15PH - 0623

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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
14 June 2001 (14.06.2001)

PCT

(10) International Publication Number
WO 01/42467 A2

(51) International Patent Classification[7]: C12N 15/12, C07K 14/47, 16/30, G01N 33/68, C12Q 1/68, A61K 31/7088 // A61P 35/00

(21) International Application Number: PCT/US00/33312

(22) International Filing Date: 8 December 2000 (08.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/169,681	8 December 1999 (08.12.1999)	US
60/171,350	21 December 1999 (21.12.1999)	US
60/189,315	14 March 2000 (14.03.2000)	US
60/203,791	12 May 2000 (12.05.2000)	US
60/210,600	9 June 2000 (09.06.2000)	US
60/220,114	21 July 2000 (21.07.2000)	US

(71) Applicant: MILLENNIUM PREDICTIVE MEDICINE, INC. [US/US]; One Kendall Square Bldg. 700, Cambridge, MA 02139 (US).

(72) Inventors: SCHLEGEL, Robert; 211 Melrose Street, Auburndale, MA 02466 (US). DEEDS, James; 39 Charnwood Road, #1, Somerville, MA 02144 (US). BERGER, Allison; 1105 Massachusetts Avenue, #8A, Cambridge, MA 02138 (US). ZHAO, Xumei; 6 Wildwood Lane, Burlington, MA 01803 (US).

(74) Agents: SMITH, DeAnn, F. et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/42467 A2

(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

(57) Abstract: The invention relates to compositions, kits, and methods for detecting, characterizing, preventing, and treating human cervical cancers. A variety of novel markers are provided, wherein changes in the levels of expression of one or more of the markers is correlated with the presence of cervical cancer.

NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

RELATED APPLICATIONS

The present application claims priority to U.S. provisional application serial no. 60/169,681, filed on December 8, 1999, U.S. provisional application serial no. 60/171,350, filed on December 21, 1999, U.S. provisional application serial no. 60/189,315, filed on March 14, 2000, U.S. provisional application serial no. 60/203,791, filed on May 12, 2000, and U.S. provisional application serial no. 60/210,600, filed on June 9, 2000, all of which are expressly incorporated by reference.

FIELD OF THE INVENTION

The field of the invention is cervical cancer, including diagnosis, characterization, management, and therapy of cervical cancer.

BACKGROUND OF THE INVENTION

The increased number of cancer cases reported in the United States, and, indeed, around the world, is a major concern. Currently there are only a handful of treatments available for specific types of cancer, and these provide no absolute guarantee of success. In order to be most effective, these treatments require not only an early detection of the malignancy, but a reliable assessment of the severity of the malignancy.

Cancer of the cervix is one of the most common malignancies in women and remains a significant public health problem throughout the world. In the United States alone, invasive cervical cancer accounts for approximately 19% of all gynecological cancers. In 1996, it is estimated that there will be 14,700 newly diagnosed cases and 4900 deaths attributed to this disease (American Cancer Society, Cancer Facts & Figures 1996, Atlanta, Ga.: American Cancer Society, 1996). In many developing countries, where mass screening programs are not widely available, the clinical problem is more serious. Worldwide, the number of new cases is estimated to be 471,000 with a four-year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer* In: "Human Papillomavirus", New York, Oxford Press, pp 9-39; National Institutes of

Health, Consensus Development Conference Statement on Cervical Cancer, Apr.1-3, 1996).

The precursor to cervical cancer is dysplasia, also known in the art as cervical intraepithelial neoplasia (CIN) or squamous intraepithelial lesions (SIL). While it is not understood how normal cells become transformed, the concept of a continuous spectrum of histopathological change from normal, stratified epithelium through CIN to invasive cancer has been widely accepted for many years. A large body of epidemiological and molecular biological evidence has established human papillomavirus (HPV) infection as a causative factor in cervical cancer. HPV is found in 85% or more of squamous cell invasive lesions, which represent the most common histologic type seen in cervical carcinoma. Additional cofactors have also been identified, including oncogenes that have been activated by point mutations and chromosomal translocations or deletions.

In light of this, cervical cancer remains a highly preventable form of cancer when pre-invasive lesions are detected early. Cytological examination of Papanicolaou-stained cervical smears (also referred to as Pap smears) is currently the principle method for detecting cervical cancer. Not surprisingly, the effectiveness of Pap smear screening varies depending not only upon the quality of the sample being used, but also upon subjective parameters that are inherent to the analysis. In addition, despite the historical success of the test, concerns have arisen regarding its ability to reliably predict the behavior of some pre-invasive lesions (Ostor *et al.*, 1993, *Int. J. Gynecol. Pathol.* 12: 186-192; and Genest *et al.*, 1993, *Human Pathol.* 24: 730-736).

It would be therefore be desirable to provide specific methods and reagents for the diagnosis, staging, prognosis, monitoring, and treatment of diseases associated with cervical cancer, or to indicate a predisposition to such for preventative measures.

SUMMARY OF THE INVENTION

The invention relates to novel genes associated with cervical cancer as well as methods of assessing whether a patient is afflicted with cervical cancer. "Cervical cancer " as used herein includes pre-malignant conditions, *e.g.*, CIN and SIL. The methods of the present invention comprise the step of comparing the level of expression of a novel marker in a patient sample, wherein the marker is listed within Tables 1-4, and the normal level of expression of the marker in a control, *e.g.*, a sample from a

patient without cervical cancer. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer or has a pre-malignant condition (*e.g.*, CIN and/or SIL).

In one method, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%. Also preferred are embodiments of the method wherein the marker is differentially-expressed by at least two-fold in at least about 20% of any of the following conditions: stage 0 cervical cancer patients, stage I cervical cancer patients, stage II cervical cancer patients, stage III cervical cancer patients, stage IV cervical cancer patients, grade I cervical cancer patients, grade II cervical cancer patients, grade III cervical cancer patients, squamous cell (epidermoid) cervical cancer patients, cervical adenocarcinoma patients, cervical adenosquamous carcinoma patients, small-cell cervical carcinoma patients, malignant cervical cancer patients, patients with primary carcinomas of the cervix, patients with primary malignant lymphomas of the cervix and patients with secondary malignant lymphomas of the cervix, and all other types of cancers, malignancies and transformations associated with the cervix.

In one embodiment of the methods of the present invention, the sample comprises cells obtained from the patient. The cells may be found in a cervical smear collected, for example, by a cervical brush. In another embodiment, the patient sample is a cervical-associated body fluid. Such fluids include, for example, blood fluids, lymph, ascitic fluids, gynecological fluids, urine, and fluids collected by peritoneal rinsing.

In accordance with the methods of the present invention, the presence and/or level of expression of the marker in a sample can be assessed, for example, by detecting the presence in the sample of :

- a protein corresponding to the marker or a fragment of the protein (*e.g.* using a reagent, such as an antibody, an antibody derivative, or an antibody fragment, which binds specifically with the protein or a fragment of the protein)
- a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by a protein corresponding to the marker

- a transcribed polynucleotide (*e.g.* an mRNA or a cDNA), or fragment thereof, having at least a portion with which the marker is substantially homologous (*e.g.* by contacting a mixture of transcribed polynucleotides obtained from the sample with a substrate having one or more of the markers listed within Tables 1-4 fixed thereto at selected positions)
- a transcribed polynucleotide or fragment thereof, wherein the polynucleotide anneals with the marker under stringent hybridization conditions.

The methods of the present invention are particularly useful for identifying patients with a pre-malignant condition such as CIN and/or SIL. The methods are also useful for further diagnosing patients having an identified cervical mass or symptoms associated with cervical cancer. The methods of the present invention can further be of particular use with patients having an enhanced risk of developing cervical cancer (*e.g.*, patients having a familial history of cervical cancer and patients identified as having a mutant oncogene). The methods of the present invention may further be of particular use in monitoring the efficacy of treatment of a cervical cancer patient (*e.g.* the efficacy of chemotherapy).

The methods of the present invention may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of markers. According to a method involving a plurality of markers, the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-4 is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer. A significantly enhanced level of expression in the sample of one or more of the markers listed in Tables 1-4, or some combination thereof, relative to that marker's corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. The markers of Tables 1-4 may also be used in combination with known cervical cancer markers in the methods of the present invention.

In a preferred method of assessing whether a patient is afflicted with cervical cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

a) the level of expression of a marker in a patient sample, wherein at least one marker is selected from the markers of Tables 1-4, and

b) the normal level of expression of the marker in a control non-cervical cancer sample.

A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer.

The invention further relates to a method of assessing the efficacy of a therapy for inhibiting cervical cancer in a patient. This method comprises comparing:

a) expression of a marker in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, wherein the marker is selected from the group consisting of the markers listed within Tables 1-4, and

b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting cervical cancer in the patient.

It will be appreciated that in this method the "therapy" may be any therapy for treating cervical cancer including, but not limited to, chemotherapy, radiation therapy and surgical removal of tissue, *e.g.*, a cervical tumor. Thus, the methods of the invention may be used to evaluate a patient before, during and after therapy, for example, to evaluate the reduction in tumor burden.

The present invention therefore further comprises a method for monitoring the progression of cervical cancer in a patient, the method comprising:

a) detecting in a patient sample at a first time point, the expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4;

b) repeating step a) at a subsequent time point in time; and

c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer in the patient.

The invention also includes a method of selecting a composition for inhibiting cervical cancer in a patient. This method comprises the steps of:

a) obtaining a sample comprising cancer cells from the patient;

b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;

c) comparing expression of a marker listed within Tables 1-4 in each of the aliquots; and

d) selecting one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

In addition, the invention includes a method of inhibiting cervical cancer in a patient. This method comprises the steps of:

a) obtaining a sample comprising cancer cells from the patient;

b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;

c) comparing expression of a marker listed within Tables 1-4 in each of the aliquots; and

d) administering to the patient at least one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

The invention also includes a kit for assessing whether a patient is afflicted with cervical cancer. This kit comprises reagents for assessing expression of a marker listed within Tables 1-4.

In another aspect, the invention relates to a kit for assessing the suitability of each of a plurality of compounds for inhibiting a cervical cancer in a patient. The kit comprises a reagent for assessing expression of a marker listed within Tables 1-4, and may also comprise a plurality of compounds.

In another aspect, the invention relates to a kit for assessing the presence of cervical cancer cells. This kit comprises an antibody, wherein the antibody binds specifically with a protein corresponding to a marker listed within Tables 1-4. The kit may also comprise a plurality of antibodies, wherein the plurality binds specifically with a protein corresponding to a different marker listed within Tables 1-4.

The invention also includes a kit for assessing the presence of cervical cancer cells, wherein the kit comprises a nucleic acid probe. The probe binds specifically with a transcribed polynucleotide corresponding to a marker listed within Tables 1-4. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a transcribed polynucleotide corresponding to a different marker listed within Tables 1-4.

The invention further relates to a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer. The method comprises isolating a protein or protein fragment corresponding to a marker listed within Tables 1-4, immunizing a mammal using the isolated protein or protein fragment, isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for production of an antibody which specifically binds with the protein or protein fragment to isolate the hybridoma. The invention also includes an antibody produced by this method.

The invention further includes a method of assessing the cervical carcinogenic potential of a test compound. This method comprises the steps of:

a) maintaining separate aliquots of cervical cells in the presence and absence of the test compound; and

b) comparing expression of a marker in each of the aliquots.

The marker is selected from those listed within Tables 1-4. A significantly enhanced level of expression of the marker in the aliquot maintained in the presence of (or exposed to) the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses cervical carcinogenic potential.

Additionally, the invention includes a kit for assessing the cervical carcinogenic potential of a test compound. The kit comprises cervical cells and a reagent for assessing expression of a marker in each of the aliquots. The marker is selected from those listed within Tables 1-4.

The invention further relates to a method of treating a patient afflicted with cervical cancer. This method comprises providing to cells of the patient an antisense oligonucleotide complementary to a polynucleotide corresponding to a marker listed within Tables 1-4.

The invention includes a method of inhibiting cervical cancer in a patient at risk for developing cervical cancer. This method comprises inhibiting expression or overexpression of a gene corresponding to a marker listed within Tables 1-4.

It will be appreciated that the methods and kits of the present invention may also include known cancer markers including known cervical cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than cervical cancer.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to newly discovered genes associated with the cancerous state of cervical cells. It has been discovered that the level of expression of these individual genes, also referred to as markers, and combinations of these genes correlates with the presence of cervical cancer or a pre-malignant condition in a patient. Methods are provided for detecting the presence of cervical cancer in a sample, the absence of cervical cancer in a sample, the stage of cervical cancer, and with other characteristics of cervical cancer that are relevant to prevention, diagnosis, characterization and therapy of cervical cancer in a patient. As used herein, "cervical cancer" includes pre-malignant conditions including CIN and SIL.

Definitions

As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

A "marker" is a naturally-occurring polymer corresponding to at least one of the novel nucleic acids listed within Tables 1-4. For example, markers include, without limitation, sense and anti-sense strands of genomic DNA (*i.e.* including any introns

occurring therein), RNA generated by transcription of genomic DNA (*i.e.* prior to splicing), RNA generated by splicing of RNA transcribed from genomic DNA, and proteins generated by translation of spliced RNA (*i.e.* including proteins both before and after cleavage of normally cleaved regions such as transmembrane signal sequences). As used herein, "marker" may also include a cDNA made by reverse transcription of an RNA generated by transcription of genomic DNA (including spliced RNA).

As used herein a "polynucleotide corresponds to" another (a first) polynucleotide if it is related to the first polynucleotide by any of the following relationships: The second polynucleotide comprises the first polynucleotide and the second polynucleotide encodes a gene product; 2) The second polynucleotide is 5' or 3' to the first polynucleotide in cDNA, RNA, genomic DNA, or fragment of any of these polynucleotides. For example, a second polynucleotide may be a fragment of a gene that includes the first and second polynucleotides. The first and second polynucleotides are related in that they are components of the gene coding for a gene product, such as a protein or antibody. However, it is not necessary that the second polynucleotide comprises or overlaps with the first polynucleotide to be encompassed within the definition of "corresponding to" as used herein. For example, the first polynucleotide may be a fragment of a 3' untranslated region of the second polynucleotide. The first and second polynucleotide may be fragments of a gene coding for a gene product. The second polynucleotide may be an exon of the gene while the first polynucleotide may be an intron of the gene; 3) The second polynucleotide is the complement of the first polynucleotide.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example a marker of the invention. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic monomers.

A "cervical-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through cervical cells or into which cells or proteins shed from cervical cells are capable of passing. Exemplary cervical-associated body fluids

include blood fluids, lymph, ascites, gynecological fluids, cystic fluid, urine, and fluids collected by peritoneal rinsing.

The "normal" level of expression of a marker is the level of expression of the marker in cervical cells of a patient, *e.g.* a human, not afflicted with cervical cancer.

"Over-expression" and "under-expression" of a marker refer to expression of the marker of a patient at a greater or lesser level, respectively, than normal level of expression of the marker (*e.g.* at least two-fold greater or lesser level).

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue-specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

A "transcribed polynucleotide" is a polynucleotide (*e.g.* an RNA, a cDNA, or an analog of one of an RNA or cDNA) which is complementary to or homologous with all or a portion of a mature RNA made by transcription of a genomic DNA corresponding to a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the transcript.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A marker is "fixed" to a substrate if it is covalently or non-covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.* standard saline citrate, pH 7.4) without a substantial fraction of the marker dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.* encodes a natural protein).

Expression of a marker in a patient is "significantly" higher than the normal level of expression of a marker if the level of expression of the marker is greater than the normal level by an amount greater than the standard error of the assay employed to assess expression, and preferably at least twice, and more preferably three, four, five or ten times that amount. Alternately, expression of the marker in the patient can be considered "significantly" higher or lower than the normal level of expression if the level of expression is at least about two, and preferably at least about three, four, or five times, higher or lower, respectively, than the normal level of expression of the marker.

Cervical cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, cervical cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (*e.g.* a package or container) comprising at least one reagent, *e.g.* a probe, for specifically detecting a marker of the invention, the manufacture being promoted, distributed, or sold as a unit for performing the methods of the present invention.

<u>Description</u>

The present invention is based, in part, on identification of novel markers which are expressed at a higher level in cervical cancer cells than they are in normal (*i.e.* non-cancerous) cervical cells. The markers of the invention correspond to nucleic acid and polypeptide molecules which can be detected in one or both of normal and cancerous cervical cells. The presence, absence, or level of expression of one or more of these markers in cervical cells is herein correlated with the cancerous state of the tissue. The invention thus includes compositions, kits, and methods for assessing the cancerous state

of cervical cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells).

The compositions, kits, and methods of the invention have the following uses, among others:

1) assessing whether a patient is afflicted with cervical cancer, including assessing whether the patient has a pre-malignant condition, *e.g.*, CIN and/or SIL;

2) assessing the stage of cervical cancer in a human patient;

3) assessing the grade of cervical cancer in a patient;

4) assessing the benign or malignant nature of cervical cancer in a patient;

5) assessing the histological type of neoplasm (*e.g.* squamous cell, small cell, etc.) associated with cervical cancer in a patient;

6) making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer;

7) assessing the presence of cervical cancer cells;

8) assessing the efficacy of one or more test compounds for inhibiting cervical cancer in a patient;

9) assessing the efficacy of a therapy for inhibiting cervical cancer in a patient;

10) monitoring the progression of cervical cancer in a patient;

11) selecting a composition or therapy for inhibiting cervical cancer in a patient;

12) treating a patient afflicted with cervical cancer;

13) inhibiting cervical cancer in a patient;

14) assessing the cervical carcinogenic potential of a test compound; and

15) inhibiting cervical cancer in a patient at risk for developing cervical cancer.

The invention thus includes a method of assessing whether a patient is afflicted with cervical cancer which includes assessing whether the patient has a pre-malignant condition. This method comprises comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a non-

cervical cancer sample. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer. The marker is selected from the group consisting of the markers listed within Tables 1-4.

The polynucleotides set forth in Tables 1-4 represent previously unidentified nucleotide sequences. These nucleotide sequences were identified through subtracted library experiments described herein. Also provided by this invention are polynucleotides that correspond to the polynucleotides of Tables 1-4. In one embodiment, these polynucleotides are obtained by identification of a larger fragment or full-length coding sequence of these polynucleotides. Gene delivery vehicles, host cells, compositions and databases (all describe herein) containing these polynucleotides are also provided by this invention.

The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but which produce the same phenotypic effect, such as an allelic variant. These altered, but phenotypically equivalent polynucleotides are referred to as "equivalent nucleic acids." This invention also encompasses polynucleotides characterized by changes in non-coding regions that do not alter the polypeptide produced therefrom when compared to the polynucleotide herein. This invention further encompasses polynucleotides, which hybridize to the polynucleotides of the subject invention under conditions of moderate or high stringency. Alternatively, the polynucleotides are at least 85%, or at least 90%, or more preferably, greater or equal to 95% identical as determined by a sequence alignment program when run under default parameters.

Any marker or combination of markers listed within Tables 1-4, as well as any known markers in combination with the markers set forth within Tables 1-4, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in cervical cancer cells and the level of expression of the same marker in normal cervical cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method,

and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater.

It will be appreciated that patient samples containing cervical cells may be used in the methods of the present invention. In these embodiments, the level of expression of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker in a cervical cell sample, *e.g.*, cervical smear, obtained from a patient. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.* storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the sample. Likewise cervical smears may also be subjected to post-collection preparative and storage techniques, *e.g.*, fixation.

It will also be appreciated that certain markers correspond to proteins or fragments thereof, which are secreted from cervical cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the protein or fragment thereof, corresponding to each of these markers can be detected in a cervical-associated body fluid sample. In addition, preferred *in vivo* techniques for detection of a protein or fragment thereof, corresponding to a marker of the invention include introducing into a subject a labeled antibody directed against the protein or fragment of the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

Although not every marker corresponding to a secreted protein is indicated as such herein, it is a simple matter for the skilled artisan to determine whether any particular marker corresponds to a secreted protein. In order to make this determination, the protein corresponding to a marker is expressed in a test cell (*e.g.* a cell of a cervical cell line), extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein corresponding to a marker of the invention. About 8 x 10^5 293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO_2, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424-54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-^{35}S™ reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO_2 atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris. The presence of the protein in the supernatant is an indication that the protein is secreted.

Examples of cervical-associated body fluids include blood fluids (*e.g.* whole blood, blood serum, blood having platelets removed therefrom, etc.), lymph, ascitic fluids, gynecological fluids (*e.g.* cervix, fallopian, and uterine secretions, menses, vaginal douching fluids, fluids used to rinse cervical cell samples, etc.), cystic fluid, urine, and fluids collected by peritoneal rinsing (*e.g.* fluids applied and collected during laparoscopy or fluids instilled into and withdrawn from the peritoneal cavity of a human patient).

Many cervical-associated body fluids can have cervical cells therein, particularly when the cervical cells are cancerous, and, more particularly, when the cervical cancer is metastasizing. Cell-containing fluids which can contain cervical cancer cells include, but are not limited to, peritoneal ascites, fluids collected by peritoneal rinsing, fluids collected by uterine rinsing, uterine fluids such as uterine exudate and menses, pleural fluid, and cervical exudates. Thus, the compositions, kits, and methods of the invention can be used to detect expression of markers corresponding to proteins or fragments thereof, having at least one portion which is displayed on the surface of cells which

express it. Although the proteins having at least one cell-surface portion are not set forth herein, it is a simple matter for the skilled artisan to determine whether the protein corresponding to any particular marker comprises a cell-surface protein. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods (*e.g.* the SIGNALP program; Nielsen *et al.*, 1997, *Protein Engineering* 10:1-6) may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker corresponding to a protein or fragment thereof, having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed molecule or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods. *In situ* hybridization (ISH) and immunohistochemistry (IHC) methods are preferred.

In another preferred embodiment, expression of a marker is assessed using an antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin}), or an antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a protein or fragment thereof, corresponding to the marker, such as the protein encoded by the open reading frame corresponding to the marker or such a protein which has undergone all or a portion of its normal post-translational modification.

In yet another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a polynucleotide comprising the marker, and fragments thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction

methods prior to hybridization with the reference polynucleotide. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker of the invention may be used to detect occurrence of a marker in a patient.

In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.* at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker of the invention. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (*e.g.* detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (*e.g.* a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of assessing marker expression is used which involves hybridization of one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it is preferable that the level of expression of the marker is significantly greater than the minimum detection limit of the method used to assess expression in at least one of normal cervical cells and cancerous cervical cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over- (or under-)expressed in cancers of various types, including specific cervical cancers, as well as other cancers such as ovarian cancer, breast cancer, etc. For example, it will be confirmed that some of the markers of the invention are over-expressed in most (*i.e.* 50% or more) or substantially all (*i.e.* 80% or more) of cervical cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with cervical cancer of various stages (*i.e.* stage 0, I, II, III, and IV cervical cancers, as well as subclassifications IA1, IA2, IB, IB1, IB2, IIA, IIB, IIIA, IIIB, IVA, and IVB, using the FIGO Stage Grouping system for primary carcinoma of the cervix (see Gynecologic Oncology, 1991, 41:199 and Cancer, 1992, 69:482)), of various

histologic subtypes (*e.g.* squamous cell carcinomas and squamous cell carcinoma variants such as verrucous carcinoma, lymphoepithelioma-like carcinoma, papillary squamous neoplasm and spindle cell squamous cell carcinoma (see Cervical Cancer and Preinvasive Neoplasia, 1996, pp. 90-91), serous, mucinous, endometroid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal {Müllerian} mixed tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant cervical tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue}). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in patients.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%, and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with a cervical cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a positive predictive value (PPV) of greater than about 10% is obtained for the general population (more preferably coupled with an assay specificity greater than 99.5%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly enhanced level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. When a plurality of markers is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-cervical origin in a patient sample), it is preferable that the marker of the invention used therein be a marker which has a restricted tissue distribution, *e.g.*, normally not expressed in non-cervical tissue.

Only a small number of markers are known to be associated with cervical cancers (*e.g.* bcl-2, 15A8 antigen, cdc6, Mcm5, and EGFR). These markers are not, of course, included among the markers of the invention, although they may be used together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

Known oncogenes and tumor suppressor genes include, for example, *abl*, *abr*, *akt2*, *apc*, *bcl2α*, *bcl2β*, *bcl3*, *bcr*, *brca1*, *brca2*, *cbl*, *ccnd1*, *cdc42*, *cdk4*, *crk- II*, *csf1r/fms*, *dbl*, *dcc*, *dpc4/smad4*, *e-cad*, *e2f1/rbap*, *egfr/erbb-1*, *elk1*, *elk3*, *eph*, *erg*, *ets1*, *ets2*, *fer*, *fgr/src2*, *fli1/ergb2*, *fos*, *fps/fes*, *fra1*, *fra2*, *fyn*, *hck*, *hek*, *her2/erbb- 2/neu*, *her3/erbb-3*, *her4/erbb-4*, *hras1*, *hst2*, *hstf1*, *igfbp2*, *ink4a*, *ink4b*, *int2/fgf3*, *jun*, *junb*, *jund*, *kip2*, *kit*, *kras2a*, *kras2b*, *lck*, *lyn*, *mas*, *max*, *mcc*, *mdm2*, *met*, *mlh1*, *mmp10*, *mos*, *msh2*, *msh3*, *msh6*, *myb*, *myba*, *mybb*, *myc*, *mycl1*, *mycn*, *nf1*, *nf2*, *nme2*, *nras*, *p53*,

pdgfb, phb, pim1, pms1, pms2, ptc, pten, rafl, rap1a, rb1, rel, ret, ros1, ski, src1, tal1, tgfbr2, tgfb3, tgfbr3, thra1, thrb, tiam1, timp3, tjp1, tp53, trk, vav, vhl, vil2, waf1, wnt1, wnt2, wt1, and *yes1* (Hesketh, 1997, In: *The Oncogene and Tumour Suppressor Gene Facts Book*, 2nd Ed., Academic Press; Fishel *et al.*, 1994, *Science* 266:1403-1405).

Known growth factors include platelet-derived growth factor alpha, platelet-derived growth factor beta (simian sarcoma viral {v-sis} oncogene homolog), thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor), erythropoietin, B cell growth factor, macrophage stimulating factor 1 (hepatocyte growth factor-like protein), hepatocyte growth factor (hepapoietin A), insulin-like growth factor 1 (somatomedia C), hepatoma-derived growth factor, amphiregulin (schwannoma-derived growth factor), bone morphogenetic proteins 1, 2, 3, 3 beta, and 4, bone morphogenetic protein 7 (osteogenic protein 1), bone morphogenetic protein 8 (osteogenic protein 2), connective tissue growth factor, connective tissue activation peptide 3, epidermal growth factor (EGF), teratocarcinoma-derived growth factor 1, endothelin, endothelin 2, endothelin 3, stromal cell-derived factor 1, vascular endothelial growth factor (VEGF), VEGF-B, VEGF-C, placental growth factor (vascular endothelial growth factor-related protein), transforming growth factor alpha, transforming growth factor beta 1 and its precursors, transforming growth factor beta 2 and its precursors, fibroblast growth factor 1 (acidic), fibroblast growth factor 2 (basic), fibroblast growth factor 5 and its precursors, fibroblast growth factor 6 and its precursors, fibroblast growth factor 7 (keratinocyte growth factor), fibroblast growth factor 8 (androgen-induced), fibroblast growth factor 9 (glia-activating factor), pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1), brain-derived neurotrophic factor, and recombinant glial growth factor 2.

Known proteases include interleukin-1 beta convertase and its precursors, Mch6 and its precursors, Mch2 isoform alpha, Mch4, Cpp32 isoform alpha, Lice2 gamma cysteine protease, Ich-1S, Ich-1L, Ich-2 and its precursors, TY protease, matrix metalloproteinase 1 (interstitial collagenase), matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase), matrix metalloproteinase 7 (matrilysin), matrix metalloproteinase 8 (neutrophil collagenase), matrix metalloproteinase 12 (macrophage elastase), matrix metalloproteinase 13 (collagenase 3), metallopeptidase 1, cysteine-rich metalloprotease (disintegrin) and its precursors, subtilisin-like protease Pc8

and its precursors, chymotrypsin, snake venom-like protease, cathepsin l, cathepsin D (lysosomal aspartyl protease), stromelysin, aminopeptidase N, plasminogen, tissue plasminogen activator, plasminogen activator inhibitor type II, and urokinase-type plasminogen activator.

Known protein kinases include DAP kinase, serine/threonine protein kinases NIK, PK428, Krs-2, SAK, and EMK, interferon-inducible double stranded RNA dependent protein kinase, FAST kinase, AIM1, IPL1-like midbody-associated protein kinase-1, NIMA-like protein kinase 1 (NLK1), the cyclin-dependent kinases (cdk1-10), checkpoint kinase Chk1, Nek3 protein kinase, BMK1 beta kinase, Clk1, Clk2, Clk3, extracellular signal-regulated kinases 1, 3, and 6, cdc28 protein kinase 1, cdc28 protein kinase 2, pLK, Myt1, c-Jun N-terminal kinase 2, Cam kinase 1, the MAP kinases, insulin-stimulated protein kinase 1, beta-adrenergic receptor kinase 2, ribosomal protein S6 kinase, kinase suppressor of ras-1 (KSR1), putative serine/threonine protein kinase Prk, PkB kinase, cAMP-dependent protein kinase, cGMP-dependent protein kinase, type II cGMP-dependent protein kinase, protein kinases Dyrk2, Dyrk3, and Dyrk4, Rho-associated coiled-coil containing protein kinase p160ROCK, protein tyrosine kinase t-Ror1, Ste20-related kinases, cell adhesion kinase beta, protein kinase 3, stress-activated protein kinase 4, protein kinase Zpk, serine kinase hPAK65, dual specificity mitogen-activated protein kinases 1 and 2, casein kinase I gamma 2, p21-activated protein kinase Pak1, lipid-activated protein kinase PRK2, focal adhesion kinase, dual-specificity tyrosine-phosphorylation regulated kinase, myosin light chain kinase, serine kinases SRPK2, TESK1, and VRK2, B lymphocyte serine/threonine protein kinase, stress-activated protein kinases JNK1 and JNK2, phosphorylase kinase, protein tyrosine kinase Tec, Jak2 kinase, protein kinase Ndr, MEK kinase 3, SHB adaptor protein (a Src homology 2 protein), agammaglobulinaemia protein-tyrosine kinase (Atk), protein kinase ATR, guanylate kinase 1, thrombopoeitin receptor and its precursors, DAG kinase epsilon, and kinases encoded by oncogenes or viral oncogenes such as v-fgr (Gardner-Rasheed), v-abl (Abelson murine leukemia viral oncogene homolog 1), v-arg (Abelson murine leukemia viral oncogene homolog, Abelson-related gene), v-fes and v-fps (feline sarcoma viral oncogene and Fujinami avian sarcoma viral oncogene homologs), proto-oncogene c-*cot*, oncogene *pim*-1, and oncogene *mas1*.

It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing cervical cancer and their medical advisors. Patients recognized as having an enhanced risk of developing cervical cancer include, for example, patients having a familial history of cervical cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients determined through any other established medical criteria to be at risk for cancer or other malignancy.

The level of expression of a marker in normal (*i.e.* non-cancerous) human cervical tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of cervical cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the cervical cells which is suspected of being cancerous. For example, the normal level of expression of a marker may be assessed using a non-affected portion of the cervix and this normal level of expression may be compared with the level of expression of the same marker in an affected portion of the cervix. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cervical cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the presence of cervical cancer cells in a sample (*e.g.* an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a parafinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the

sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of cervical cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a nucleic acid or polypeptide corresponding to a marker of the invention. Suitable reagents for binding with a polypeptide corresponding to a marker of the invention include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal cervical cells, a sample of cervical cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer. In this method, a protein corresponding to a marker of the invention is isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the vertebrate exhibits a robust immune response to the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened

using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the protein or protein fragment. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test compound for inhibiting cervical cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of cervical cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of cervical cells, it is likewise recognized that changes in the levels of expression of other of the markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit cervical cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous cervical cells).

This method thus comprises comparing expression of a marker in a first cervical cell sample and maintained in the presence of the test compound and expression of the marker in a second cervical cell sample and maintained in the absence of the test compound. A significant decrease in the level of expression of a marker listed within Tables 1-4 is an indication that the test compound inhibits cervical cancer. The cervical cell samples may, for example, be aliquots of a single sample of normal cervical cells obtained from a patient, pooled samples of normal cervical cells obtained from a patient, cells of a normal cervical cell line, aliquots of a single sample of cervical cancer cells obtained from a patient, pooled samples of cervical cancer cells obtained from a patient, cells of a cervical cancer cell line, or the like. In one embodiment, the samples are cervical cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various cervical cancers are tested in order to identify the compound which is likely to best inhibit the cervical cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting cervical cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significant decrease in the level of

expression of a marker listed within Tables 1-4, or blocks induction of a marker listed within Tables 1-4, then the therapy is efficacious for inhibiting cervical cancer. As above, if samples from a selected patient are used in this method, then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be efficacious for inhibiting cervical cancer in the patient.

As described herein, cervical cancer in patients is associated with an increase in the level of expression of one or more markers listed within Tables 1-4. While, as discussed above, some of these changes in expression level result from occurrence of the cervical cancer, others of these changes induce, maintain, and promote the cancerous state of cervical cancer cells. Thus, cervical cancer characterized by an increase in the level of expression of one or more markers listed within Tables 1-4 can be controlled or suppressed by inhibiting expression of those markers.

Expression of a marker listed within Tables 1-4 can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be provided to the cervical cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein corresponding to the marker(s). Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of the marker(s). The compound so identified can be provided to the patient in order to inhibit expression of the marker(s) in the cervical cancer cells of the patient.

As described above, the cancerous state of human cervical cells is correlated with changes in the levels of expression of the markers of the invention. Thus, compounds which induce increased expression of one or more of the markers listed within Tables 1-4 can induce cervical cell carcinogenesis. The invention thus includes a method for assessing the human cervical cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human cervical cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significant increase in the level of expression of a

marker listed within Tables 1-4 in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human cervical cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to novel isolated nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention or a portion of such a polypeptide. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention, and fragments of such nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or mutation of nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA

of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid encoding a protein corresponding to a marker listed in Tables 1-4, can be isolated using standard molecular biology techniques and the sequence information described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual, 2nd ed.,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A process for identifying a larger fragment or the full-length coding sequence of a marker of the present invention is thus also provided. Any conventional recombinant DNA techniques applicable for isolating polynucleotides may be employed. One such method involves the 5'-RACE-PCR technique, in which the poly-A mRNA that contains the coding sequence of particular interest is first reverse transcribed with a 3'-primer comprising a sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer with a known sequence, which preferably contains a convenient cloning restriction site attached at the 5'end. The tagged cDNA is then amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, *e.g.*, BRL Life Technologies Inc., Clotech) according to the manufacturer's instructions.

Isolating the complete coding sequence of a gene can also be carried out in a hybridization assay using a suitable probe. The probe preferably comprises at least 10 nucleotides, and more preferably exhibits sequence homology to the polynucleotides of the markers of the present invention. Other high throughput screens for cDNAs, such as those involving gene chip technology, can also be employed in obtaining the complete cDNA sequence.

In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a database called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone. Software programs exist (TIGR assembler and TIGEM EST assembly machine and contig assembly program (see Huang, X . , 1996, *Genomes* 33:21-23)) that allow for assembling ESTs into contiguous sequences from any organism.

Alternatively, mRNA from a sample preparation is used to construct cDNA library in the ZAP Express vector following the procedure described in Velculescu *et al.*, 1997, *Science* 270:484. The ZAP Express cDNA synthesis kit (Stratagene) is used accordingly to the manufacturer's protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert *et al.*, 1988, *Mol. Cell. Bio.* 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes except that the hybridization temperature is reduced to a room temperature. Washes are performed in 6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with ^{32}P-ATP trough use of T4 polynucleotide kinase.

A partial cDNA (3' fragment) can be isolated by 3' directed PCR reaction. This procedure is a modification of the protocol described in Polyak *et al.*, 1997, *Nature* 389:300. Briefly, the procedure uses SAGE tags in PCR reaction such that the resultant PCR product contains the SAGE tag of interest as well as additional cDNA, the length of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)-3', contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads.

Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

cDNA constructed utilizing this or similar modified oligo-dT primer is then processed as described in U.S. Patent No. 5,695,937 up until adapter ligation where only one adapter is ligated to the cDNA pool. After adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Gene trapper technology can also be used. The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithsburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the ^{32}P-labeled oligonucleotide, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a nucleic acid corresponding to a marker of the invention or to the nucleotide sequence of a nucleic acid encoding a protein which corresponds to a marker of the invention. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker of the invention or which encodes a polypeptide corresponding to a marker of the invention. Such nucleic acids can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a protein which corresponds to a marker of the invention, and thus encode the same protein.

In addition to the nucleotide sequences described in the Tables, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 0.1-0.5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a nucleic acid corresponding to a marker of the invention or to a nucleic acid encoding a protein corresponding to a marker of the invention. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 75% (80%, 85%, preferably 90%) identical to each other typically remain hybridized to each other. Such stringent

conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions for annealing two single-stranded DNA each of which is at least about 100 bases in length and/or for annealing a single-stranded DNA and a single-stranded RNA each of which is at least about 100 bases in length, are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C. Further preferred hybridization conditions are taught in Lockhart, *et al.*, Nature Biotechnology, Volume 14, 1996 August:1675-1680; Breslauer, *et al.*, Proc. Natl. Acad. Sci. USA, Volume 83, 1986 June: 3746-3750; Van Ness, *et al.*, Nucleic Acids Research, Volume 19, No. 19, 1991 September: 5143-5151; McGraw, *et al.*, BioTechniques, Volume 8, No. 6 1990: 674-678; and Milner, *et al.*, Nature Biotechnology, Volume 15, 1997 June: 537-541, all expressly incorporated by reference.

In addition to naturally-occurring allelic variants of a nucleic acid molecule of the invention that can exist in the population, the skilled artisan will further appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino acid residues that are conserved among the homologs of various species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a polypeptide of the invention that contain changes in amino acid residues that are not essential for activity. Such polypeptides differ in amino acid sequence from the naturally-occurring proteins which correspond to the markers of the invention, yet retain biological activity. In one embodiment, such a protein has an amino acid sequence that

is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of one of the proteins which correspond to the markers of the invention.

An isolated nucleic acid molecule encoding a variant protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of nucleic acids of the invention, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule corresponding to a marker of the invention or complementary to an mRNA sequence corresponding to a marker of the invention. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-

coding region of the coding strand of a nucleotide sequence encoding a polypeptide of the invention. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polypeptide corresponding to a selected marker of the

invention to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into a cervix-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α-units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a polypeptide corresponding to a marker of the invention can be designed based upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS

RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742). Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a polypeptide of the invention can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the polypeptide (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup (1996), *supra*; or as

probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNASE H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996, *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975, *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide,

hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

II. Isolated Proteins and Antibodies

One aspect of the invention pertains to novel isolated proteins which correspond to individual markers of the invention, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a polypeptide corresponding to a marker of the invention. In one embodiment, the native polypeptide corresponding to a marker can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, polypeptides corresponding to a marker of the invention are produced by recombinant DNA techniques. Alternative to recombinant expression, a polypeptide corresponding to a marker of the invention can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material

includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a polypeptide corresponding to a marker of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the protein corresponding to the marker (*e.g.*, the amino acid sequence listed in the GenBank and IMAGE Consortium database records described herein), which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

Preferred polypeptides are encoded by the nucleotide sequences in Tables 1-4. Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the protein of the corresponding naturally-occurring protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then

compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions (*e.g.*, overlapping positions) x100). In one embodiment the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for

comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins corresponding to a marker of the invention. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a polypeptide corresponding to a marker of the invention operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the polypeptide corresponding to the marker). Within the fusion protein, the term "operably linked" is intended to indicate that the polypeptide of the invention and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the polypeptide of the invention.

One useful fusion protein is a GST fusion protein in which a polypeptide corresponding to a marker of the invention is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a polypeptide corresponding to a marker of the invention can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook *et al.*, *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a polypeptide corresponding to a marker of the invention is fused to sequences derived from a member of the immunoglobulin protein family.

The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a polypeptide of the invention. Inhibition of ligand/receptor interaction can be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a polypeptide of the invention in a subject, to purify ligands and in screening assays to identify molecules which inhibit the interaction of receptors with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, *e.g.*, Ausubel *et al.*, *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of the secreted protein or other proteins of interest. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to the described polypeptides having a signal sequence, as well as to polypeptides from which the signal sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a protein which is ordinarily not

secreted or is otherwise difficult to isolate. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the polypeptides corresponding to individual markers of the invention. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

Variants of a protein of the invention which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, 1983,

Tetrahedron 39:3; Itakura *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the coding sequence of a polypeptide corresponding to a marker of the invention can be used to generate a variegated population of polypeptides for screening and subsequent selection of variants. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

An isolated polypeptide corresponding to a marker of the invention, or a fragment thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polypeptide or protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues

of the amino acid sequence of one of the polypeptides of the invention, and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with a marker of the invention to which the protein corresponds. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent.

Accordingly, another aspect of the invention pertains to antibodies directed against a polypeptide of the invention. The terms "antibody" and "antibody substance" as used interchangeably herein refer to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site which specifically binds an antigen, such as a polypeptide of the invention, e.g., an epitope of a polypeptide of the invention. A molecule which specifically binds to a given polypeptide of the invention is a molecule which binds the polypeptide, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and $F(ab')_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred

polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be harvested or isolated from the subject (*e.g.*, from the blood or serum of the subject) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected or (*e.g.*, partially purified) or purified by, *e.g.*, affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, *i.e.,* one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, *e.g.*, when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B

cell hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology,* Coligan *et al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining

regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521- 3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

Antibodies of the invention may be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having cervical cancer. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*, U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent

5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

An antibody directed against a polypeptide corresponding to a marker of the invention (*e.g.*, a monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in an ovary-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

Further, an antibody (or fragment thereof) can be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy

anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*, dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp.

303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

Accordingly, in one aspect, the invention provides substantially purified antibodies or fragments thereof, and non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. In various embodiments, the substantially purified antibodies of the invention, or fragments thereof, can be human, non-human, chimeric and/or humanized antibodies.

In another aspect, the invention provides non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of: the amino acid sequence of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing

in 0.2 X SSC, 0.1% SDS at 65°C. Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies.

In still a further aspect, the invention provides monoclonal antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to an amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

The substantially purified antibodies or fragments thereof may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a polypeptide of the invention. In a particularly preferred embodiment, the substantially purified antibodies or fragments thereof, the non-human antibodies or fragments thereof, and/or the monoclonal antibodies or fragments thereof, of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of the present invention.

Any of the antibodies of the invention can be conjugated to a therapeutic moiety or to a detectable substance. Non-limiting examples of detectable substances that can be conjugated to the antibodies of the invention are an enzyme, a prosthetic group, a fluorescent material, a luminescent material, a bioluminescent material, and a radioactive material.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the invention is a pharmaceutical composition comprising an antibody of the invention and a pharmaceutically acceptable carrier. In preferred embodiments, the pharmaceutical composition contains an antibody of the invention, a therapeutic moiety, and a pharmaceutically acceptable carrier.

Still another aspect of the invention is a method of making an antibody that specifically recognizes a polypeptide of the present invention, the method comprising immunizing a mammal with a polypeptide. The polypeptide used as an immungen comprises an amino acid sequence selected from the group consisting of the amino acid sequence of the present invention, an amino acid sequence encoded by the cDNA of the nucleic acid molecules of the present invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. After immunization, a sample is collected from the mammal that contains an antibody that specifically recognizes the polypeptide. Preferably, the polypeptide is recombinantly produced using a non-human host cell. Optionally, the antibodies can be further purified from the sample using techniques well known to those of skill in the art. The method can further comprise producing a monoclonal antibody- producing cell from the cells of the mammal. Optionally, antibodies are collected from the antibody-producing cell.

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a polypeptide corresponding to a marker of the invention (or a portion of such a polypeptide). As used herein, the term "vector"

refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the

host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide corresponding to a marker of the invention in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter

mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.,* 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.,* 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.,* 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.,* 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al.*, *supra.*

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-

specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss, 1990, *Science* 249:374-379) and the α-fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny

of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*, insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a polypeptide corresponding to a marker of the invention. Accordingly, the invention further provides methods for producing a polypeptide corresponding to a marker of the invention using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the marker is produced. In another embodiment, the method further comprises isolating the marker polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a polypeptide corresponding to a marker of the invention have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a polypeptide corresponding to a marker of the invention sequences have been altered. Such animals are useful for studying the function and/or activity of the polypeptide corresponding to the marker and for identifying and/or evaluating modulators of polypeptide activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a nucleic acid encoding a polypeptide corresponding to a marker of the invention into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S.

Patent No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA encoding the transgene in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which contains at least a portion of a gene encoding a polypeptide corresponding to a marker of the invention into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (see, *e.g.*, Bradley, *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant

female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, *e.g.*, Lakso *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") corresponding to a marker of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and

agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.* 37:2678-85);

spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a marker can be accomplished, for example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (*e.g.*, marker substrates) can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the activity of a marker or a biologically active portion thereof. In all likelihood, the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of the marker to identify its natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent No. 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al* ,1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker or downstream elements of a marker-mediated signaling pathway. Alternatively, such marker binding partners may also be found to be inhibitors of the marker.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.*, affect either positively or negatively) interactions between a marker and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an cervical cancer marker identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker and its binding partner involves preparing a reaction mixture containing the marker and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the marker and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker and its binding partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance interaction of the marker and its binding partner.

The assay for compounds that interfere with the interaction of the marker with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that

interfere with the interaction between the markers and the binding partners (*e.g.*, by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test compounds that disrupt preformed complexes, *e.g.*, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (*e.g.*, physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker or a marker binding partner can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated

marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the protein-immobilized surfaces can be prepared in advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (*e.g.*, by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and

densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993 Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, *e.g.*, Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, nondenaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, all proteins binding to an antibody specific to one of the binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be compared, thus offering information about the ability of the compound to modulate interactions between the marker and its binding partner.

Also within the scope of the present invention are methods for direct detection of interactions between the marker and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer may be utilized (see, *e.g.*, Lakowicz *et al*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al*, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.*, marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.*, marker or test compound), which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in the preformed complex will result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of mRNA or protein, corresponding to a marker in the cell, is determined. The level of expression of mRNA or protein in the presence of the candidate compound is compared to the level of expression of mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA

or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA or protein.

In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, an marker modulating agent, an antisense marker nucleic acid molecule, an marker-specific antibody, or an marker-binding partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of

subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic

water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium, and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically

acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the cervical epithelium). A method for lipidation of antibodies is described by Cruikshank *et al.* (1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193.

The nucleic acid molecules corresponding to a marker of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, *e.g.*, Chen *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

V. Computer Readable Means and Arrays

Computer readable media comprising a marker(s) of the present invention is also provided. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. The skilled artisan will readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a marker of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the markers of the present invention.

A variety of data processor programs and formats can be used to store the marker information of the present invention on computer readable medium. For example, the nucleic acid sequence corresponding to the markers can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. Any number of dataprocessor structuring formats (*e.g.*, text file or database) may be adapted in order to obtain computer readable medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in computer readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the invention in computer readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The invention also includes an array comprising a marker(s) of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development and differentiation, tumor progression, progression of other diseases, *in vitro* processes, such a cellular transformation and senescence, autonomic neural and neurological processes, such as, for example, pain and appetite, and cognitive functions, such as learning or memory.

The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

The array is also useful for ascertaining differential expression patterns of one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

VI. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of polypeptides or nucleic acids corresponding to one or more markers of the invention, in order to determine whether an individual is at risk of developing cervical cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit cervical cancer or to treat or prevent any other disorder {*i.e.* in order to understand any cervical carcinogenic effects that such treatment may have}) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample involves obtaining a biological sample (*e.g.* a cervical smear) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a polypeptide corresponding to a marker of the invention include enzyme linked immunosorbent assays (ELISAs),

Western blots, immunoprecipitations, immunohistochemistry and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a polypeptide corresponding to a marker of the invention include introducing into a subject a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345 and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real

time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the

absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of mRNA corresponding to the marker can be determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA. For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from cervical cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA corresponding to a marker of the present invention in a sample involves the process of nucleic acid amplification, *e.g.*, by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA,* 88:189-193), self sustained sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the cervical cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a gene that is not a marker, *e.g.*, a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, *e.g.*, a patient sample, to another sample, *e.g.*, a non-cervical cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

Preferably, the samples used in the baseline determination will be from cervical cancer or from non-cervical cancer cells of cervical tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker assayed is cervical specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cervical cells provides a means for grading the severity of the cervical cancer state.

In another embodiment of the present invention, a polypeptide corresponding to a marker is detected. A preferred agent for detecting a polypeptide of the invention is an antibody capable of binding to a polypeptide corresponding to a marker of the invention, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Proteins from cervical cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A*

Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis, immunohistochemistry (IHC) and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can readily adapt known protein/antibody detection methods for use in determining whether cervical cells express a marker of the present invention.

In one format, antibodies, or antibody fragments, can be used in methods such as Western blots, IHC or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody, proteins or cell containing proteins on a solid support. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from cervical cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample (*e.g.* a cervical smear). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing cervical cancer. For example, the kit can comprise a labeled compound or agent capable of detecting a polypeptide or an mRNA encoding a polypeptide corresponding to a marker of the invention in a biological sample and means for determining the amount of the polypeptide or mRNA in the sample (*e.g.*, an antibody which binds the polypeptide or an oligonucleotide probe which binds to DNA or mRNA encoding the polypeptide). Kits can also include instructions for interpreting the results obtained using the kit.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide corresponding to a marker of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

B. Pharmacogenomics

Agents or modulators which have a stimulatory or inhibitory effect on expression of a marker of the invention can be administered to individuals to treat (prophylactically or therapeutically) cervical cancer in the patient. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, *e.g.*, Linder (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the

identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

This invention also provides a process for preparing a database comprising at least one of the markers set forth in Tables 1-4. For example, the polynucleotide sequences are stored in a digital storage medium such that a data processing system for standardized representation of the genes that identify a cervical cancer cell is compiled. The data processing system is useful to analyze gene expression between two cells by first selecting a cell suspected of being of a neoplastic phenotype or genotype and then isolating polynucleotides from the cell. The isolated polynucleotides are sequenced. The sequences from the sample are compared with the sequence(s) present in the database using homology search techniques. Greater than 90%, more preferably greater than 95% and more preferably, greater than or equal to 97% sequence identity between the test sequence and the polynucleotides of the present invention is a positive indication that the polynucleotide has been isolated from a cervical cancer cell as defined above.

In an alternative embodiment, the polynucleotides of this invention are sequenced and the information regarding sequence and in some embodiments, relative expression, is stored in any functionally relevant program, *e.g.*, in Compare Report using the SAGE software (available though Dr. Ken Kinzler at John Hopkins University). The Compare Report provides a tabulation of the polynucleotide sequences and their abundance for the samples normalized to a defined number of polynucleotides per library (say 25,000). This is then imported into MS-ACCESS either directly or via copying the data into an Excel spreadsheet first and then from there into MS-ACCESS for additional manipulations. Other programs such as SYBASE or Oracle that permit the comparison of polynucleotide numbers could be used as alternatives to MS-ACCESS. Enhancements to the software can be designed to incorporate these additional functions. These functions consist in standard Boolean, algebraic, and text search operations, applied in various combinations to reduce a large input set of polynucleotides to a manageable subset of a polynucleotide of specifically defined interest.

One skilled in the art may create groups containing one or more project(s) by combining the counts of specific polynucleotides within a group (*e.g.*, GroupNormal = Normal1 + Normal2, GroupTumor1 + TumorCellLine). Additional characteristic values are also calculated for each tag in the group (*e.g.*, average count, minimum count, maximum count). One skilled in the art may calculate individual tag count ratios between groups, for example the ratio of the average GroupNormal count to the average GroupTumor count for each polynucleotide. A statistical measure of the significance of observed differences in tag counts between groups may be calculated.

C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for cervical cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent can be desirable to increase expression of the marker(s) to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent can be desirable to decrease expression of the marker(s) to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

D. Surrogate Markers

The markers of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states, and in particular, cervical cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection

of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am, J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

The markers of the invention are also useful as pharmacogenomic markers. As used herein, a "pharmacogenomic marker" is an objective biochemical marker which correlates with a specific clinical drug response or susceptibility in a subject (see, e.g., McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker is related to the predicted response of the subject to a specific drug or class of drugs prior to administration of the drug. By assessing the presence or quantity of one or more pharmacogenomic markers in a subject, a drug therapy which is most appropriate for the subject, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein for specific tumor markers in a subject, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be present in the subject. Similarly, the presence or absence of a specific sequence mutation in marker DNA may correlate with drug response. The use of pharmacogenomic markers therefore permits the application of the most appropriate treatment for each subject without having to administer the therapy.

VII. Experimental Protocol

A. Subtracted Libraries

Subtracted libraries are generated using a PCR based method that allows the isolation of clones expressed at higher levels in one population of mRNA (tester) compared to another population (driver). Both tester and driver mRNA populations are converted into cDNA by reverse transcription, and then PCR amplified using the SMART PCR kit from Clontech. Tester and driver cDNAs are then hybridized using the PCR-Select cDNA subtraction kit from Clontech. This technique results in both subtraction and normalization, which is an equalization of copy number of low-abundance and high-abundance sequences. After generation of the subtractive libraries, a group of 96 or more clones from each library is tested to confirm differential expression by reverse Southern hybridization.

SEQ ID NOS: 1-705 were identified through the above-described subtractive library hybridization technique, wherein the "tester" source for the subtracted libraries was comprised of cDNA generated from four independent stage IB cervical tumors. The "driver" source for the subtracted libraries was comprised of cDNA generated from at least three independent samples of normal ectocervix that were manually dissected to isolate the epithelial component of the tissue. In some cases, the driver also included cDNA generated from B-lymphocytes, T-lymphocytes, and other white blood cells, in activated and resting states.

SEQ ID NOS: 706-1428 were also identified through the above-described subtractive library hybridization technique, wherein the "tester" source for the subtracted libraries was comprised of cDNA generated from four independent CINIII cervical samples. The "driver" source for the subtracted library was comprised of cDNA generated from six independent normal ectocervix samples that were manually dissected to isolate the epithelial components. The "driver" source also includes cDNA generated from B-lymphocytes, T-lymphocytes, and other white blood cells, in activated and resting states.

B. Proteomics

Proteins that are secreted by normal and transformed cells in culture are analyzed to identify those proteins that are likely to be secreted by cancerous cells into body fluids. Supernatants are isolated and MWT-CO filters are used to simplify the mixture of proteins. The proteins are then digested with trypsin. The tryptic peptides are loaded onto a microcapillary HPLC column where they are separated, and eluted directly into an ion trap mass spectrometer, through a custom-made electrospray ionization source. Throughout the gradient, sequence data is acquired through fragmentation of the four most intense ions (peptides) that elute off the column, while dynamically excluding those that have already been fragmented. In this way, approximately 2000 scans worth of sequence data are obtained, corresponding to approximately 50 to 200 different proteins in the sample. These data are searched against databases using correlation analysis tools, such as MS-Tag, to identify the proteins in the supernatants.

VIII . Summary Of The Data Provided In The Tables

Table 1 shows 1428 novel nucleotide sequences identified through subtracted library experiments. These 1428 novel sequences were determined to be novel through various BLAST searches of available databases. The sequences of Table 1 were reinterpreted and those sequences are set forth in Tables 2 and 3. Table 4 sets forth additional sequence (*e.g.*, full-length sequences) for the sequences of Tables 1-3.

The contents of all references, patents, published patent applications, and databases cited throughout this application are hereby incorporated by reference.

Other Embodiments

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed is:

Claims

1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleotide sequence of Tables 1-4, or a complement thereof;

b) a nucleic acid molecule comprising a fragment of a nucleic acid comprising the nucleotide sequence of Tables 1-4, or a complement thereof; and

c) a nucleic acid molecule comprising the nucleotide sequence of Tables 1-4, or a complement thereof.

2. A vector which contains the nucleic acid molecule of claim 1.

3. A host cell which contains the nucleic acid molecule of claim 1.

4. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleic acid comprising a nucleotide sequence of Tables 1-4.

5. An antibody which selectively binds to a polypeptide of claim 4.

6. A method for producing a polypeptide comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

7. A method for detecting the presence of a polypeptide of claim 4 in a sample comprising:

a) contacting the sample with a compound which selectively binds to the polypeptide; and

b) determining whether the compound binds to the polypeptide in the sample to thereby detect the presence of a polypeptide of claim 4 in the sample.

8. A kit comprising a compound which selectively binds to the polypeptide of claim 4.

9. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample comprising:

a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and

b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample to thereby detect the presence of a nucleic acid molecule of claim 1 in the sample.

10. The method of claim 9, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

11. The method of claim 9, wherein the sample is isolated from cervical tissue.

12. The method of claim 9, wherein the sample is a tumor sample.

13. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1.

14. A method of assessing whether a patient is afflicted with cervical cancer or has a pre-malignant condition, the method comprising comparing:

a) the level of expression of a marker in a patient sample, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4, and

b) the normal level of expression of the marker in a control non-cervical cancer sample,

wherein a significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer or has a pre-malignant condition.

15. The method of claim 14, wherein the patient has CIN.

16. The method of claim 14, wherein the patient has SIL.

17. The method of claim 14, wherein the marker corresponds to a secreted protein.

18. The method of claim 14, wherein the marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

19. The method of claim 14, wherein the sample comprises cells obtained from the patient.

20. The method of claim 19, wherein the sample is a cervical smear.

21. The method of claim 19, wherein the cells are in a fluid selected from the group consisting of a fluid collected by peritoneal rinsing, a fluid collected by uterine rinsing, a uterine fluid, a uterine exudate, a pleural fluid, a cystic fluid, and an cervical exudate.

22. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a protein corresponding to the marker.

23. The method of claim 17, wherein the presence of the protein is detected using a reagent which specifically binds with the protein.

24. The method of claim 23, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.

25. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide or portion thereof, wherein the transcribed polynucleotide comprises the marker.

26. The method of claim 25, wherein the transcribed polynucleotide is an mRNA.

27. The method of claim 25, wherein the transcribed polynucleotide is a cDNA.

28. The method of claim 25, wherein the step of detecting further comprises amplifying the transcribed polynucleotide.

29. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide which anneals with the marker or anneals with a portion of a polynucleotide wherein the polynucleotide comprises the marker, under stringent hybridization conditions.

30. The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with cervical cancer by a factor of at least about 2.

31. The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with cervical cancer by a factor of at least about 5.

32. The method of claim 14, comprising comparing:

a) the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-4, and

b) the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer,

wherein the level of expression of more than one of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with cervical cancer or a pre-malignant condition.

33. The method of claim 32, wherein the level of expression of each of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with cervical cancer.

34. The method of claim 32, wherein the plurality comprises at least three of the markers.

35. The method of claim 32, wherein the plurality comprises at least five of the markers.

36. A method for monitoring the progression of cervical cancer or a pre-malignant condition in a patient, the method comprising:

a) detecting in a patient sample at a first point in time, the expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4;

b) repeating step a) at a subsequent point in time; and

c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer or a pre-malignant condition in the patient.

37. The method of claim 36, wherein the marker corresponds to a secreted protein.

38. The method of claim 36, wherein marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.

39. The method of claim 36, wherein the sample comprises cells obtained from the patient.

40. The method of claim 39, wherein the patient sample is a cervical smear.

41. The method of claim 39, wherein between the first point in time and the subsequent point in time, the patient has undergone surgery to remove a tumor.

42. A method of assessing the efficacy of a test compound for inhibiting cervical cancer in a patient, the method comprising comparing:

a) expression of a marker in a first sample obtained from the patient and exposed to the test compound, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4, and

b) expression of the marker in a second sample obtained from the patient, wherein the sample is not exposed to the test compound,

wherein a significantly lower level of expression of the marker in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting cervical cancer in the patient.

43. The method of claim 42, wherein the first and second samples are portions of a single sample obtained from the patient.

44. The method of claim 42, wherein the first and second samples are portions of pooled samples obtained from the patient.

45. A method of assessing the efficacy of a therapy for inhibiting cervical cancer in a patient, the method comprising comparing:

a) expression of a marker in the first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4, and

b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy,

wherein a significantly lower level of expression of the marker in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting cervical cancer in the patient.

46. A method of selecting a composition for inhibiting cervical cancer in a patient, the method comprising:

a) obtaining a sample comprising cancer cells from the patient;

b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;

c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4; and

d) selecting one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

47. A method of inhibiting cervical cancer in a patient, the method comprising:

a) obtaining a sample comprising cancer cells from the patient;

b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;

c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4; and

d) administering to the patient at least one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

48. A kit for assessing whether a patient is afflicted with cervical cancer or a pre-malignant condition, the kit comprising reagents for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-4.

49. A kit for assessing the presence of cervical cancer cells or pre-malignant cervical cells or lesions, the kit comprising a nucleic acid probe wherein the probe specifically binds with a transcribed polynucleotide corresponding to a marker selected from the group consisting of the markers listed in Tables 1-4.

50. A kit for assessing the suitability of each of a plurality of compounds for inhibiting cervical cancer in a patient, the kit comprising:

a) the plurality of compounds; and

b) a reagent for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-4.

51. A method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with cervical cancer or a pre-malignant condition, the method comprising:

isolating a protein or protein fragment corresponding to a marker selected from the group consisting of the markers listed in Tables 1-4;

immunizing a mammal using the isolated protein or protein fragment;

isolating splenocytes from the immunized mammal;

fusing the isolated splenocytes with an immortalized cell line to form hybridomas; and

screening individual hybridomas for production of an antibody which specifically binds with the protein or protein fragment to isolate the hybridoma.

52. An antibody produced by a hybridoma made by the method of claim 51.

53. A kit for assessing the presence of human cervical cancer cells or pre-malignant cervical cells or lesions, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker selected from the group consisting of the markers listed in Tables 1-4.

54. A method of assessing the cervical cell carcinogenic potential of a test compound, the method comprising:

a) maintaining separate aliquots of cervical cells in the presence and absence of the test compound; and

b) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4,

wherein a significantly enhanced level of expression of the marker in the aliquot maintained in the presence of the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses human cervical cell carcinogenic potential.

55. A kit for assessing the cervical cell carcinogenic potential of a test compound, the kit comprising cervical cells and a reagent for assessing expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-4.

56. A method of treating a patient afflicted with cervical cancer, the method comprising providing to the patient an antisense oligonucleotide complementary to a polynucleotide corresponding to a marker selected from the markers listed in Tables 1-4.

57. A method of inhibiting cervical cancer in a patient at risk for developing cervical cancer, the method comprising inhibiting expression of a gene corresponding to a marker selected from the markers listed in Tables 1-4.

Table 1

Sequence 1
GCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGGACATACTGAGAGAATTTGGAATTATAT
GTTATGGTAGAATAAAGATCGAGGTCCATTTTTCTATACATGAAAANTTAAATATTTAG
T
TTGGGATTTGAGACTTCGATCTAGGCCTCTGNATTTCTTTCTAGTTTTTTCCCTACCAT
T
CTTTAATCGGAGTATCCAAGCCCAATCACCCTGTANCCTATGTCCTAAAGCATCTTGAAT
TGNTTGNTTCANGTTTTTNCTTCATGNAGGAGTGTCTTTTGCNCACNCCTCTTAAGCC
TA
TCTGGATCCCCACTTCANNCCTCTGAAGGGTTCTGTTAAAANTTCTAACCCTATCTNT
AT
NGAATTTGTCCCC
Sequence 2
GCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGTC
CGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCCT
TTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATTT
GCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAG
CATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTGG
AATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 3
CGGAGAGGAGTCCTTACTTAGAGTNAAGCTGAAGGAGCATCACAACCCCAAAGACTGTTA
TGTTGTGAAATTTAGGCTGTGTTTTAATAATACTGATGATGATANGATGAAATAGTAAT
T
TATTGATTACTATATCTACTATATGTCCGTAAGATAGCAGGGTCTTTATACTCGGAATC
T
CATTTGATCCTCATAGTTTTTATTGGTGTATTATTATCCTCATTTTACAGATACAGAAAC
TGAGGCTTCAGAGAGGCTGTGTAATCAAGAGTTTGTATGCCTTTCATCTGAGGAGGTTGA
GGACAATCCCAAGTTAGAAAAATAAATGTCTTTAGCATTATTTTTCCTTAATGTTTAGAA
TATTAATAAGTTACTCAGATAATCTATTGGAATTTTCTTCATGGCAGGGGGAAGAGGCTA
GAGTTG
G
Sequence 4
TACTCAGTTTCCTTATCTATAACATGGGGATAATATTANGTATGCTACATCCGTTGTTA
T
GAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTNTACTAAATGGGNAAGG
TCTGGCNGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGGAAGGCTGAGGNGGGG
GCAGTTGGGGAGCGAGGGGTTGTACTACTNCAATGTAACTTGCTTTCTCAGAAATTNAGG
CNAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAACAGTCTCNTGCCTTT
AAGGAGCTTATAGTCTAGTTANGAAACCAGACTTAAACATATGAAAAGTTTAAACATTGG
Sequence 5
CTCTTTCATTGAAAGGAAATTANGGTTGAACCTCCAGGAGCCCGTCAGAGTCTGAGGAGA
GGCTGGCTTNATGTCTAGATACGACGACAGCAAGGCTGCTTAGAGCTAACAGCGCATTGC
CTTTCACTACCGGACTCTCCTTTGCAGCTGCCTTGGTGATCTCATCAGTCAGCATGTC
TC
TAACCCAGAGCCAGGCTGTGCTTTTTTTGTACCT
Sequence 6
CGCGGTGGCGGCCGCCCGGGCAGGTACCTATGACCATCTTACATTATTTTTATGGGTGGG
GGGCATTGGCTGTGGAATGTGGGCAGTAACTTGCACAGTCAGTAACCGTNNGAGTAACTG
GTTGTTGGCATCCCCATTCTGGCACTCCTCCTCTAGGTCTCCACCTCACACGCTGGTTTG
TGGGCGGAGGGGCAGGTTGGTGCCGTGGGGTGTCCGGGCACTGGCTGTGCATGCCTTCTT
CCTCTTCTGTCTCTTGGCCACCTTTTCCAAAAAGTCACCAGTGACCAATTCTCCCAGT

Table 1

GT
TTCTTTGGGACTCAATGCCTTGGGCTTGGCATTGGGTAAAGCCGACTGGCAAGTTTCATT
CTGACCAAGCTCTATAGTAGTCCGGNGTGGACCTCTTGCCCTCCCTGCTCTGCGGAAAGC
TTNCTCAGCCTTTGCTTCTTCACTTATTTACTATTTGCGGGGTCCTGGGGGTACCCTC
GG
NCGCTCTAGAACTAAGTGGGATCCCCCCCGGGCTGCAAGGAATTCGAATATCAAGCCTTA
TCGAATCCGTCNAACCTTCGAAGGGGG
Sequence 7
GGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCTCC
ATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATTGAC
TCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAGTTT
GGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAGGATC
ATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCCGGA
TT
CCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 8
AGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGTCCGCGAAAC
CAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCCTTTTGAGGT
CCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATTTGCAAAACC
ATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAGCATCCAGA
GAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTGGAATCTAAC
TCAGCGGAATTGTATCCGTACCTCGGCCGTTCTANACTAGGGGATCCCCCGGCC
Sequence 9
GGTGGCGGCCGAGGTACCACATGCACTGATAGCTCTCTTTGTATGAACAGGAGCTGTGGC
AGGCCCTATGCCAGGGAGAAAGTAAGATTGGAAAAGAGCTTACCAAGGAGGTGGCATTTG
CACTGTGCTTAAGGGGCAAGAAAAACGTCTTCCAATCAGGAGCCACAAATGCTTGGCTGA
AGTGCTACTGCTCTTTCATCCTGGAGCTGGAACAGACGTCACCAGTCAATCATGATGGCT
GCTGGGTGCACTGGCTAACATCTATAATCCCAGCACTTTGTGAGGCTGAGGGTGGGAAGA
TTGCTTGGGGCCAGGAGTTTGAGACCAGTTTTGGGCAAATTGCAAGACCCTGTCTCTGCA
AAAAAATATAAAATGTAGCTGAGTGTGGTGGCACCTGTAGACCCAGCCCCAGCTACTCGA
GAGGCTGAGATGGGAGGATCGCTTGGGCCTAGGAGTTCGAGGCTGCAGTGAGCTATGATT
GCACCACTGCACTCCAGCCTNGGTGACAGAACANGACCTGTCTNTAAAAANCATTAAATT
AAATCAAAAAAAAAAAAAAAAAAAAAG
Sequence 10
GGTGGCGGCCGAACATCCTGTTTTAACTAGCACAGACAAAACCTATGTGTTACTATCAAA
ATAAAATTTAGAAAAACAATTTTCTTATAAAATTTTCTGTTTGTATTTGGACTACATAAA
CTGGCTTTAAAATTGAGAAATATGCCCTAAAACCATAAGGAAAAAGCCAACAGAAAGAAC
AAAAAGATCACAGCAATTAGGCCCGTTCTATTCAATTTTGCCATGAGCTAAAAATCACAT
TCTTCACAAAGTAAATTACCGCCCTGTTTTTTATTCTTAAGCACTAGGGTTAGGATTGT
G
ATCTGAGCTTTACTAAATCGGAAAAGAAAATCTCAATTATAGAACATTTAGTTTATTTAT
ACCTTAATGCCCGGAGAGGTAATATTTTACTTTAAAATGCATAACCCATGTGGACATGCT
AGGTCTTCCAAAA
Sequence 11
GGTGGGGCCGGGCCCGGACCCGGNCCAAGACCTACCCGCCGGNGNANTTGGCCTNGGGCC
CTGGGGTTTCCTCCCNAGGGGAAGCCTTGTAGAATCCACCTNGGAAANCCTTGTNGGGTN
CCGCTTGCCCCGTNGNATGGNTGGNGTAGGGGAAGGGCAAAGTACGCCTTCAAGAATAGG
NAAAAAAGGGANGGGGGGGGGNACCACTCAAGGCCTGGCAAAGGCCAAGTGGGACCAAG
TGGCCCAAGGGGGCTTCTTGGAATGGTGGNTCTCTCACAAGCTTTGTAANAAAGGTGGTG
GAAGAACCAAGCCTTGNCCCTTTTGTGGGTCGNGNGACCTTGGAATAAAGGGCCAAAAGG

Table 1

AAGTTTTGGTTTCCCTTGGCCCCCNTTTTTCCCTTNTTTGNTTGGAACCTTTTGGGAAA
A
GAAAACCCCCCTTGGGACCTTTTTTGGTTTTTTCCTTTGGCNAAAAAAGGGGGCCACCCC
TTGGCCAAATTGGATGGTTCCTTGNATTGGTTTTTCCGGTCGCTTTANGGGGCCAATT
NA
NAANTTGGTTTGTAAAGGGGAAAG
Sequence 12
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTGTTTTGTATTTTTAGTAG
AGATGGGGTTTCACCGTGTTGGCCGGGCTGGTCTTGAACTCTTGATTTCAAGTGATCCGT
CCACCTCAGCCTCCCAATGTGCTGGGATTACAGGTGTGAGCCACCATGCCTGGCCTTTTT
CTTTTTTTTTTTTAAACGAAAAAATGTTTTTAATTGACAAATAAAAATGATGTATATTTA
TGGTGTTTTTTCTCTTTTGCATCATCAGTCTCTTTCTCATCACTGAAACCTACAAATATT
TTAAAATCTTTCCATTAAAAAAATTTTGCTGATCATTCAACCTCTTCAAATTATTAAGAG
ATACTTACTTTGTATGAAAAATTTTGTCGAGATGTATAATCCATTTTTTTCTGGGAAG
Sequence 13
TTACTTAGGGCGAATTGCGNCCGAGGTACCAGGTGTCATTCCTGCAGCAGGATTTAACAC
GATGCAGATCTGGCCCCAGTGTGAGCATCTGTGTTAATGGTATCAGACTTAAAGAAGGAA
AGACCTGATTTGACTGCTGTTGGTTTGGTAGTGTTCCCTGATCCGGAGCCAGTTTTGTGG
GAGGGAGTCCCAAAGCAGGTTTGAGCTGTGGTAATGACCGAGTTGATCCTAGAAGACAAA
ACAGTAGAATCGTACCTGCCCG
Sequence 14
TGGCGGCCGAGGTACGGTATTCTCTTCAAACAAGAGCAAGCCCATGATGATGCCATTTGG
TCAGTTGCTTGGGGGACAAACAAGAAGGAAAACTCTGAGACAGTGGTCACAGGCTCCCTA
GATGACCTGGTGAAGGTCTGGAAATGGCGTGATGAGAGGCTGGACCTGCAGTGGAGTCTG
GAGGGACATCAGCTGGGAGTGGTGTCTGTGGGACATCAGCCACACCCTGCCCATTGCTGC
ATCCAGCTCTNTTGATGCTCATATTCGTCTTTGGGACTTGGAAAATGGCAAACAGATAAA
GTCCATAGATGCAGGACCTGTGGATGCCTGGACTTTGGCCTTTTCTCCTGATTCCCAGTN
TCTGGCCACAGGAACTCATGTCGGGAANGTGAACATTTTTGGTGTGGAAAGNGGGAAAAA
GGAA
Sequence 15
GCCCCTGCCCGGCTGGTTATGTAACAAACAAAGTCTGTGTCTGTGTGGAGTGTTGCAGGA
CGAGTGGAAATGACTGTTTCCAAGTTCATGGCAATTCAGAAGGCCCTTCAGCCAGACTGG
TTCCAGTGCCTCTCCGATGGAGAAGTATCTTGTAAGGAAGCAACTTCCATAAAAAGGGTC
AGAAAGTCTGTTGACCGATCACTTCTTTTCTTGGATAACTGTCTGCGGCTGCAGGAAGAG
TCAGAGGTTCTTCAGAAGAGTGTGATCATTGGAGTGATTGAAGGTGGAGATGTGATGGAA
GAGAGGCTGAGGTCAGCACGAGAGACAGCCAAGCGGCCTGTGGGTGGCTTCTTCTGGATG
GTTTTCAAGGAAATCCAACA
Sequence 16
CGGTGGCGGCCGCCCGGGCAGGACGCGGGAAGAGGTAATTTTAATGCCATTTTCATGGGA
CACTTGGGAGCTAGATTAGAAGAAGCCAAGACTAGAATCGGGGAGATGAGTTGCAGAGGG
NNGTGGTGAAGGTCTGAAGGAAGGTAGGAAAAGGTCGGACACATTCCAGACATATTTAGG
GGTGGAGGTGGTTGGATATGGGGAGTT
Sequence 17
TTCGCGGTGGCCCGGCCGCCCGGGCAGGTGACTTTAGTCCTCACTCTGTGGGCAGGGGCA
TTACAGCATAGGGGTCCCTTTTGTCAGGGATTTATGATGGCATCACACGCAGGATTCAGA
GAGCATNAATTGAAAAATACATATGATTGGCTGGGCGTGGAGGCTTATGCCTGTAATCCC
AGCACTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGTCTG
ACCAACATGGAGAAACCCTTTCTCTACTAAAAATACAAAATTAGCCGGGCGTGGTGGCAC
ATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATTGCTTGAACC

Table 1

Sequence 18
TNCCGCGGTGGCGGCCGAGGTACGATTCTACTGTTTTGTCTTCTAGGATCAACTCGGTCA
TTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACTGGCTCCGGATCAGGGA
ACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATT
A
ACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACA
CCTGGTACCTGCCCG
Sequence 19
CCGCGGTGGCGGCCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTATTTTTTTTTT
T
TTTTTTTTTTTTTNCCCCCGGGAGAGGAATTGGGAAGAGCAAATTGCTGCTGAAAATT
TC
TACATTGATCCAGACAAACAAGTTAGAGCAGGCTGAAAAAGAACCCTTGGTGTTTTTCTG
TGTTCAACCAGATCAACTGGAAAAGTATAGATACCTTAATTAGCACTGTGCTCTGNGGGA
TTCTGGTCAGCCTGGCCCAGTGGTTTTTTTCCCCTGAACACNCCTGAAAGGGGAGCTCAT
AATGACTGCTGTGCAGGTGGGCGGGGAGGGGGCTTCCTATTTGATTTAGNGGCTGATCAA
TGCCAGTTACCAATTNTNGGTNGCCCCATTTATACATGGNGGAAAAAAAGTACCT
Sequence 20
GAGGTACCCAATTTTTTTAAGTTCTAAGGTAGCTTTCTCAAAGAAAACCATTTCAGGGT
G
TCCATTAAAAGAGCATCTGCGAATTGTTTTTGCAGGGACTCCTAATCAGTCAGGAGAAGT
AGAATGTAAGCAAAGTCACAAACCTCCCGTAAGAATTTGGTTCACCAGGACACAGCTCCT
CTCTTATGAAGGGATGAGAAGCAGACCCCAAACCCAGTGCCACAGTCTCCCTGGAAACAG
CAGCAGGCTTGGGGAATGCTTCCAAAAGGCTATGCCATTCAAGGTCTCAGGTTTTTTGGT
TAAAAATACAACTTAGGCCAACTGCAAGTGGCTCATGCCTGTAATTAATTCCAAC
Sequence 21
GTGGCGGCCGAGGTACGATTCTACTGTTTTGTCTTCTAGGATCAACTCGGTCATTACCAC
AGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACTGGCTCCGGATCAGGGAACACTAC
CAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACACAGA
TGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACGCCTGGTA
CCTGCCCG
Sequence 22
CGCGGTGGCGGCCGAGGTACAGAGTAGAGAGAGTTCTGCAGGGATGAAGTGGGAGACGTT
GATAGGACCAGACCAGACCAGGCCTTGTAGGCCATGGAAGGACTTTGGATTTTACACCAA
GTGCAACAGGTAACTGCTGGAGGGAATTCAGCAAGAGAGTGACAGGAGCTGATTGACAAT
TTGAACGCCCACTCTGGCTGCCATGTGGCAAATAGATTGTAGGAAGAAAAGAAGAAAAGG
AAGAGAGCAGTTTGGAAGCTACTACTGTTGTCCCAGAAATATGTAATGGTGGCTTGG
C
Sequence 23
CGCGGTGGCGGCCGAGGTACANAGTAGAGAGAGTTCTGCAGGGATGAACGTGGGAGACGT
TGATATGGACCAGACCAGACCAGGCCTTGTAGGCCATGGAAGGACTTTGGATTTTACACC
AAGTGCAACAGGTAACTGCTGGAGGGAATTCAGCAAGAGAGTGACAGGAGCTGATTGACA
ATTTGAACGCCCACTCTGGCTGCCATGTGGCAAATAGATTGTAGGAAGAAAAGAAGAAAA
GGAAGAGAGCAGTTTGGAAGCTACTACTGTTGTCCCAGAAATATGTAATGGTGGCTTGGC
CCAGGTTGGGGT
Sequence 24
CCGCGGTGGCGGCCGAGGTACAAAAAAAGCACANGCCTGGCTCTGGGTTAGAGACATGCT
GACTGATGAGATCACCAAGGCAGCTGCAAAGGAGAGTCCGGTAGTGAAAGGCAATGCGCT
GTTAGCTCTAAGCAGCCTTGCTGTCGTCGTATCTAGACATGAAGCCAGCCTCTCCTCAGA
CTCTGACGGGCTCCTGGAGGTTCAACCTAATTTCCTTTCAATGAAAGAGTGGGTTTCCAT

Table 1

GGTACCTGCCCG
Sequence 25
CCGCGGNGGCGGCCGCCCGGGCAGGTACGCGGGAGGCACATTCTTTTCTACGTGAAGAGT
TTTGTAAACTGAACTTTGTTTTCAGTTCCGGCTCCAGCCATCCTGGGGTNGCTTGCCA
AT
AGATGAATCCCACTCGTTTGACCCATGACGCTCCTTCTTTTCATTTCTCCCTCTTTCCC
C
ACAGCAGTGCATGTCCACCATACCACCTGAGAGTCTGTGGAATCTAATTTTCTGTTATAC
TTCTTTCCTTACAC
Sequence 26
GCGGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCT
CCATCACACGCCCCAGAAAGGACAAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATT
GACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAG
TTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAGG
ATCATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCC
GG
ATTCCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 27
ACGCGGCGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCT
CTCCATCACACGCCCCANAAAGGACAGTAGCCAGCTTNTCTGGATGCTTTGCCAAGCAAT
TGACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCA
GTTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATGTAAAGCAG
GATCATAGTTTCTTGGAACTCTCTGTAAGNCNCAACTTGGTTATCGCCGGACATAATTGG
ACCCGGTATTTCCGGCTCAGNCATCTTCACCTTTCATCTAAGGNTTGCATNTTCCGGGCC
CGNTCTAAGAACTAGTGGGATCCCCCCGGGGCCTGCAGGGAATTCCGATAATCAAAGGCT
TAATCTGAATACCCGGTCGGACCCTTCGGAGGNGGGGGGCCCCGGNTACCCCAAGCTTT
TTTGGTTTCCCTT
Sequence 28
CGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTAGCTACATCGT
TGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTACTAAATTT
TAAGGNCTGGCAGGCGCGGTGGCTCACACCTGGNATCCCAGCACTGTGGAAGGCTGAGGT
GGGGGCAGTGGGGAGCGAGGGGNTGTTACTACTCCAATGTAACTGCTTTCTCAGAAATTA
AGGCAAAAAGTCTTACTGACCATGTNAAGGAAATCCAACAATTATAAACAGTCTCTGCCT
TTAAGGAGCTTATAGTCTAGTTAAGAAACCAGACTTAAACATATGAAAAGTTAAACATTG
GCCAGGCACAGTGGCTCATGCCTATAATCCCAGCACTTTGGGAGGCCAAGGCAGGAGGAT
CACCTGAGGTCANGAGTTCGAGACCAGCCTGACCAGCNTGGAGAAACCCCATCTN
Sequence 29
GCGGTGGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTAGCT
ACATCGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTA
C
TAAATTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGGAAG
GCTGAGGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTTCTC
AGAAATTAAGGCAAAAAGTCTTACTGACCATGTAAAGGGAAATNCAACAATTATAAACAG
TCTCT
Sequence 30
GGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTACGTAGCTACAT
CGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTTCTACTAA
A
TTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTATCCCAGCACTGTGGAAGGCTGA
GGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTTCTCAGAAA

Table 1

TTAAGGCAAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAACAGTCTCTG
CCTTTAAGGAGCTTATAGTCTAGTTAAGAAACCAGACTTAAACATATGAAAAGTTAAACA
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GATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGACCAGCATGGAGAAACCCCATCTTTA
CTAAAAATACAAAACTAGTTGGGCATGGTGGCGCATGCCTGTGATCCCAGCTACTTGAGA
GGCTGAGGCGGGAGAATCACTTGAACCCGGGAGGTCGAGCGGCCGCCCGG
Sequence 31
CCCGCGGTGGCGGCCGAGGTACTCAGTTTCCTTATCTATAACATGGGGATAATATTAGTA
GCTACATCGTTGTTATGAGGATCAATATCTGTAAAGCTCTTAGAACATGCATTTTTCTT
C
TACTAAATTTTAAGGTCTGGCAGGCGCGGTGGCTCACACCTGGTAATCCCAGCACTGTGG
AAGGCTGAGGTGGGGGCAGTGGGGAGCGAGGGGTTGTTACTACTCCAATGTAACTGCTTT
CTCAGAAATTAAGGCAAAAAGTCTTACTGACCATGTAAAGGAAATCCAACAATTATAAAC
AGTCTCTGCCTTTAAGGAGCTTTATAGTCTAGTTAAGAAA
Sequence 32
GCGGCCGAGGTACGTATGCACTTGCTTGCCATCTAAGCAGGGACAATGGCAGTTCATATC
ATGATGTTACTTTGATTCTCTGACCAAACTGGCCTGTGAGCACCCTGGGCCTTTCTTC
CT
CTGTCAAAGGCCTTAAGACAGGTTTACCCTGTAGCCAGGTCTGGAAGACAGAGCTGGGTT
AAAGCTGGGTGGGAGAAGTGAAAAAGGTCAGGTTTACATTCCTACGCGGAAAAGGATGTA
ACACGGGGCCACATCCTATGCCCAATCCCAAGGCAGGGAGGCAGGGAAGTGGCTGCCAAA
CCTGTTGTAGGAGAGTAATAAATGACTTGAGAGTAAGCCTAAGCAAACTCAAGTGGGAAG
GGGAGTGGGCTGTAAAATAGTTTAAGAGACTCTCTCAGGAAGTCAGCGTAATTGATGTGT
AGAAAGGTAACAGTCAACAGTTCTCCTAACAAGACAGCTTCAAAGCAGCAGCTATAGTGG
AGCATTCCTGAGGCCTGCTGCAGATCAAAGCATGAATGTGCAGACTGGTCCTCTTGCCCA
GCGTTTCTTTC
Sequence 33
CCGCGGTGGCGGCCGAGGTACGTATGCACTTGCTTGCCATCTAAGCAGGGACAATGGCAG
TTCATATCATGATGTTACTTTGATTCTCTGACCAAACTGGCCTGTGAGCACCCTGGGC
CT
TTCTTCCTCTGTCAAAGGCCTTAAGACAGGTTTACCCTGTAGCCAGGCTCTGGAAGACAG
AGCTGGGTTAAAGCTGGGTGGGAGAAGTGAAAAAGGTCAGGTTTACATTCCTACGCGGAA
AAGGATGTAACACGGGGCCACATCCTATGCCCAATCCCAAGGCAGGGAGGCAGGGAAGTG
GCTGCCAAACCTGTTGTAGGAGAGTAATAAATGACTTGAGAGTAAGCCTAAGCAAACTCA
AGTGGGAAGGGGGAGTGGGCTT
Sequence 34
GCGGCCGAGGTACCAGTTAAAGTCTTCTAGCCTGTATCCCCACTCCTTTTTGCCACTTGC
AAATTCGGTAGCCCAGTTACCCAGAGGGAGGCATAGGAGGGAAAACGAAGACTGAAAAGG
GCTAATATGAGTTTTGTCTCTTACAATTTATCTGCATCTTATCCTTCCCCCACCCCCCA
T
CATTAAATCATTAAACATTCTATCCAAATAGGATGCCCTTCTGTGGAACTGCATATTTG
G
AAACCATACTGCCTGTTTAACTTATGCACTCCACTGGGAACTTACAGTATCTGTTTCCC
A
CAATACTTGCAGTCATATCAGTTACAACCGCTGGGTGTGTATTGGTTCAAAAGGACCTAC
CTACAAGGTTATATCAATCCATTGTCCAATTTGAGAGATTTTTTCTGAATCCAGTTAAA
A
TAATTTTTGGCTACACCTGGGGACACTTCCCAGGACAACAATGACTTGTAGTCTAGTGCC
CAAGAAAGCCAAAAAGGCCCGGCAAC
Sequence 35
GGTGGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTCTAACCTCTCC

Table 1

ATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCAAGCAATTGAC
TCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTCGTTCCAGTTT
GGTAGCATTTAAAGCTCTTATATATTCTCGTGGACCTCAAAAGGATGTAAAGCAGGATC
ATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCCGGA
TT
CCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 36
CATNTGTGTTTTATTGTGAAGGGTCCTCAACTGTGTGGCTGATTCAGGCTGTCCCCACTG
CAATGTAGGGAGAGGAGAGAAAGGGATGAAAGTGAAGGCAGGGGGGGGGATGTTTGTTNC
ACCGGGGTGAACTTCTGCCTGAGCAAGNTGATGTTGGCTTCCGANNGTATTTGGGACACT
TTCTTTCAATACATNTNTTATTTAAGCACTTTATTCTGTGNCTGCTGCCCTG
G
Sequence 37
CCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCAACATGGCGGCCTTAGCAAGCTAT
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GCTTCGTGCGATTCGCGTCCGAGCTCAGACGAGCTCCCTGGAGACCCCTCTTCACAAGAA
GAAGATGAGGACTATGATTTTGAAGATCGGGTCAGCGACTCGGGTTCATATTCCTCAGCG
AGTAGCGATTATGATGATCTTGAGCCTGAATGGCTGGACAGTGTGCAGAAAAATGGAGAG
CTGTTTTATTTGGAATTGAGTGAGGATGAAGAAGAAAGCCTCCTTCCTGAGACACCAACT
GTGAACCATGTCAGGTTCAGTGAAAATGAGATTATCATTG
Sequence 38
CCGCCGAGGTACTTAAGTTTTTCTTCAGTTACAGCTACCATGTGAAAATAATTCTCTGC
T
TATCAAGTTTACAACTTTAGAATTTCCTGTTTTAAAGTTTTCTCATTTACTTATCACACA
GTCATCTTCTTTTTGCCAAACGCTATAGTAGCACATTAAAAGGAGACTGATGTGAAATCA
ACTCTGTGCAAAAAGTATTGGGTGCTTTGGTAGAAGTCTATACAGAAGACACTGGAGACA
CAAAAATGAATTTTGTCCAGGTGAGTTGATGTCAGAAAAGGCTTAATAATGGAGATGAGG
CCGGGCATGGTGGTTCACACCTGTAATCCCACCTGTTTGGGAGGCTGAGGCAGGTAGATC
ACTTGAGACCAGGAGTTTGAGACCAGCCCAGCCAACATGGAGAATCCTGTCTCCACTTTT
NAAAANTNAAAAANATNNGGTTCCTGCCCGGGCGGGCGCTTAGAACTAGTGGGATCCCCC
GGGCTGCANGAATTTCGATATCA
Sequence 39
TCCCCGCGGTGGCGGCCGCCCGGGCTGGTACGCGGGAAAGCAAAACGACAAGCACGCCCT
GAGCAGAGCCCCGGGAATTCAACCTTTAAGTGGATAACTTGGCTTCTGGTTTGCCAAGGA
ACCAGGGCATCAAACAGATGAAACAGCCTATTGTCCATTTCAACAGGATTTTTCAGGAGT
GGGGATGATCTTTCAAATTATCCACAACTTAATTATTTAATATTTTGATAGTCAATTACC
TAAGACACGGCATCGTCACTGACCAATCAGAAGAGATGCCAGTAGTTGGGCGCAGTGGCA
GCACTTTGGGAGGCTGAGTGGACAGATCACCTGGGGTCAGGAGTTCGAGACCAGCCTGGC
CTACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATGAGCCAGGCATGGTGGGCAC
CTGTAATCCCAGCTACTTGACAGAGTGAGCCTCTGTCTCAAAAAAAAAAAAAAAAA
Sequence 40
GCCTCCCCGCGGTGGCGGCCGAGGTACAGTTTAGAAAACTGTGGGGCTGAGTCCTCGGGG
CCGTGGGGCGCAGCGTGGCTGATCACCATCATAACGGGCCTATGGGGATACATTCTCTTA
GACATTTTGAAGTAATTAATGCTCTCGTTAGTGATTAAGTCTGTGAAGTAGTCCTTTGC
A
TAATCAAATCCATGCTTTTCTTTGATGCCATTGCGACAAACAGTGTAATTATAGAAGCG
A
GAATTCTTGATTAATCCAAGCCATTCTCGCCACCCAGGGGGGATGTAGCTGCCATTATAT
TCATTGAGGTATTTTCCAAAAAAGGCTGTTCTGTAGCCAGTGTTGTTAAGATATACAGCA
AAAGTCCGAGGCTCATGCATGGCCTGCCACGAGGGGGAAGAGCAGTTCTCGTTGTTGGTG

Table 1

TAGACATTGTGATTGTGCACATACTTNCCGGTGAGCATGGAGGACCGTGACGGGCAGCAC
ATGGGGTGTAGTCACAAAGGCATTGATGAAGGTGGCCCCCCATGTT
Sequence 41
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGTGCACATTGTGCAGGTTAGTTACATAT
GTATACATGAGCCATGCTGGTGCGCTGCACCATGGCACATGCATATCTATGTAACAAACT
TGCATGTTCTGCACATGTATCACAGAACTTAAAGTGTAATAAAAAAAGAAAGAAAAACAG
CATGCAATTCAGCCCACACAAAAAAAAAGAAGTCAAAGACAGCGAGAATTCTTAAAACAGC
AATAAAAAGTATAAAGTCACTCTAAAGGAATCCCCGTTAGATTAACAACACATTTCTTAA
GAGAAATCTAACAGGCCAGGAGAGAATGGGATGACATATTCAAAGTGTTAAAGGGGGGA
AAAAACTCCACTCAAGACTACACCCAGAAAAGCTATCTTTCAGAAATGGAGATAAAAACA
TCTTTCCCAGACAAAGAAAAACTAAGAGAATTTACTACCACTCACCAGCCTTACCAAAAA
A
Sequence 42
NTTGGAGCTCCCCGCGGTGGCGGCCGGAGAGCAACCGAGATGAAGGTGAAGATGCTGAGC
CGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAAC
TATGATCCTGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGC
T
ACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGAT
GGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGT
GATGGAGAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 43
ATTGGAGCTCCCCGCGGTGGCGGCCGGAGAGCAACCGAGATGAAGGTGAAGATGCTGAGC
CGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAAC
TATGATCCTGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGC
T
ACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGAT
GGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGT
GATGGAGAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 44
GGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTCTACTCTGGAAG
C
TGAGGNGGAAGGATTGCTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGCTATGATCACAAC
ACTGCACTCAAGCCTGGGCAACAGAGCAAGACCCTGACTGTAAAAAAATTTTTTTACATT
AATTTTTAAAAGTGAGGTTTTTACCTGATGATTGNGTAGGTTTCTCCTAGCTCCAAAGT
A
TCCGGCTCCTACGACTCTAAATATAACCTTCAAGGAAAGNGGAGCTGGTTTACTCTTTTC
TGATAATATCAAGCCATTCCTGGCTGGGCGTGGNGGCTCATGCCTATAATCCCAGCACTT
TGGGAGGCCCCGCGTACCT
Sequence 45
GGGNGGCTCCCACCGCGGTAGGCNGGCCGCCCGGGCCAGGTACGCGGGNAATTCAAGGAT
GGGATTAAAGGATTTAAACCGTTTAGGACCCTAAAAGCATAAAAACCCCTTAGAAAGGAA
AATCTTAGGGCAATACCCATTGGAGGGACCTTAGGGCCTTGGGACCAAAGGACTTTCATG
GACTTAAAAACCACCCCAAAAGGCAATTGGGCAANCCAAAANGCCCCAAAATTAGGNCCA
AATNGGGGATTCTTAACCTTAAAACTTTAAAGGAGGCTTTNTTGGCCCCAGGCCAAAANG
GAAAACTTTCCCCTTCNAGANGGNGGGACCCNGGGCCANCCCTTTCCNGGGAATNGGGGG
GGGAAAAATTT
Sequence 46
GGAGCTCCCCGCGGTGGCGGCCGAGGTACTCGGGAGATCGTGCCACTGCCCTCCAGCCTG
AGAGAAAGAAACTCTGTCTCTAAAAAAAAAAAGAAAGAAAGATGTCAGTGCTATTTATAG
TAATACAAAAATTTAATGTAATTTTTGTCAAAATCTCAATGGTATATTTTTGCAGATTTT

Table 1

TCAAATTATATATATATGATTTATAAATTATTGTTATAGATTCCTGGAAAGTTAATCCAT
CTCACCATTACATAATACCAATCTCTCTCGGCCGGGCGCAGTGGCTCACGCCTGTAGTCT
CAGCACTTTGGGAGTCCGAGGCGGGTGAATCATGAGGTCCAGAGATCGAGACCATCCTGG
CCAACAAGGTGAAACCCCATCTCTACTAAAAAT
Sequence 47
CTAACCTCACATTTAATTGCGTTTGCGCTCACTGCCCCGCTTTTCCAGTCGGGAAACCT
TGTTCGTGCCAGCNTGCAATTTAATNGAATCGGGCCCAACNGCCGCCGGGGGGAGGAGGG
CCGGGTTTTTGGCGGTATTGGGGGCGCCTTCTTTCCCGCTTTCCTTTCGCCTCACTT
GAA
CTTCGCCTNCCGCCTTCGGGGTCC
Sequence 48
CGCGGTGGCGGCCGCCCGGCCNAGGTACAAGNGACAATGCTGGATGCCAAGCAGNTCCCC
CCTACCGTCTCACTGCCCCTCAAGACTTCAAGGCCACTCTCCCCATAAACATCATGACTA
CAGATTTAGGTGGAAGAGCAGCCATGTTTGAAGGGCACATGTGATGAGTGGGGGGCAGCA
AGATGCCATTTCTGCATCTCCCAGAAGGGATGAGTCTTTGTCCCGATGCAAGCCCCCTCT
TCGTTGGGCTCCCAGCAGTGCTTNCCTNCTCCACCCTGCACTTCATTTNGTTCTTTCC
CC
CCCNAACTTTT
Sequence 49
GCGGCCGAGGTACAACTAATGGAGCTCAGAAGCTGTCAAGGATATAAGCAGTGCAACCCA
AGACCTAAGAATCTTGATGTTGGAAATAAAGATGGAGGAAGCTATGACCTACACAGAGGA
CAGTTATGGGATGGATGGGAAGGTTAATCAGCCCCGTCTCACTGCAGACATCAACTGGCA
AGGCCTAGAGGAGCTACACAGTGTGAATGAAAACATCTATGAGTACCTGCCCGGGCGGCC
GGCTCTAGAACTAGTGGATCCCCGG
Sequence 50
GGCGGCCGGANGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCCGGAATCCGGACAATT
ATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTAC
ATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAG
TATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGG
CAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAA
TTTGGAATCTAACTCAGCGGAATTGTATCCCGTACC
T
Sequence 51
NGGCGGCCGAGGTACCTCAGCATATATTGGAAGTGTTTTAGAGTTGGTGAGTTCCCCGTG
CCTTCCAGAACTGAACGCTAGGAGGAGCAGNCAGNGAGGACAGACGTCTATGCAGAAACA
TGGNGAACCTCTGGAAATGACACACTCTCCGGGCNCAGGGGGCCATTCGTCCATCTTTGA
GGTGGACTAATCATGGAGATTCTNGCAGGGCCGGCTGCTATCTCAGATTTTCTAATCGGA
GAAGGAGAGAGATCAACTTCCATCGACTCCAGTCTGTCGGGGGCTGATGAGTGAGGTGGC
AGCAGGCATCCGCGTGGTTTTGTTGAAACTGGACTTTTTATTGTGCTGAAAGCTGTTT
GT
TGTGATGATCTCATACTTTGNAGTTGNTCTATCTGCANCACTGACTTTC
Sequence 52
TCGTTNGAAGCCCCCCCGCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTGG
CA
TTCTGAAAATTCATGAGGCTGTGTTTTAGGTGAGGCTATTTCTTCATTCACTGAACNG
GG
CACCCAACAGGCTCTTAATATGAAGACTTGGGCCCTTCCTGAGTTCTAGAAAAGCATTTT
TACTAGTTCTTCAGTAATTTCCCCTCCCCTTCATTCTCTGTTCTCTTTTCCTCGGACTC
C
AATTGGATCTTGGGCCTCTAAGTATAGGCAAGATCATGTTTCTAAAAAGGTTCTTAGAGG
GAGGGAGTTCCTGGGAGTGTTATGTGGGGTGGTGCANAAGGTGCTAACAGGTGGNTTTNT

Table 1

CTTTAGGATGAGCAGGTGG
Sequence 53
GTGAAGATGCTGAGCCGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACAG
AGAGTTCCNNGAAACTATGATCCTGCTTTACATCCTTTTGAGGTCCCACGAGAATATATA
AGAGCTTTAAATGCTACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTG
GATGGTCACCGTGATGGAGTCAATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTC
CTTTCTGGGGCCGTGTGATGGAGAGGTTAGAAATTTGGAATCTAACTCAAGCCGGAAATT
GTAATCACGTACCTCGGCCCGCTCTAAGAACTAGTGGATCCCCCGGNGCTGCAGGGAAA
TTCCGATATCAAGGCTTTATCGATACCGGTCNACCCTNGAGGGGGGGGCCCCCGGGTACC
CCAANCTTTTTGG
Sequence 54
CCCCCCGCGGGGCGGCCGAGGTACACTGGGAAAATGAAGAACTTAACTACATAAAAATAG
AGGGACAGTCAAAACTTCACAGGGGGGAAATCAAGTTAAATTCAGAGCTGGATTTAGATG
ATGCCATTCTAGAGAAGTTTGCTTTCTCCAATGCTCTATGCCTTTCTGTAAAACTGGCA
A
TTTGGGAAGCATCACTGGATAAATTTTATTGAATCTATTCAAGNCAATTCCTGAGGCTT
T
AAAAGCTGGGAAGAAAGTGAAACTATCTCATGAAGAAGTTATGCAGAAAATCGGTGAACT
CTTTGCTCTAAGGCACCGTATAAACTTTGAAGTTCAGGACCTTCCTGATTACTCCTGA
TT
TCTTACTGGGGACAGGAGAAAACCNNGGGAAGGGACTTTACCGATAAAAACCGTGGTCAA
ATTCCTTTAGCCATTTGGCCCCGAAAGANGTTAAGGGTCCAATGAAATTGAAA
Sequence 55
TAGCAGGAGCCCCAGGAGTCTGAGCGGNGGGACCCTCATGTCCATGCCTGTTGTCCCTGG
ACNTGAAGACCTGAACTCCCCCCGCGTACTCTCGGCCCGNTTCTTAGGAACNTAGGTGGG
ATTCCCCCGGGCCTGCTAGGGGAATTTCCGAATATTCAAAGGCTTAATTCGAATACCCCG
GTCCGAACNCTTCGNAGGGGGGGGGGGGCCCCCGNNTTACCCCAAGC
Sequence 56
GCGGCCGAAGAGCACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGACAATTATGT
CCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGCTTTACATCC
TTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATT
TGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTGCTTGGCAAA
GCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAGAATTTG
GAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 57
CAGGGAATGGGNGGNGGCTNCACCTGGGGANNCCTGAGGCCCGTGTTTGTGGAAGATGTA
GATTCCTTCATGAAACAGNCTGGNAATGACGACTGCNGATACAGTATTAAAGAAGACTGG
ATGAACAGTACCT
Sequence 58
CGGCCGCCGGGCAGGTACGCGGGCTATTGTGATTCCCAGTGACCCATAGAACAGGATTTC
ACTAGTCCTATGACATGTGACTGGGCTTGGGAAGTTCNCGTGTCAGNTCCAAAAATCCTA
AGGTGGGATCTTCGCTTTGTGAAGCAAATTAATTACACAACCAAATATTGCCACATTCT
T
GAGGTCTATTGACACAATGGGAACTTCAACCCCTACTTAGCTTAGCATTTTTTTTTTCA
A
GAGTGAAAAGTGGTCCACGTAGAGCACAATATAATTTAAGTAAAGGAAGATTAAAACATA
TTTTTATCCATTTCTTATGGTGGNNNNATTACATGTTTTAGATTTGAGGTCCCCCTCTC
A
GGAAAACCCTTTCAACTTCGTATTATTCACTCCTGAGTAGTATGGGGGTAGAAAAATGAG
TGGGAAATCAGTTTGGTCCACTATTTTCCCGAGTCTTTCTTGCACTTGCAAATACTTTC
A

Table 1

TCAAATATTTTACCAAAAATTCTCANGCNCCTGTTTACCAGGATGGTGGTATCACNATC
A
GGGCTCAAACCAAAGNTTACAGGAAATTCTNTTGGNGGGTTTTTTATCCTGGGACNATTC
TAAATTTTAAAAAACCTAAAAAAGGTTATTTATTTCTTCNCNAATTTATTCANNTGNTTT
TTTAAA
Sequence 59
CACGCGGGAAAGATCAGTTGNTTTACCTTGGCATTCAAAGACTTTTCTTTGACTCCCATG
GTTCTCAAAGCGTGATCCTGGTCCACCACCATCAGCATGGNNGGNGGGAACGTGTTAGCA
CTGCAAATTCTCATTCCTCCCTAATTTTCTGAATCANAAATTACGGAGGTGGAGCCCAGC
AATCTGTTTTAACCAAACTTCCACATAATTCTAATTAATTTATGCTTTGGAGAACNCGC
T
GATCTAGTTTGTCCCTCTCATTTTGCAGGCAAAGAATTGAATTCTAGAGAGGTTAATTG
A
CCTTGTCCAGTCATACAGCTAGGGTCTGTTTTCTATTATTTATTTATTTATTTATTTTTA
TTTTATTCACTTTACCCCCCAGGTATTCATAGNTTTCTTTCTAAATACTCCATATTTGGA
CTTGACTTTTTACAAGTTTGTAATTACCAAATAAAGTCTAAAGATGGGGAAAGGTTGTGG
GAAAACTTTATAGAGAACATGAGATTTTGACTGAACCAGTNAACATTAAGTAGAGAGNAA
AAAGAAAGGGGTGTTCTAAAGCAGTAGGGACCACAGTGAATAAAGGGAGAAGATAGGGAA
GNTTTAAAAAAAA
Sequence 60
ACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACG
AGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGNGATGGAGTCAATTGCTT
GGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGAGAGGTTAG
AATTTGGAATCTAACTCAGCGGAATTGTATCCGTACCT
Sequence 61
TCCACTCCCGCGGTGGCGGCCGAGGTACACGTTACTGTTCCGTCGTATTTTGTAGTCTCT
GTTCTGCCCTTTGGAACATCTNTTCGGTGTTCCTGTGGGATCTCTCTACTGCATTNTA
CT
TTATGTAATAATCTGTTCAATAAATAATTTTTAAAAGGAGACAACAACGCCGCAGGTGAT
CTGGAGGCTCCTGGAGGACCTCAGCGACTCAGGTCCAGTCCAAGGAGGGCCGCAGATCAG
GCTGAAGGATGGATCCACATGTTTAGAGGAGATCGAGAAATGCAGAAGAGAGATGCAGCA
GAGAAATGCCACAGAAAGGGGAGCTGGAGAGAATCAAAGCATGAGAGGAATTCAACCTGC
TGTCACTGGAAGGGGTCCAGATGGAACGCTTGAGAAGAAACGTGTGTAGCATCTAGGAGT
AAAGACTCGCCCTGGCTGACAGCTAGTAAGGAAATGGGAACCTCANTGCTGCAGCCTCAA
AGAATTGACTTTAA
Sequence 62
TGGCGGCCGCCCGGGCAGGTACAATGATGGCTGTCAACTTCGTTTGTTTAAAAAAAGACA
ATTTGAGCAGGACGACCCTCTCCAATCTGGGTAGCATGGTTAGCCTGTGCAGTAACAACG
TAGGCTCGGAGGATGGGTACCT
Sequence 63
TGAGTGAGCCTAACTCACATTTAATTTGCGTTTGGCGCCTCACTGCCCGCTTTTCCAG
TT
CNGGGGAAACNCTGTTCGTTGCCCAGNCTGCATTTAATGGAAATCCGGCCAACGCCGCCG
GNGGNAGGAGGGCGGGTTTTGCCGTATTTGGGGCGGCTCTTTCCCGCCTTCCTTCGGCCT
TCAACTTGACTTCGGCTTGCNCCTTCGGGGTCNGTTTTCTGGCTTGCCGGGTCGAGNCCG
GGNTATTCAANCCTTCAACTTCNAAAGGGGCCGGGGNAATTACCGGGTTTAATTCCCAAC
CAGGAAATTNAAGGGGGGGAATAAACCGCCNAGGGAAAAAGGAAAACANTTGTTGGAAGC
CAAAAAA
Sequence 64
GGGCGNTGGGCTGGAGGAGNGGAGCGGCNNCAGNAGGGGGGCGCCGGCCNCCCCAGCAGA

Table 1

NGNCTCCAGCAGCAGNNGNANCTCTGAGGCTCCANCNCCCACAGCACCGAACAGNGGGNN
CCAGCNNCCACCAGGGGACCCNGGANCCCGGGCGACGGCNGANCCAACNCNGAAGGAGNC
NNAAACCTNNNCNNTTGAGCGGNGGNNCNCNCCCGCGACCCCGAGCAAAAGGAAGCCCAG
CNGGAGGGGCGGNGGANNGACGCCCNCGGGGGGCACAAACAACCNNCNAAAGGAAGAANN
NGCCACCCACCAANCCNNANCAANACAACAAANGAANCAANACAAACANAACCCAAAAAC
GAGNAAAAAAAAAA
Sequence 65
ACCTTTTTTTTTTTTTTTTTTTTTGGAGGAGATGGACAGTGTCAGTCTCCTGATANGGNGG
T
GATGGGTAGGTAATTTAAAAGCTTCTATTATAAAATCTAGTCTCTCTGACACTGCCCTG
T
CCACTGCAGTCACATCTCCCAATACTGAAGGATCCTGAGAATACCGAGCNGGTCATGACA
CTTACTCACGTCATTCACCANTTTTTTTGNACCTGCCCG
Sequence 66
GCGGTGGCGGTNTCCCGGGCAGGCCACGCGGAAATCCCCTAACTTCCTTGCTATCTTCCC
ATCCCATATTTAGGTTAGATAGAGAAGTGTGTATGTGTGTGTGTGTGTGTGTTGCTCGCA
CAGTGATGAACTGTAAACATAAATGAAGATATGGAAAAATACATCAATTAGGACAACATG
ACAATTTCATTAGACTCCTATCAAAGAGTATCAGTTCACAGTTNNNTNTAGATACTAGTA
T
AAAATTCAGATCTTGACTGTTTTCTGGGGATAAAGCANGGCTTTACAATTTAGCAGTNTG
NAGCTAGCTTGAAACAGTAAAACAACAACAGCAGAGCCTTAAGTGTATTTTTGTGACCTA
AAACATGAACTCAGGGTTTCCAAATTCCTAACAA
Sequence 67
AGGTACTTGAAGGATAAGAAATTACTGTGTCAAATTACCCACAAGTTAAATGCCCATGTT
CCAGACCTGTGGCTCTTAGTATCAGGCTTGTGATAGAGAAAAGGCTGCTATGAATTCTAC
TCAGTGTGCTTAGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 68
GGATAAGAAATTACTGTGTCAAATTACCCACAAGTTNTTTGCCCATGTTCCAGACCTGTG
GCTCTTAGTATCAGGCTTGNGATAGAGAAAAGGCTGCTATGAATTCTACTCAGTGTGCTT
AGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 69
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCATTTCATCTTGCACCCGCAATAC
CAGGGATTGTTGCGAAGAATCAGTTGTGTTATATTGTCCAAATCATCAAAGATACCCTGA
GGTAAATTACTTAGGTTATTATTGGACATATCCAGTCGATAGAGCTGCCTTAGATAAGAA
AAAGCATTTGGGGGCACCCGATTGATGTGGTTATCTTGAAGATAAAGCTTCCTCAGGTTT
GTGCCTGGAAGGTTTACTGGTGCAGCAGTCAGGGAATTCCGCACCAGGGACAGCTCTGTC
AAATTAACTAGGTTGAAGAAAACTTTGTCACCTAAACCATGATTGTTCAACAGGTTTCCA
TCTAGAACCAGGCGTTTTAGACTAGTGAGACCTTGAAGAGATGGTGATGAAATAGTGGAT
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CTAAGGTGATTACGGGACAGGAAAAGCAGTCGGAGATAGTTGCTGTCTCGGAATGCTCCC
TCTTNTATGCTAACTGCAGAGACAGAGTTGNCATCTAAATGTAATTCTTCCAGATAGG
Sequence 70
NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTGAATAAAAGGCTTTGGTTTCTCTG
ATGTCTTCCAATCAATCACACAGAGCTTGCCCTGATACTCAGCCACACAGTCCAGCAGAC
CTATATAGTTTAAGGTTTCATGTTGAACAGCACTTTCAAGAGCTCGCACTCCACTGAC
AT
CTTTCAGAATATGCTGGACACTTTCAATGTAACCAGACTTGAGGAGATTTTCATCTCTC
T
CTTTTAAGGTTTCCTGGGGTGAAAGTATGCTTTCCAAGGCTTCGTGGAACCGTTTCCC
TT

Table 1

GTAAAAAGACGTTTGAAGTGTATTCTTTAAAGCCATCTTCTCCCAGTTCCAGAATCATC
C
CGCTGTTTCCACCTCTCCAACAAAGAAAACCTGTTGTTTTGGTCATGGTCTGCTGAAGGA
CTCGGGTCACACTTGGTATCACATTCCTTTGCAAGGGGATTTTCAAA
Sequence 71
AGGTACTTGAAGGATAAGAAATTACTGTGTCAAATTACCCACAAGTTAAATGCCCATGTT
CCAGACCTGTGGCTCTTAGTATCAGGCTTGTGATAGAGAAAAGGCTGCTATGAATTCTAC
TCAGTGTGCTTAGACCAAAGGAAACCACCACAGGGATTTCACAGGC
Sequence 72
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATATATCATTTATTCAAGAGGCAGA
TTTTAAACGTTTTTGTAAAAAGCTAAATAACACCCAGAGTGACTCAAAAAATTTCTCAA
C
TTTGCCCAAGTGAATAGTAAGTCTAGAGTTTTTTGGGTTTTTTTTTTGTGACAGAGTTT
C
TCTCTGCCGCCCAGGCTGGAGTGCAGTGGCGATCTTGGCTCACTGCAACCCCTGCCCG
Sequence 73
GGCGGTTNTGGGGGGCAACACCGANCCGCAGAGNCACACTNGCAACAAAAGGNACTTNTT
TGGGGGGGGGAAAAACCCCGGCCCCNCCNGNCCAGCNGGACCATCNATTTNNTCCNCCNC
CNCGGAGCNGCNCCCNAAAAAGCNCANAACAGNAGAGANCAGNNGNCNCNGGNNGCAAAN
CNAACANANANNCANGCAANGGAGGNGNANCNCCATGCTTTTTNGNNGGGGGGGGNNGCG
CNACGCNCCCNNGAAGAAAAAAACGCCNCAGNAACGGGGGGGGGGNAGGACCCAGCCNGG
GCGGNCGCNCNAGAACCAAGNGGAACCCCCCGGGCCNGCAGGAAANCCGAAANCAAGNCN
NANNGAAACCCGNNNAACCNAGANGGGGGGGGNCC
Sequence 74
CCGCGGTGGCGGCCGCCGGGCAGGTACCTTGTGAGAAGAGGAAGAAGGTGATAAGAACTA
AGATCAGAGCATAGTAGAGAAAGTAGCCCTGTAAACAGAGGAGAAGCAGAAAGAGAGAGG
GGAGGACAGAGCTTTTATTTTGCTCCAGGTTAAAAAGAAAAAAAAAGCACATTCAACTCT
ATGTAGTGTCTGTCCCAGGTCCTAGAACTGGAATAGACCAACCAAGCCCAACCCTTCTTA
AAAGTAAGACTNGGTGCTTCCTGATTATATATTCAACTGCCTGGAAGCATGCAAGTAAAA
TTTCCTTGATGGCATTTCTAAGTTTCAAACATATTCTTNCTAACAAATGCATTTACAAAA
AAATATTAGGGATTGNGGTTTTTTTGGTTNGGACTTTAAAAAAAAATTGTTTTNAAANC
C
ATAATTGGGGGCCCTACCCCAAAATGGATTCTTCTCCCCTACAGGTGGAGGGTTTCATTT
TTTC
Sequence 75
GCGGCCGAGGTACGCGGGGAGGCGTTGTGGGAGGAGGTGCGGGGAGAGAGGAAGGGGCCT
GTGCACTGAGCNGGCATCAAACTATTAGTGGATGGCCTTGCGTCTCAATCTGCAGTAAAN
AGGAAACTAATCTGAAAGGGAANGANAGGACTGTGTGNCTTTTTATTTTTTAAAATACGG
AGTGTGCANTTTTACTGAATCTTGAATCATGCCC
Sequence 76
CTTGGCCCTTGGNTCGGGGGCCNTTTNCCCCCCCAAGGGATGGGGNCCCNTGGNGTANGT
GTTNGNGGGCCCAAATANGAGCGGANAGGTTAAAANCNAAGTAACNAACGACCGTAATCG
TTGTAGTTCCAAATGGGGAAATTGGGGTNTTTTCGGGNGGAACCTTAAGAAAGNGGCCTT
CCAAAATTGGNGGTTNGGGGGGAAAGGAAAGGAATTCCCCCCTTGGCCAANAAAAAACNC
CCACNCCAAACCCCCAAGGAAAACCGGTTGGGGNTTTTTTGGGCCCCNTNGGAAAGGGGC
NTNGTTCATACCTTGGGNANGGAAGGNAAAAAATGGAATTTTCTTGGGGGGGGGGCTTTG
GTTCTTTTAATTGNAAAAAAANATTNAATTAACGGACCCATTTTTNCTTCNAACNAAATT
AAAAGGCCCCCCACGTTNNTTCAATTCCATCCCCCAATTTTTTNTCCCCTNCCCCTTTT
T
TTANCCCCTTTTTTTTCTAAAGNATTGGGCCAAAGNNTTNTCTTCCNTTTNTTTTNCCA

Table 1

A
CCNATTTTNAANGGGGGCCTTGGGGTTTTNGNGTTNTTCAANAANAACNTTTTTTTT
GN
GGGGTAAGTCCCNACCCGNGNTANCNTTGGGTNCAAGNTTTCNNTTTCTTTGGGGGGGA
AAAGGCTTGGNGGTTTCCAANGTCCNTCCAATTNTCCTTGGGCCAAANGGGGGGCCTTTT
NCCTTCCCCTTCCCCTTNCTTTGGTNNCTTTTT
Sequence 77
AAAAAGNGAATTCCANCNTGGGGGGNCTTGGNGAAAAAGCCTTCTTAAACCANGGGCCAA
TTTGGCNCAGGCCCCTAAAGCCTTACCCTGGCCAAGTTTTTTGAAGAGCCAAAGGGGGGC
CAAGNGGGTTCAACCTTTTAACCCCCTTGCTTGGTTCTTGGAAATTGGTCNTCCCCTTGG
GGGGAACCAAAACAAGGGNAGGGGGCNTGGCCACCTTCAACTTGGGCCTTGGAGGTTCCA
AGAACCAGGAAAAGGAAGGGGGAATCCATTCCGGGGACCTTGGGAAAAGNCCTCCTTGGG
CCAAGGGGGTAATTGGGGCTTAGGCCCCNTGGGGTTTNACCCCCGGTTAAGTTGGAAGAA
AAATTNGGGAAGNAAGGGGGGCCCCAACCCTTGGCCCCCAAGCCNTTAACCACCAAGGAA
ATGGTTTTTTTCCCCCAAGGGGAACAAAACCAAAGGGGAAGGGGCTTTGGTTGTTTCCCC
ACCTTTGGNACCAAGGTTTTTCAAGNACCAAGGGAAAAGGTTGGGGGAAAACCCCAACCT
TGGGGGNACCCCCGGGGAAAAGNCCTTCNTTANNCCAAAGGNTGGGTTTTGGCCCCCCAA
CCCCTTGGGGGCCTTAANCTTTANAANTTGGGAAGGCCCCTTTTTGGAAANAACCCCCAG
GCCCGGAAAAAAACCCAAAATTTAAAAATTTCAAAAAAGGGAAAGGCCAAGNTTTTCNTT
GGTNCCCNAANAAGGN
Sequence 78
TCCCTTTAAGTGAGGGGTTAATTGCGCCGCTTGGGCCGTAATCATGGTCATTAGCCTGGN
TTCCTGTGTGGAAATTGTTANTCNCGCCTCACAAATTTNCAACACCAACCATTACGGAAG
GCCCGGGAAAGNCATTAAAAGTTGGTAAAAAGCCCTNGGGGGGTGCCTAAATGGAAGNTG
GAGCCTAANCTTCAACATTTTAAATTTNGCGGTTTGCCGCCTTCACCTGGNACCCGGCTT
TTTTCCAANTTCCGGGGGAAAACCCCTTGTTCCGGTNGCCCANCCTTGNCCATTTTAAAT
GGAAAATCGGGCTCCAAACGNCCCCGGGGNGNAGAAGGGCCNGGTTTTTGGCCGGTTATT
TTGGGGGCCNGCCNTTCTTTTNCCGGCNTT
Sequence 79
GAGGTACTTTGGGCCTCTCTGGGATAGAATGTTATTCACGCAGGCACACCAAACAAGAAG
GGCAAGTTTCCAAGGATTTCAACCTGCTTCAATCAAGAATGGGGCGGGGGGGAAAGAATG
AAAGAACCAGGAATGGGTGGCCAAGGCCCACCAGGTTTCGTTTTTNGANTCCTCCCACCC
TTTGGGGTTCCCCTTCCCGGCCCCGAAAAGGTGGAACCCCGNATGGTCCCCTTTCCCATA
ATTGGTTTTAACAGGGTAAAAATAACAACCTNGCAAGAAAATNCTTTCAAAGGGCCTCCC
AAGNCCCTTGCNTTGGAATTGGGTTGGAAGAAGGTGGAAAAGGTTCTTGGTTCCCCCAAG
NACCCCCACCTTGGCCCAACTTGGAAACCCCTTGGTCCTTGGCCGAATTGNTCCAAGGTN
GGGGCCCCCNTTGGTTTTGGGGAATTGGTAATTCCAAGNAAGGAATTGNAAGNGGGAAGC
CCCTTTGGGGGGNAANGCCCCTTGGGGCCCCAAGGGGTTTTTTCCTTGGGCNTTGGGGTT
AACCCTTGGCCCCCCGGGGGCCCGGGGGCCCCGGNCTTTCTTAAGAAAACCCTAAGGTNG
GGGGAATTCCCCCCCCCGGGGGCCTTTNGCNAGGGGNAANTTTTCNCAATTANTTCCAAA
AGNCCTTTAATTCNGAATTNCCCCCGGTTTNGAACCCCTTTTGNANNGGGGGGGGGGGC
CCCCCGGGGTTNACCCCCAAAGNCNTTTTTTGGGGNTNCCCCCNTTTAAANTNGGAAGGG
GGGTTTAA
Sequence 80
TGGCGGCGATTACTGTGCGAGAGGTAAAGGATATATGTGGCTACGATTACGGCCTCTCT
Sequence 81
GCGGTGGCGGCCGAGGTACAGCCAACCCCCTAGGTGTGGACCAGCTGAGGCACGGTGGGC
ATGATATGCAGAGGGACTTGGGGCTTTGCCAAAGGGTAAGCACAAAGAAGGAGTCACGGG
TTCTGTTCGAGGCACTGTTGGGATTAGGAGCCGGAGGGGACCTACTTTTGCAGGAACCTA

Table 1

GCATAACTTTGTGTGACGAGACTGCACAAGACAAAGCTCANGCAAGTGGCTCAGTAGTTG
GCCAGCCCAGCAGGGTCCTCTGTATGAGTGTGCACCCAGCTGAAGAGAAGAAATGGAGAG
CAGCAATTGGAGCTTNAGGACCGGCTTGCACTGTGGCTCCAGGTTATACCACCACTGCCC
AAAGCAAAAGCTAGAGAAGCAAGTGGAGAAATGCTGGGAGAAAGCTG
Sequence 82
TGGCGGCCGAGGTACGCGGGGGAGTCAGTCTCAGTCAGGACACAGCATGGG
Sequence 83
CGAGGACCTTGTTGCAGCTCTTTATTTCTTAAGTCCCCTCCCCCGAGGTAACACATTT
CT
GCTTTTTTAGCTGTTTCCTCTAGTGTAGGTTCACCTNGCTAATTTTTGATTCAATCACT
T
AACCACCGTTACATACTACAAAATATCACTATATTATGACCATGATTATATTTTNTTTTC
TTTTTCCCTTCATCAAGGAAGTTCATCAAAGAATTTCATCAAAGTTCAATGATGACCTC
T
TTTTAAAATTTTCTTAGTATTCTATGTAACTATCACCGATCTTTTCCCCACACACTTCAA
GAGGCTTTTTTAAANATAATNTTTTACATAGGCCNTTGAGGCACANGATTAACCAAATCC
CTNTTTT
Sequence 84
GTGGCGGCCGANGNACTNNGGCCTATNTGNGANANAAGGTATTNACCNNGNNCACAACAA
ANGCATNNTCCATATTNNAACNGCTCATCATATGGNGNNAANATNNNGACAGANGGTGCA
ANCACNNTNCACTNGATATACNCCTTGGTNCCTCCGGCCGCTCTAGAANCTNANTGGGAT
CCCCCCCGGGGCCTGCAAGGGAAANTTTTCGAATAATCAAAAGCCTTTATTCGGAATAAC
CCCGNTGCNGACCCCTTNCGAAGTGGGGGGGGGCNCCCCGGGTAAACCCCCCAAGACCT
NTTTATGGTTTTCNCCCTTTTTTAAAGATTGNAAGNGGGGTTNTAAAATNTAGGCCNG
CC
CGCCTTTTGGGNCNGNTTAAAATTNCAATNNGNGTTACAATTAAAGNCCTTGGGTTTT
TT
CCCCTTGGTTGGTTAGGAAAAAAATNTTNGATTTTAATTACCCNGGCCTTTNCNAACNAA
AAATTTTTCTTCCACCAACCCAAAACCAAATNAAACCTNAANTCCCCGNGGGGNAAGNC
CNAATTAAAAAAANGATTTGGTTAAATAAGGCCNCTTGGGGGGGGGGTT
Sequence 85
CCGCGGTGGCGGCCGAGGTACTTATATTACATTATGCTCAAATGCAAACACTTATGCTAA
ATGTTATATTTGGGAACAAATTGTGTAAATATACTGATGACGTCAATGGATCATTACAA
T
TAATGTAGGTGCCGTGGGCAGGAAAGCTAACTTTANCTGAAAGCATCTNNAACGTGCTTA
TTTTTCATGGGCCCTCAAAGGAAAGGGATGAGGCCAGCCATAAGGAANGGCTTGGCCAAA
TATAGTTCTTGTTTGTCAAGAACAACAAATCCCATTTCACAACAGAACTAACGCTGGCAT
GCCATTCTNTCCTNAGGTTCTTGGCGTGCAGTGAGCGAGGCCNGGATGGCAGTCAAGGAT
TCATTCCTTTG
Sequence 86
CCCCGCGGTGGCGGCCGAGGTACATCCCTGTTTATCCCATTCCATCCACCGAGGCCCAAC
AGCATGGATGATCTGTTTGCAGGGAAGCCTCCCTGCTCCCGTGACAGCTATCTCACCAGC
TGACACTTTACCATATCTGGCAACAAACTGTTTGCTCTCTTCTTGGATTTCAAATCCAC
C
AGCTTTTACCAGGGCCAGGGCCAGGCCTCCCCCATGCAGAAGATCTTCATTGGCTGCATT
CACCACAGCATCAACAGCATGTGTGGTGAGGTCATCTTTCCACACTGATAACTCTATCCT
AGGAGTCAGCATTTTTCTGAACACTTGCAGAGATTTGCTGTTGCCTTCCTGAACTGGAGA
GACCAGGGTAGAGATACAGCCAAACTTATTCTGGAGGACTTCACACAGCTGACGCTCATT
ATTTTTTAAAATTTTAGAAGTCATTGGTGGTTAATGG
Sequence 87
CGGTGGCGGCCGAGGTACTCTTCAAAATTGTCAAGGTCATGAAAGACAGCAAAAAGTGAA

Table 1

GAATTCTTACAAACTAGAGGAGACAAAGATTGGAGAAGAAACAATGACTGGCTGGGCACG
GTGGCTCATGCCTGTAATCCACTTTGGGAGCACTTTGGGAAGGCCNGAAGAGGGACAGAT
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CNNCATCCCNTACCTATAATAAATACCAGGAAATTACGCCTTGGGGTCGTNGGTTGGNTG
ACATTGCCCTTATTAAATNCCCCAGCCTTACCTTTGTGAAAGGGCNCTTCCGGNCAGGGA
AGAAATTNNACCTTTNTATACNCNCGGGGGAGGGGCATGAAGTGTTTTGTTGNGTTTGAA
GCNCCAAAAAAAATTTGGCCGCCCATTTTGGNCAACNTCCCANGCNCCTNGGGGCCAANC
AAAGAAGCCGAA
Sequence 88
GCCCANAAAACCGTAAAAAAGGCCGCCGTTGCTTGGCGTTTTTTCCATTAGGGCTCCGCC
CCCCTTGACCGAGCCATCACCAAAAAAATTCGACGCTCAAGGTCAAGAAGGGTTGGGCGG
AAAACCCCCGACCAGGGAACNTATTAANAGAATACCCAAGGGCCGTTTTTCCCCCCCTGG
GAAAGGCTTCCCCTCCGTGGCGCCTCTTCCTTGTTTTCCCCGAACCCCNTGGCCGCCTTT
NACCCGGGNATTAACCCTTGTTCCCGCCCCTTTTTTCTTCCCCCNTTNCCGGGGGGA
AA
Sequence 89
CGGGCAGGTACCGCTCAGCCTGCTTGGTTGCATCCTCCGCATGGCGAGTCAGCTCTGAGA
TCTGAAGGTCAGCATGCTTACGCTCGGCCTCACATGTGTCAAAGTGATTCTGGATCTCCT
TAAGTCGATCCAACATCTGCAGNTGCTGGTTTTCCCCATTCTCCAGTTCACGTGTTAA
AT
TCTCTACTTGTGATGCCAAATGTGCTTTCTNCTTGTCTTTTCTTTCCATGCACCGTTTN
A
CTTCCTTTAACT
Sequence 90
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATCACAAAGCAGACAAACAG
GAAAGACTGAACCATCTATTTGAAAAAAGTGACTTCATTCAATTGGTTCAGCCACCCGTA
TCTGTAATCTCTCCATTCTGCCCTCTTGATTTTAATGCAGCTATAAAGGAGAGTATTTT
A
AAAGTGCCTCCCAGTAGGAAGAACAGTCACAAGGCACTGTTATATCAATTCAGTGTGACA
CAAGCCCTGATTATTTAATAGTATAACAGCAGTGAATCAGAGTTCTTTCATCTGACTTT
G
CTGACATTNCCAGCAGCTGNATATTTAATTCACAGTTAGGGGCTGGACAAACTACAGCCN
TTGATCAGAATGGAAGCAGGCATCCTTGAGCTTCTTCTAGGAACAAATACAGATGTGCAC
AAAATTTTCATTTATTCAGT
Sequence 91
GATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATCACAAAGCAGACAAACAGGA
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TGTAATCTCTCCATTCTGCCCTCTTGATTTTAATGCAGCTATAAAGGAGAGTATTTTAA
A
AGTGCCTCCCAGTAGGAAGAACAGTCACAAGGCACTGTTATATCAATTCAGTGTGACACA
AGCCCTGATTATTTAATAGTATAACAGCAGTGAATCAGAGTTCTTTCATCTGACTTTGC
T
GACATTTCCAGCAGCTGTATATTTAATTCACAGTTAGGGGCTGAACAAACTACAGCCATT
GATCAGAATGTAAGCAGGCATCCTTGAGCTTCTTCTAGGAACAAATACAGATGTG
Sequence 92
CCCCANGAGGNCACCAAGCATCCCANCACCCTTNNTCCGGGNGGTGNAAANCCCANGGCC
GCCAGGCAANGGCACANCAAAANCCGGGCTGCGNCNNGAGCACNGGGCANCCCGAGAAAA
CAAGGNCNCAACNACNGACNGGCNAAGAAGGGGCCNGCCCCNGGCCAACNNCACCANACA
GNNNAGAGCAATCTTTTTTNGGGGGNGGAGCACCGGGACCACCACCCNGACAACAAAGGA
CCCCGGCCGGGGGN
Sequence 93

Table 1

CCCGCGGNGGCGGANATTGGGGGNGAAACCTNANANCANGGAANCTTTGCTTTNNGNCCA
GATTANATTGGGGGGNCTTAAANCCCCAGCGGCNNNNGACAGNTAATACACCTCACGTTT
TTNGNAACTGGGGGGGGCAGNACCN
Sequence 94
TTTCCCGGGCAGGNACAGCTCCATGAGGTCACCAAGCATCCCATCACCCNTTNCCGGCAG
TTGCATGGCAATGGCTGCCAGGCAATGGCACATCAAAATCCGGGCAGCGTCTTGAGCACT
GTGCAATTGAGTCAACAAGGTCTCAACTACTGACTGGCTAAGATGGGGCCTGCCCTTGGC
CAACTTCACCATACAGTTTAGAGCAATCTTTAAAGTGGNCTGAGCACCTGGACTATCATC
TTGACTACAAAGTACCT
Sequence 95
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTGTATGATAACATTGCAGTCAAACATA
TCTTGTGACAGGACAGTTTTTTGTGGGGAGGAGAATTAGACCAAGTTCGGAGATATATTT
TAGGAACTAAAAGGAACGTAAGATCTGGGGTAGGGGGATGAGCAGCTCCACACCCTGCTC
CTGTGTGAGCTGTGCGCTCCCGACTGGGAAATGTCTAACTCCATCGAAAACATGAGATGA
GGGGCAGGGAAGGGGCTACTTCCAAGCCTTTCATTATAATACTGTGTGTAACCTTTTGCA
TATTTTCAGAAAAGAAACCAGTAAGGTGGGTTCAGTTGTGGGCTCATCCTGACTTAGAAA
ATTTTAAATAATTTAGCCCATTGAAATGTTGATAATATAAGGCATGCATGAATAATAATT
TTTGCTTCTT
Sequence 96
AGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGCTGCGACAAACACCCCACAAAA
TGGCGGCAGCGCCGTCGCCCTAGAATCCCCCGAGTCGCCTCTCCCCGCGTACCT
Sequence 97
AGCTCCCCGCGGTGGCGGCCGAGGTACCTTCCCCTGAGGAGCCCCCTTCAGAGGGGCGAA
GAGCAGTATCTTCAGAGGCCATCCAAGTTTTAGCATAACAAGGAGGGAAAGAGAATGCAG
AGAAGAGGCTGGTGATAGACAAGTTTCATGTTCACAACTTGAATTGCAGAGGTCAAGAGT
TTAAAGAGTTTGGGATGGAAAGAAATCGAGAATTGGGCT
Sequence 98
GCTCCCCGCGGTGGCGGCCGAGGTACCAGCAGAGATGGCTTCAAGATGATTTAGGACTTG
GGTCAGTAGCACTTACTGATGTAGTGGTTTGATACACACTGATTACCTTCTTCCTTTTT
T
ATTCTCTGGCATTTCTCCTATATAACTAGCCACTTTTAAACAATATTTGTCGGCTCTTTT
CTTCTGCTTGTCTGTAAATATTAGGGTTCCTGAGTCCTTACCTAGATTTTCTTCTCTTC
T
TACTCCTGGCCTTTCCTTGGGAGAGTTCATAATTCACCTACTCCATCTAGATATTTGTG
A
TGTCCAAACACATCTCCACGTTAGGCTTCTATTTGTAGCATCAGACCCACACTTTCAA
CT
GTCCACTAGATAGCCTCACTTGGATGCTCTGCAGGCCTAAATAACCTTTGCGGACAGATT
AACAGGGAAAAAATATTAATAGGAAAAAATATAGATTTTTATCTGATGGTAAT
Sequence 99
TGCGTTGCGCTCACTTGCCCGCTTTCCAGTCGGGGAAACCTNGTCGTGGCCCAGCCTGCA
TTANATTGAAATCGGCCAAACCGCCGCCGGNGGAAGAGGGCCGGTTTTGCGGTAATTGGG
GCGCCTCTTTCCGCTTTCCTTCGCTTCACTGGACTCCGCCTTGCGGCTTCGGGTNCNGTT
TCCGGNCTTGGCCNGGCCGAAGGCCGGGTTANTTCAGGCCTCCACNTCAAAAAGGGCGGG
GTAAATNAACCGGGTTAATCCCACCANGAAATTCAGGGGGGGAATNAACCGCCAGGGAAA
AANGAACCATTGTTTGAAGCCAAAAAAGNCCCANCCAAAAA
Sequence 100
GAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA
ATATGTTTTAATATGCATATCATCCAGGCAGCATAATGTTATATTTCAAAGACAGATTTA
TCCATTGAATTATTGTTTTTAAAAGTTGGGATTCTCTACATAGAACATATTTTCTGAAAT

Table 1

TTCAAGAATATTTTCAGGTAAATTAAGAATTAATTTCTTCTAAGACTATCCAATGNGTCT
CAATCTATTCCATAATATAATCAATGATAAAGATTCACATGTATCACCAAATTCGAGGC
A
GCTTAGTTGAAAAAATTTGAAACAGCTTACTGAATTCCATTTGCTGATTCTGNGGGGCT
TCCCCAATGGCATGNGTGCTCCTTTGGATGCCTGCAGGGGTGGTCACTGCAAAGTCGTCA
TNTGTGCCACTGGGAGTTGGGGAGGCGGCCTGCTGGGGTTCCCTGGGT
Sequence 101
GGCCGAGCCCAATTCTTGATTTCTTTCCATCCCAAACTCTTTAAACTCTTGACCTNTGC
A
ATTCANGTTGTGAACATGAAACTTGTCTATCACCAGCCTCTTCTCTGCATTCTCTTTCC
C
TCCTTGNGTACTGCTAAAACTTGNATGGNCTNTGAAGATACTGCTCTTNACNCCTCTGAA
GGGGGCTTCCTNAGGGGAAGGTACCTCGGCNCGCTCTAGAACTAGTGGAATCCCCCGNGC
TGCAGGAAAT
Sequence 102
CGGGTCCATAATAATGCAATTAACAAAATCCAGGATTTAAGGATTTNTATAAGATTAAAA
AAAAAATGAGGTGGTGTCGAGTGGGGAGAGAAAAAAGCAGGAAACAAAACTGGTGAGAGG
AAATGACCCCCTGATGAAAGATCTTAAACACCAGGCTGAAGATTTTAGATTTCTACCTAT
TAGAAATGAATATTCACTGAGGTTTGATGAAGAGTCACTGAAGTGTCACAAAGAAAACAA
GATTTGAGAAAGATTCTTGAGAACTCGTGCATAGGAATGAACTGCAATAAGGGCAGATTA
GAGAAGAACTAGGCCATGAGGGCCTAGTATCCAGAATGAGGCAGAGGGAGGGACGCTGGA
TGTGAGCAG
Sequence 103
ATTGAGCTCCCCGCGGTGGCGGCCGAGGTACTCCTTTCTTGTTTAAACGCCTCACCACTG
ACCACGGAACGTCTTGATAGAGCCATCTAGTAATTCTTAAGTCCTACCTCATCCAACCTT
GTTTTGACTCCTGCAGTGAGCACAGCTGCCCTCACCCTCCCCTCTCTATGCCCTCACCTT
TGCAGGAGACTCTCAATTTCTCAGTCCACATCAGCTCTNAGACCACCAAANGCAAGGGTT
N
Sequence 104
TGGATTGAGCTCCCCGCGGTGGCGGCCGAGGTACACGTCAACACGGGTGGTTGCATGCAT
TCCTCAAGTCTGTATGACTCTACCAAGATACTGTGAAGTTGTCCTTCTGATTGCACAT
GG
GGAGAAAATGCTGAAACTAGTGGCCACAGATGTCTTTAATTCCAAAAACC
Sequence 105
AGCTNCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTCTAGGTATATCATGTGCCCTAATG
TGCTCCTAATATCATAAATGTTTACTTTCCGAAAAGTATTTCTGAAAGGGAGCATATTT
T
GGAAAGTGCATAGGCTTGTAATCATACTTGTTTTCAAGTTTCAACTTTGCTATTCAACT
A
GAATAATCTTGTGCAAAACCTGAGCTGATTTTCTCATCTATAAAATGGAAACAATACTT
T
CTGTGATAATGGGTGCAAAACACAAGGTATACTGGTTTCTTTGCTCTGGATTCAAGTT
TT
CTTCTTAGTTTCAAAATTTTAAAGGGAAACCAAAAATGTTTCATGGNCCNNNCTNGCNGG
NANGGGANTTTTCCCNCNAAAAAAAAAANTCAACGGGGGGGGTTTTTNCCNNTGGGGANN
CCCAAAAAGCCGNNTNTNGGCCANGTTTTTNNGNNNCTTTTTGTNAGGGGNTTTNGGGCC
NCCCTGCTTTACCCCNTTTTTTANATAACNNCCCCCCCTTTTGGNNTNGGGGNGGGGNNT
TATATATNTTTNTGGGGGGGG
Sequence 106
GTAGTGGGCAGCGATNAGGGCTGGGGCTCTTTCCTGAGTTGTGTCAAGGTGAGAGATTGT
GAAGAACTTGGCTTGCAGGGTTTGGGCATCAGCTGCCCATTGAGGGGCCGTTCATTGTCT

Table 1

CAAAGTGAATGTGGGGTGGTTTGATCTGCATGTGTCATTTGTATCCACACAAGTTAATTA
TTCTGCTTTTGTTGTAGTACCTTGGTTGTGAAGCAGAAGCTACCAGGCGTNTATGTGCAA
GCCATCTTATCGCTCTGCATTAAGTAAGATGAGGATTCACTCTTAATTTATGGGCACAT
T
TTAGTTCCTTCCACACAAATTTAAGGCCTTAACTCTTNATTTTTTCCTACANTGGNGGG
T
TTTGGAAGTAATATTCATACGGGCATGGGACCT
Sequence 107
CAGAGAAAGCTTGCCAACGGTGATAAGTAGGTTTGTCTAGCAGCACTGATGCGTCGTGGA
AGTTGATGGTCATGAACATACAGTGTGATAACCTATCTGCCCTCTTGACCTTTTCTAGT
A
GTGCTATGTCATTTTGGTACTAAGGTAGGTGAATTTTCCAAGTGTTCTTGGAAATAAG
GA
AACATCAAGAATAATGTAAAAGCCTCATATACAATAATGAATAATAAAGAATAATGTGAA
GGCTTCATTCAAGGTTGGGGTTTGCCAGATACATTGCAACAAAATGACAGAGCAGCCAAG
GTATTTAGGGATAGTGGCCAAAGTATTGTAATGATGGCTTATGGGAGTGTCAAGCTGGAT
AAAAGAGTGAAAAATGGAAATAAAAAACTAATGGGATTGGTTCNANTCCGAAATAGGCAG
CNCNGCCCCAATGGCNCCCATNGCCCCGGTTTNAAATTAGGGGG
Sequence 108
NCCGGAATGGAATTCTACATCAAGTGTCTGTGCCTCGCTGCTGAAGGATAACCCAGAGTG
CAAGGTCATCTTTGTTGCTGAACAGGGCTGGACCTGTCGCACTTAAGCACACTTAAAGGA
TTCTATTCTTCATTCAGGTCCCCCAGAGAAATTGGCTCCTTATTTTTCTTTACCTATTC
C
TAGACTTCCTTTTGTCTAGAGCCAGTTTTGCAAAGGGCACTTTTATCCATCTCAGTTAT
T
CCCAGAGGTGACAGAATGAGTAAACCATATGGGGCAAATAGCATATATGAGCTAAACCAG
NTAACTGTTAACCAAGGCACATGGTCAATGCCTTAGTATTTTTTTTTTTTTAATTCTTCC
TAAACGGTTATTTTCTAGCTGTACATTCCCAAAA
Sequence 109
GCGTCCGAGACACTTCTCTGACTAACCATAGACTATGTGGAAAATGGTAGCTGGATTGCC
TTTGGGTGGAGTCCTTGCCCTGTGGCATAGGAAACAAAGGAAAGGAGAGAGATGCCCTTT
GAGATTAATGAAAATGCTCTCAGCCAAATAAAATCTAAAAATAGCCTCCTTGTGATACGA
ACGCGTGGCCCCTAAGGGTCCTAAAGAGAGAGCTAGGGGAGGTTCAGCTGGCCACAGAGA
TGCTAAAGGTCAGGAGCAGACTTTTAGGGTTTGCTGTTTTATAGGTTTAAAGACCAGGTC
TGTGTTTTGATAACTGAACTTGCTAATAGCTGGCCACTTGAGTTGCTTCTTCCAGCTCT
T
TGTTTGTTTTAAATAAAGAGATTCAGCCAGTAATAATGGGAAGAGCTGCAAATGACTTCC
CCAG
Sequence 110
GTGCTGCCTGCACTGTGACTAAGACTTTCTGGACTATCATCATGTTTAGGAGTTGATGAG
ATTATAGTTTCATGTAAGTGTATCATTAGATGACAACTCTACATCTTTAGGCATGGAAA
C
AAAAATTTTTCCTGGAAGAAAAAAAAGTGAACATCCAACCTCCATTTAAACAAATTNGAT
TGTTTCTTTGCTATTAAGAAACTCGGTGCTCTTTCTCCCACTCTATTATATTGTCAAAAT
ACATCTGGAGACACTTTATAAACTTTTTCTCCTTTAAATTACCTGGTTTATATATTATCT
CCTGTAGCCTGCATAAACGATAAAGGGTTAAACATA
Sequence 111
GCNCGCGGGATTGGCCGACGCAGCCATGGTAGGTCCAGATCCCGTAGAAGGGAGCGGGGT
CCCATAGGTTACGGCCGATTCCTGGAGCTTCTGGACTGAGGGCCGCGGTAAGCAGTGGTC
TGGGCTCCCGC
Sequence 112

Table 1

CGTGGCCGAGCGGTTTGCATCGCCGCTCGCGCAAGGCCATGAGGTTGGTCTGGGTGAAGA
ACGCATCGATGGCGGCACGGGCCTGTTCCGGCACGTAGACCTTGCCGTCACGCAGACGCT
CCAGCAATTCGCGCGATGGCAGGTCGATCAGCAGCAGCTCATCGGCTTCCTGCAAGACCC
AGTCAGGCAAGGTCTCGCGCACTTGCACGCCGGTGATGCCGCGCACCTGGTCGTTGAGGC
TTTCCAGATGCTGGACGTTGACTGTGGTGAATACGTTGATGCCGGCAGAGAGCAATTCCT
GAATGTNTTGCCAGCGCTTTTCGTGGCGGATTGCCGGGGGCGTTGCTGTGGGCCAGTTCG
TTCACCAGCACCAGTTTTGGGCTTG
Sequence 113
GCGGCCAGCCAGACTGGACCCCTTAGCCTCGAGGCCTTTGCTGAAGCTCATGTGAGGGGG
CGACTGCCCCTGACATGGTGTTGGATTCCAGCTGCTGTGGCCCTGAAGGTGGGTGGTGGG
AAGAACGGGAGAATGAAGCCAGCCTTGGGAGAGGTAGGACGCCAGCCCGGCCCAGCTGCT
TCCAGCATCTGGATCCAGCCTCACCTGAAGCCAGCCACCTNCTGGACTGCAAAGTCATTT
GTNAACACCGAAACACAGGGTTTCTGACCATTGCAACCCAGGGTCCCGGCGTGTCGTGGC
T
Sequence 114
TTGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGAAGCAACTGTCAGCTAGTGAGATTA
CTGTGTATGGCCAATCCAGATAAATAAGACGATCAAGTCTTTATGAAAAGGAAAGAAAAA
TTTGGAATGCACATCTCTGTCCAGCTCAATTCCTCACTCCTTTTTTAAGATGGAGAGCT
G
TTAGGTTTGTCTACACAGTAGGAAACACCTGATTAAATAACAGCATGGAGCCAATCTTGA
CAAAGAAATTGGCTGCATCCAATAGAATCCCAGGGCCGGTCGTGGTGGCTCATGCCTGTA
ATCCCAACACTTTG
Sequence 115
GGCCGGAATCGTTGCACCAGACNAGGCCCCCAGGGCCCAGCTACTCGAAGAACAAGCCAA
TGGATTGGAACGTCCTAGGACAGATGCCACGGCTTTGACCCAGGCTGGGGGTGCACGGAT
CTCACTGGGGTTAGTTGGTCGGAGGGGGAAGCCCCATGGGTCCACCAGGATGAGGTGTTT
AACTCTATCAGGGTACCT
Sequence 116
GGGGCTCGTCGGTGGCGGCCAGCGAATTGGTGACGACGCTGATCTTCACGTTGCGCCCGC
GGATCTCGCGCATCACCTCCAGCCCCGTGGCACCCGGAATCAGGTAGGGCGAGACGATGG
TCACTTCGGAACGCGCGCGGCGCATCTGCTCGACCACGTTGTAGCGCACGCTGTCGACAT
CCAGCAGCGGCACGCCGCCGTACGACGCGGTCTTGCCCGATCACGCGGTCAGGCGAATCG
GCATACGCCTCGGCGGTGGTCCAGATCAGGCCGAGCTTGCCGGCGTTTGAAGGTCTTCGA
CCATCGGGCTGTAGCCGAGCAGGGTTCGTTTGGGGCGCCGGGCTTCGGCGGGGGCCGGGC
GTTTGGTGTCGGGGGNCCCGGTGGGCCGGCGT
Sequence 117
GATGATGAGCTCCCCGCGGTGGCGGCCGAGGTACTCTAATGGAGCCCTCAGGACTGTCTT
AAAAAGACAAAAATACCTCCTACAGTTGTTATCATCAACGTCAGTTGCTGGCTTTTCCT
A
AATTTGTCTTCTACCTCAGATCTAAACCATTTGATAACATTAGGGCAATATCATGGCAA
T
CGTGGCCCAGTAAAACCATAGCAAATGTTTTCTCCCTAGGACACTATCTGTTTTCACAGG
AAAATTTTTCTCATAGAAAAACTGTAGGAAAAGCCATGGGATGAGCTGAGAAGACCAAAC
CTATCTCTTGGAAAACAACAGTAGGGAGCGTNGGATTAGGAATGTCCTTGGTGCGTGAAA
CAGGCAGACCAATCCTGAAACATCTTTCTCTGGGGACCGTAAGGCATGGAAAAATTTTCT
ATTACACTTANGGAGGGCTTCTAGGGAAACAGGAAACCGACCAAAAATGGGAATGGGGCC
TTAATTCATTTTTTT
T
Sequence 118
CTCCCGCGGTGGCGGCCGAGGTACGCGGGGAACCGAGGCAGCAGCGGACGTGAGCGATAA

Table 1

TGGCGGATATGGAGGATCTCTTCGGGAGCGACGCCGACAGCGAAGCTGAGCGTAAAGATT
CTGATTCTGGATCTGACTCAGATTCTGATCAAGAGAATGCTGCCTCTGGCAGTAATGCCT
CTGGAAGTGAAAGTGATCAGGATGAAAGAGGTGATTCAGGACAACCAAGTAATAAGGAAC
TGTTTGGAGATGACAGTGAGGACGAGGGAGCTTCACATCATAGTGGTAGTGATAATCACT
CTGAAAGATCAGACAATAGATCAGAAGCTTTGGAGCGTTCTGACCATGAGGGACAATGAC
CCCTCAAGATGTTAGATCAGCACAGGTGGGATCAGAAAGCCCCTAATG
Sequence 119
GGTGGCGGCCGAGGTACCTGAACACCAGGCTCTTTACGGTCCCCTGGCCAGTGAAAGGGT
CTAATATAAAACACACCGAGGCTGAAATAGCCCGCTGCTTGTGAGACCTTCCTCAAGCTC
AATGACTACCTGCAGATAGAAACCATCCAGGCTTTGGAAGAACTTGCTGCAAAGAGAAGG
CTAATGAGNTGCTGTGCCATTGTGTATGTCTGCAGATTTCCCCAGGGTTGGGATGGGTTC
ATCCTACAACGGACAAGATGAAGTGGACATTAAGAGCAGAGCAGCATACAACGTAACTTT
GCTGAATTTCATGGATCCTCAGAAAATGCCATACCTGAAAGAGGAACCTTATTTTGGCAT
GGGGA
Sequence 120
GTGGCGGCCGAGGTACCCGAGCTACCAGGCTGTGGAATGAGACCGTGGAGCTTTTTCGTG
CTAAGATGCCCGTTACGGAAACATCGCTGTCGTTTCAAGAGCTATGGGCATTGTTTCACA
Sequence 121
GCTCCCCGCGGTGGCGGCCGAGGTACAAGTTTATGTTTTCCTTGGTGTAAGGCTTTAACA
GTTCCCACCTTTCAGCTGCCTGGGCATTGATTGCTCACCTACCACTATGACTAGATATGA
TTCCATGTGCTTTTGACTAGATTCTTTGTCTCTTGTGTATGGAAAGTGAGACTTTAAGT
A
ATAGTTACTGCTGAGAGAAATAGAAGACGTGACAACGTTTGCTTTCCCATTCAGTAGTCA
GCGGTTGAATGGAATTATCTTCGTTTTTGGACTGACAGATTTGTTTTACAATTCAGCTA
T
TCCCAAGCCTTACTATTCAAAGCAGAACCCTTCTGTCTTCTTTCTGTAGTTGCTCTCTC
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CCCTATATTCTGTTGTATTTTTTTCAAATAACTTATTACTATCTCAAGTAAAATTGTTTT
ATGTTTTGTTTTTATCTACCCTCTTAATCAGGGCAGGGATATGTCTGTTGTATATTTTA
C
TTTTCCCAAATCATAAAGGTTTTGGG
Sequence 122
CCCGCGGTGGCGGCCCGAGGTACACACTGGGATCTCCTTCACTCATTTTTTAACCCTGAC
TGGGACACCAGAGACATGCTGCATCTTGTATTAGGTGTTTCATCTTGCAGAATGGCTGTG
CTCCTGAAATATTTCCTGTGAAGAAAATTGTTACAATCCCATTACATCACTGGCTTTTA
T
TATTAAATTGGAATGTTGGCTGGAAACAATTTTAACCC
Sequence 123
GCGGTGGCGGCCGCCCGGGCAGGTACGCGGGTGTGCAACTGCAAACCAGTAACCTGCTAT
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GCTCAAGCAATCTTCCCGCCCCACTTCCCGAAGCCCTAGGATTACGGGAGTGAGCCACCG
CACCCAGCCAGAAAAACGTTTCAAATATTGGAAAACCTTACTTTTTTCAATGAGCATTT
T
TGCATCAAGGGGTAACAGGGACATTAGGCTTTTTTTCTCTTAGACTCCAAACAGTAAGGT
CAGAATTTATCAAGACATTACATAGGAGTAAGGGCACAGCCAGGGGGTGGTGGGGGGGAG
GGACATTTTCCAGCA
Sequence 124
GCTCACCGCGGTGGCGGCCCGAGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGC
TGCGACAAACACCCCACAAAATGGCGGCAGCGCCGTCGCCCTAGAATCCCCCGAGTCGCC
TCTCCCCGCGTACCT

Table 1

Sequence 125
ATTCAACAAATATTTATGCATCAGCTACATGCCAGGATCTGTAATAGATTCTGGGTGTGC
AGTAGTGATTACTGCAGAATGCAGACATGGTCCCTGCATTCTTGAGAGGGAGACAGCAAC
CAAATAAACAATTACAAAAAAGTATGTAACTAATTAACAAGTGGGAGAAGGGAGTGGGAT
TACACAGCAGAAGTGGAAGGAAGGGCCCACTTAGAGTGGTCAAAGGCTTCTTGAAGGTAA
CATGTAAGCTGAGACCTGAAGAAGGATGCAAAAGGGCCAGCATGTAAGGAACAGAGAATA
AACATCCCAGAAATAGAAAATAACACACAAAAACCTAAAGTCATTAAAGAACATGATCAT
CTTTCAAGAACTAACCCTTGAGATCAGAGTAGTTTGATTATAGAGGAAAAGGGTGAGTGC
AATGGAAACGTTAAAAATAGCCCAGATCACGTAGAGCTCTTAGCCTTTTGGTAGAAAAA
Sequence 126
GCTCCCCGCGGCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCGGAATCCGGA
CAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCCTGC
TTTACATCCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGA
ACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCAATTG
CTTGGCAAAGCATNCAGAGAAGCTGCTACTGTCCTTTCTGGGGCCGTGTGATGGAGANGT
TAAAAATTTGGAATCTAACTCAAGNGGNAATGNATTCCGNACCCTNCGGNCGNTNTTANA
ACTAGGGGGATCCCCCGGGGCTGNAGGGAATTCGANTAAAGCTTNNTTANTCCCCGCCAC
CNCNNGGGGGGGGNCCCCNNCCCATTTTTTTTTTTNTTTANGGGGGNTAATNGCCCCC
GGGGGAAAAAANNNANAAAAATTTTTTTNTNGNGGAAAAATTTTCCCCCAAAANTNTNCA
NNAAAAAAAAAGGGG
Sequence 127
GTGAAAAAACAAGAAAGCTGAGAGAAATCAACATGTTCCCAAGTGCTGTATGTGAACAAT
AAATCTGAGACATACCTCTAAGGCTTTTCCAGAGACAAGAAGCTCTCAACCTGTAAAGAA
TTCCTGGGACATGACTGAGAGCAATGAGAACTCCAGTGNCAGAAGGTTAGCAGATATAGT
GTAGAGCATACACAGATATACTATAGTTCATAACACTGGTGGCTTAGCTGTAAATCACAA
AATAGCACTGGAATTATCTAGTGATCATAGCACATAGTCCAAGAAGAAAAAATTTTGATC
TTGTCTTAAACTTTGTGGAGCCAGTGGTGAAATGAGTCACACAAAGATGCAACAATGATT
GAACCCAGNCCTCTTTAGACTAACATATTCTTGGCCATCACCNCCAATATTACAATAAAA
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CAAAATGNNACTTCATGCTTAAGGAAAAAAAAGGAGNGGGAAGGAGGNCACCAAAGCNGG
TNCNGNAATGGGTNAACTTGGGGCATTATANGGGGGNGCTTTAAAATACCATTTT
Sequence 128
GCGATTGGAGCTCCCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTTGAAACG
ACAGCGATGTTTCCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAG
CCTGGTAGCTCGGTACCT
Sequence 129
CGCGGTGGCGGCCGCCCGGGCAGGTACAGTCAACGGCCGAAAACCACTGAGCTTTTCCCT
CTGCCTGGCACATATCCACTGCCCTGCCTTCCTTCAGCTGATGAACTCTTCATATGCCTC
CTTTTGGGTGTCAGTGGAAATGTCACTTCTTTCTAGAAGCTTCTCTGGCTCTCCCAGC
CT
GGCCCAGGGCTCCAGCTATGAGCTTCCATAACACCCCTAGTTTTCCTCACATTGCCCTCA
TAGTATATGGAATTTGTTCATTCAATTGCCTGGCTTCCAACAGATGCCAGCTCCAAGAAG
GCAGGAGCTGCTTCTGGGTATTGCTTGCCATCAAGGCCCTCACACCCAACCTAATGCCTG
GGCCAGAGGTAGGTGCTTAATAAAAAATTGTTTGAGGCCGGGGCGTGGTGGCTCACGGCT
ATAATCCCAGCACT
T
Sequence 130
GCCCAAGGGGGGGCCAACCCACATTATTTGNNTGGGGCNNNCTGCCCNTTTTTNAAANNA

Table 1

GAAAANCCTTNNCCCCCCTTTTTATNAAATAAACCCCCCCCNNNGGGGNGNGGGGGGGGG
GGGNGTNATANNNGNANNNNGTCTCNTNTTTTNTCCTTTAATTCCNANAAATAAACTT
GA
CNTTCGCTTGNGCTTNGGNNGGTTTCGGGCTGCGGCGAAGCCGGTATTCAANCTCACTCA
AAGGGCGGNTAATACCN
Sequence 131
CCGCGGTGGCGGCCGCCCGGGCAGGTACCTATCTGCAGAACGGTCATTAGCAGTTTTTCC
AAACAAGCGACTTTTAGCAAATTAACCGTTAATTTTAATGAGATTCAAAAGTTAATAGC
C
ATTCTTAACGTTTTATAATTAGAAGCTGTTATATAATTAGAGCTGGACACCCACATGGA
G
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C
TGTAGACCCTTGGGAGTTGTAGGGAGTTAAAGCTGATCATTATATACTATTATATACTT
A
GGGATACAACCCAAGGGCAACCCCTGGCCTTTATGAAAACCTGGAGTGAGTTATTATTTC
CTGGTAATACAATTCTCTGCCAGCCAGTTGCTGCATCAAAACAGTTCTGATACACACACC
TAAAGTCACCACTTCCTCATTCTGGTCCCCAATAACCCTATAAGCCTCTCCCTTGGAGGT
GACCTCTGCCCTGTGAAGGGTTGGGCTC
Sequence 132
CGCGGTGGCGGCCGAACCGTGGTGGCCGTGATCGTGCCGTTGGCGGACGGAACCTTGAAG
ATGTTCTGGGCGGCCAGCACAATCGCCGCCTTGCCGACGATGACATTGTTGGCCTTCAGC
CCGTCAATATCGCCCTTGATGTCGATGTTCTGGCTCTCCTCATCATGGCTCAGCGCAATG
GCGGCGTTCGCCTTGCCGGTCGCCTCCACGAGGAACAGGGCTGCGGCCGTCGACACATCG
CTGGACGCGAGGGTCAGGTTGCCCTGAAGCAGCCCCTTCTTGTCCTGGGTGACATCACCG
CGCAGCCGCGTGCCGCCGGCAATGAACTGGATATTGCTCAGGCGTTTTTCGTCCTTGTGC
AGGGCAAGTTCCGTGGCAAGATCGGCCCGCACGCCGTCGAGGAACGCCAGACCG
Sequence 133
CGGTGGCGGCCGAGGTACGATAATTCATGCCAATTTCTTTGGGAATACTTGTTTCTGATA
TAATAGGTTACAAAGCAAAATTGAGATGATTTTTAAAATGCCATGCAGTTATTTTTTCT
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AATAACATAAATTTTAAACAGAGACCTGAAAAAAACCCCAAAAGTATTAACCTTTAAATA
CATAAACTCAATAGAAATAATTTAACTGCCTTCTCTTCACAAGAGGCAATCAGAAGGCAG
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AGAAACAATTCCATAGTTTTAATTTC
Sequence 134
TNGACTCCCGCGGTGGCGGCCGCCAAGTGTTGGGATTACAGGCATGAGCCACCACGACCG
GCCCTGGGATTCTATTGGATGCAGCCAATTTCTTTGTCAAGATTGGCTCCATGCTGTT
AT
TTAATCAGGTGTTTCCTACTGTGTAGACAAACCTAACAGCTCTCCATCTTAAAAAAGGAG
TGAGGAATTGAGCTGGACAGAGATGTGCATTCCAAATTTTTCTTTCCCTTTCATAAAGA
C
TTGATCGTCTTATTTATCTGGATTGGCCATACACAGTAATCTCACTAGCTGACAGTTGC
T
TCCCGCGTACCT
Sequence 135
TTGAGCTCCCCGCGGTGGCGGCCGAGGTACCTCTCCTGCAGGGCCCTCCATTCAGGGTCT
TCCTGGAAAACCCCCTGGAGGAAGCGCTCCTGTTGCAGTCGGAGTGAACACCCGTCTTGT
TTAACCACCAGCAGGGGGATTCCTTTCTGGAGAGTCCATGTAGTCATCATCTCTTTGACC
TCTGCATTTTCCCCCAGAAAGGCGAGCATGTTACTTGTCATCTTGGGATCCGAATGACAA

Table 1

ACTCCACCAGATGTAAAATCACTTTCTAAACAACTATTTGACAGACTGCTCCACAAGTCA
TCATTCTTAGCATTTCTATAGCTGAACTTCTTTAAGTACCTGCC
CG
Sequence 136
AGCTNCCGCGGTGGCGGCCGAGGTACTTAAAAGTATATCANGGGCAGTTTCATGCCACGG
GAGCCAGGGAAGGCACCCAAGGAAGTGATGGAAGAGTAGAAGTTCACCAGGTGCAGCTCA
GGAAAGGGCTCAGCAAATTTCTCTGTAACAGGATGCAGACCCCGCGTCCTGCCCG
Sequence 137
GCCGAGGTACTAAATTTAGCAACTTTATTCATGAGGAACACCAGTCCAATGGTGGTGCTC
TTGTCCTTCATGCTTACATGGATGAACTCTCATTTTTGTCTCCAATGGAGATGGAGAG
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TTTCTGAGGAGTTTCTTGCTTTGACATTCAGTGAAAATGAGAAAAATGCTGCTTACTAT
G
CTTTAGCAATAGTGCATGGAGCGGCTGCTTATCTCCCAGACTTCTTGGACTACTTTGC
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TAATTTCCCCAACACTCCAGTGAAAAATGGGAAATTCTGGGCAAGAAAGATTTTTGAACC
ACCCCCCATTTTAAATTTTTTNACCTCAGGGGAANNAGGGACNATCCTGGNTNGGGGNCC
CNCACCGGNGGGGGNTCCNTTTTGGGGGGAAAAAANATNTTTNTTGTGGNNCNNAANAAA
AAAAAAAAAANNGGGGGNTTTNTTTTTCCCNNCCCNTTTTTTTTNTTNTANAAAAAAAA
C
CCNCTTTTTTTNAAAAAATTTT
Sequence 138
TNCCGCGGTGGCGGCCGAGGTACTCGGGAGGCTGAGACAGGACAATTGCTTGAACCTAGG
AGGTAGAGGTTGCAGTAAGCCAAGATCGTGCTACTACACTCCAGCCTGGGTGACAGAGTA
AGACTCCATCTCAAAAAAAAAAGAAAAAAATTGACTTTGGAACCTCAGATTACATATCAG
TTTGCATACATGCTAAACAGAGAAATGTCCTCAAAATTCAGTTACTAAAAATTACTGAT
A
TCTCCATGATTAGAACCACACTGTGGTTGTGTGTGTAGTCAAAGGAGGAGAATTTTTAAT
GCTATATAAGCATAACTGATAACTGCTATTACAAATAAATATTCCACAAATTTGGAAAG
T
TATTAGAGGAAGAATTTTTTTTCCTTGTAATTTCCAGGTGTTTATATTAGTTGGGCCAT
A
GTGAAAATTACATGGAGGAAAGAAAATAGGGAAAATAAGTCACAGAAAAAGAAAA
Sequence 139
TTGGAGCTCCCCGCGGTGGCGGCCGAGCCCAATTCTTGATTTCTTTCCATCCCAAACTCT
TTAAACTCTTGACCTCTGCAATTCAAGTTGTGAACATGAAACTTGTCTATCACCAGCCT
C
TTCTCTGCATTCTCTTTCCCTCCTTGTTATGCTAAAACTTGGATGGCCTCTGAAGATAC
T
GCTCTTCACCCCTCTGAAGGGGGCTCCTCANGGGAAGGTACC
T
Sequence 140
TCCCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATAGCTCTTGAAACGACAGCGATGTT
TCCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAGCCTGGTAGCTC
GGTACC
T
Sequence 141
TNCCGCGGTGGCGGCCGAGCCCATTCTTGATTTCTTTCNTCCCAAACTCTTTAAACTC
TT
GACCTCTGCAATTCAAGTTGTGAACATGAAACTTGTCTATCACCAGCCCCTTCTCTGCAT
TCTCTTTCCCCCCTTGTTATGCTAAAACTTGGATGGCCTCTGAAGATACTGCTCTTCA
CC

Table 1

CCTCTGAAGGGGGCTCCTCAGGGGAAGGTACCT
Sequence 142
NGGTTGCGCTCACTGCCCGNTTTTTCCAAGTCAGGGAAAACCTTNGCNGGCCCNNTTTNG
TTTTAANANAANNTGNGCCNNCCCCNCGGGGGGGGGGGGNNGNTTTTGNATNTNTTGGGG
CCNNTTTTTCCCTTTTCCNNNAAAAAAAAAAAAANCNCNNGGCCCCCNGGNNTTTTTGGGG
GGGNGGGGGGGG
Sequence 143
NNGACCTAACCTNACATTTAAATNGCGGTGGCGGCTTAACTGGCCCGCTTTTCCAAGTCC
GGGAAAAACCCTNTTCCNNGCCCAANCTTTGTANTAAANGAAATCCGGCCCAACCNCNCC
GGGGNGAAGGGNGGGTTTTTNGCNATTATTGGGGCNCTTTTTCCCGTTTNTTTGNTTNNN
NNNANACCCCTTNNGCCNCNGGGGGGATTGGGGGGGGGGGGGGG
Sequence 144
GAGCTCCCCGCGGTGGCGGCCGTTGCCCTTACATCTCTCATTTGGAACGTGACACGGTAT
TAAATAACGGCATATGAAAGCTTAAAAGTCATCAAATACAATCACTGGGTACTTTCGATT
ACCCAAACCAGGCACTTTCCTAAACTCCCCACTTCTTTACTTCTGCGGTCTCCTTTCTT
T
TATTCCCCCGCGTACCTGCCC
G
Sequence 145
ACTCCCCGCGGTGGCGGCCGAGGTACCGAGCTCCNGGCTGTGGAATGAGACCGTGGAGCT
TTTTCGTGCTAAGATGCCGTTACGGAAACATCGCTGTCGTTTCAAGAGCTATGAGCATTG
TTTCACA
Sequence 146
CTCCCCGCGGTGGCGGCCGTTATGCTTAGCCNGTTTATTCTTTATTTTTTTACTGGAG
TC
ATTGCCAGTGATGGAAACGGTGTTTGCTTCTCTTTCAGTCAAGATCTGCACAAAGTATAG
CATTAGGTGGTATTTATTGTTTATATTATGAGTTCTACATTCATCTTTCCAGCACTCTGA
AGTTATCAGCAAGTTCTCAGTCAGTTCAAGGCATTGGATTCTGCTTGATTTCTTTTTAA
T
TCATTGTTTTTGACCCCTTTGAGAGTTTTAATAGAGAGGAGTCTGGAAGGCAGAGATCTC
CACCACCTAACCGTGAGAAATTTGGAACTAAGGACTTGCACTGGTCCCCAAGTTAACAGG
GGATATACTTCCTGCATTTTCTCTGNTCTTTCTTGCC
Sequence 147
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCAAGGTGGGCATTTTTTTAAAAA
ACCCATGGAAATAAATGCTACTTCTTGTTAGTGTTGTTTGAAAATAAACAAAGAAAATGC
AAACAAAACAAAAACCATGGTCCATTCAAGCTCAAGAGTATTTAACCAATGCTCTGTTGC
CTCTTAAAGGATTGGTAGCTATTTCCCCATCTACAAATACATGACAATTAACTAAGCCCA
ATTCTTTAAAACTATCTGGAATTAGGTCAAAATTATCTAATTTTTTTTCTGATTTAATTAT
GGATTACCGTAATCCAATAGTTGGCAACATTATAAAACCCTAACTTTACCTCATTGGTT
T
GGCTATACCAAGGTCTCATGGACTCTTGGACATAACCACCATTCTTTCCTNCCAACACCC
CGGNGTACTTCAGAGTAAAACCCGGGAGCCTTCATGATAACCATGAAGGCCCGGAAGCTT
CTGGCTTCCAAGGCTTTCTNTNGGCCTNACCTTCCGGTGGTTCCTTTTCT
Sequence 148
GGGTGGCGGCCGAGGTACCTNTGTGCGCGGTGGNCGAAAAAGCACCTGGGTCGGGTGCAG
ACTGCGGAGCNGGGCCCTACCGTGTGCGCAGAAAGAGGAGGCGCTGGACTTATCCTACCT
TAAGTTGAAGCAGACCAGCAATTGTTGTGACCTACAATCTCCACACCCATCTTTACTCTG
AGCCAAGGAAGTGTCTGTTCTTGTGCTGAGTTTNAGGGGCCTTCAGCTNGNGGGAAATCC
CNAAGA
Sequence 149

Table 1

AGCTCCCCGCGGTGGCGGCCGAGGTACCTTCCCCTGAGGAGCCCCCTTCAGAGGGGTGAA
GAGCAGTATCTTCAGAGGCCATCCAAGTTTTAGCATAACAAGGAGGGAAAGAGAATGCAG
AGAAGAGGCTGGTGATAGACAAGTTTCATGTTCACAACTTGAATTGCAGAGGTCAAGAGT
TTAAAGAGTTTGGGATGGAAAGAAATCAAGAATTGGGCT
Sequence 150
CNCCGCGGTGGCGGCCGCTGTGAAACAATGCTCATTGCTCTTGAAACGACAGCGATGTTT
CCGTAACGGCATCTTAGCACGAAAAAGCTCCACGGTCTCATTCCACAGCCTGGTAGCTCG
GTACCTCGGCCGCTCTAGAACTAGT
Sequence 151
CCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTGTTTTTGTTT
T
TTTCTGTCCCCTCTGAGCCATGGAAGATACTGGAGTTAACAAAAATTTTATAAACTAAAG
AAAGCAACTTTATAATCTAAAAGAAAGCAACTTTCCCTCCTGTCTTTTGAATTCTTATTC
CTGAAAGAATGGATAATGAATCAGGAGATGAGCAAAAACGTATCTTTTACAAAGCTCTAG
TCTTCCAAAAGCCTCTAAACTCAAACGAAACCTTTTTAAAGTAGTTTTGTAAAAGCTCA
A
GGTATGCCATTTCCAGAAAGTTGCAGATGAGCACCATTGGGCATTACCCAAATTCTGTCA
CACATTGAGCAATGAAATTCAGGGAATTGGGACAATGACCTCTTGGGCATATGAAAGAAT
TAAAAGAGGGCTAGGGCTTAGGGAGGGGGGATCTAATCGGGAGGGGATGTTCTGTCCCNA
GCCCTTCCTTCCTTTCT
Sequence 152
TNCCGCGGTGGCGGCCGAGGTACNCCTAAAAAAGTACTGCAGCAGAGAAGAAAACATTGG
ACAAAGAAGAAAGGCGACAGAAGGCTAGAGAGAGGCAGCAGAAATTGCTTGCGGAGTTTG
CTTCACGACAGAAAGGCTTTATGGAAACTGCAATGGATGTTGATTCTCCTGAGAATGATA
TTCCTATGGAGATCACCACGGCAGAACCACAGGTTTCCGAGGCAGTATATGACTGTGTTA
TTTGTGGACAGAGTGGCCCCTCCTCTGAAGATCGACCTACTGGATTAGTTGTACCTGCCC
G
Sequence 153
GCGGTGGCGGCCGAGGTACACCTGCAACTGTGCGAATGGTCCTGTTGCCTCCTGCATTTT
GGCCTCTGTTCTATAAAGGAAGAGTAAAGATGGAGCTCCTCCTGCCTCCATCACGAAAGC
ACATATCATCTGTCCCTTTGGATTTTACTTCCAGGACGCGTGTCGTCCCCAGCGTGTG
TT
GCCTTATGGTGCCGGCAGAGCCTCAGCTATCTGCCTGGGAAGTCGGATGTCCTTGGAGAG
AATTTGGAATGCAGATAATTTTTCTTATTTCTTGAGAGCTTACTTTAATCAGCATGACA
C
TACCTAAACACTGAAGATGGCCTTATATTAGTAAGATTTGCACAAAATTAAGTATACCT
A
TGCAAACTATTACTTTGGTTTTTAGGAGTTTGATCAGATGAAGAAGTNATGGTATCACA
T
ATATATGTAAGAAGGCCAACCCATCATTATTTTTTGNAAGTGNTTTTTATTAAAAACC
Sequence 154
CNCCGCGGTGGCGTNCGGCCCCCGCCTTTTCTGCGGCTTTCAGCTGCGCGTTTCAGGTCG
TCAATGAGGTCGTCGGCATCTTCGAGACCGATGGACAGGCGGATCGTGCCCTGGCTGATG
CCTGCGCCCGCCAGCGCTTCGTCGCTCATGCGGAAATGCTGTGGTGCTGGCCGGGTGGAT
CACCAGGCTGCGGCAATCGCCCACGTTGGCCAGGTGGCTGAAGACCTTGAGGGTTTCAAT
GAACTTCTTGCCCTGCTCGCGGTTGCCCTTGAGGTCAAAGCT
Sequence 155
CGCGGTGGCGGCGCCCGGGCNGGTTATAAAAACGAACATGTATAAACGCTTACGCAAACC
CTTTTTAATGTTCTGAAGTCAGTCTTTGTAAGTGAAATCGCTGGAGACTAGAAAGTATG
A
AATGGCAGTCTACCTGGGCAACCTACAAAAAATTTAGCTTGAAAAGACTTCAGTCTCCGC

Table 1

TCCCCTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAGAACTGGAAAATTATTTA
GGAAAGTTTGTTAACTACTCTTTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAG
AACTGGAAAATTATTTGGGAAAGTTTATTAAC
Sequence 156
CTGGCGGCCGCCCGNNCTGGTNCTTNCATCTNGGCTNCCTATANGCTNTCTTTTTTACAG
ACGGCCATGAAATGCAATCCAGCTGAAGTATTATCATCTTGTAGCATTTCAAAAGGAACC
GTCGAAGTCATCCAAAGGATGGGAACCACAATGTTCTTGTTGTTCCTTGGGTTTCTTA
AT
GATTTCTGAATCATCATTATTAATTATGGAATTCTCTGGTCGAAAAGTCACATTTGGTT
T
TCTCCTCAGTTTCTCACATCTTTTTTCTTGCAGCTCTTTCTCAGCTCTTCTTCCTTGCCT
TTTTTTACTGGCCTTTCCTTGTCTTACTTCAGGTGGTTCTATTTTGACCTTTAAGAAGG
T
TGAAGGGTGGTNCAAGCATCACCTTGGTTCNAATAAAATTAATGGTGTTAGGTTTCTGGT
GGCCTTNGTTTAAAACGCAAATGGGGGTTTTTNANGGGGGGANAAGGTTGGGGT
Sequence 157
CCGCGGTGGCGGCCGAGAAATGTCGCCAAACTGCCGTCTTCCCTCCTCGGCCGCTGCGAC
AAACACCCCACAAAATGGCGGCATGCGCCGTCGCCCTAGAATCCCCCGAGTCGCCTCTCC
CCGCGTACCT
Sequence 158
CCCAGGGCCCAGCTACTCGAAGAACAGCCAATGGATTGGAACGTCCTAGGACAGATGCCA
CGGCTTTGACCCAGGCTGGGGGTGCACAGGATCTCACTGGNGNTAGTTGGTCGGATGGGA
AAGCCCCATGGGTCCACCAGGATGAGGTGTTTAACTNTATCAGGGNACCTTGCCCGCTCT
AGAA
Sequence 159
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACAGGACCAATGCTGCCCATCCCATGGAAT
TTACAAACATTCTACAGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGG
AGAGGCTGTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTACA
CCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCAT
ATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCA
A
TAGTCCCACAGATCGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTGCTGGGC
TCGACACACCTCCTGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGC
CAGGTAACAGGTTTCGAACAAACAAGAAGGCC
Sequence 160
TGGCGGCCGCCCGGGCAGGTACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAA
CATTCTACAGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCT
GTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTACACCGCCGA
CCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCATATGACTT
TGATATTCGTGTGCCTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCAATAGTC
CC
ACAGATCGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTGCTGGGCTCGACAC
ACCTCCTGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAA
CAGGTTTCGAACAAACAAGAAGGCCAAAA
Sequence 161
CGAGGTACCATCCTATTAATACTAACTTCTGCTTCTACATACTGTAGACCTTTCTGGAT
G
ATAGAAATCAATGCAGCGGGTGGGACGAGGGCACCATTTATATTGGACTGACTGATATGG
CTTTCTATACCAAAGGTAAATGCTGAATGAGAAAATCCTGACTCTTGCAAGTATCTATA
T
ACCAAGAAGTTGACCTCATCACTGCTTATACTCATCTTTATTCCCACTTAAACCATGAG

Table 1

G
TCCCAACACAGGATATAACCCATTGGGCAGTGCATTGATGTGGGGGATGTGCAACTGANT
ATNCCGGTCACCCGCCAATCACAAGTTTGCTGGTGTTGATGCTGGAAACGGTGGCCTCCA
ACGCCGCTCCCCCCTCCCGGGAA
Sequence 162
GGCGGCCGAGGTACCTGGCCTGCTGGCATAGTTCTTTGACCCGTTCATATTTGGGCAAGT
GATTTGACTGTTGGATATTCTTGCTGGATTCCTCCTTCTTACGTAGAAATTTGCCTCTT
T
CCACTAGGAATGTATCACGCCAAATTTTGGCCTTCTTGTTTGTTCGAAACCTGTTACCT
G
GCTTTTCTGGGTCCAGAAGTTTGAGGACAGACTTGCCGTCCACATCAGGAGGTGTGTCGA
GCCCAGCAATATCCAGGATCGTGGGGGCCAAGTCAATGTTGAGAACGATCTGTGGGACTA
TTGATCCTGGTTCTACACTTGGACCACGAATAAAAAAAGGCACACGAATATCAAAGTCAT
ATGGCATGGATTTCCCCTTGACCAGTCCAAACTGCCCAATATGGTAACCATGGTCGGCGG
TGTA
Sequence 163
GGGGCCNCGCGTCCGGGTGGCTCTATGTAGTTCTAATTTGCATTTCTCTAATGACTAACG
ATGTTAAACATATTTTTATGTACTTGTTTCATGTACTTGTTGATATGTCTATTCAATTCC
TTTCACCATTTTTATGGAGCTGTTTTTTATTATTGAGTTGTAGGATTTCTTTATATATG
CTGCATACCAGGCCTTTGTTATATACATGCTTTGCAATGTACATTGTCTTAAAATCTGT
G
GCTTGCCTGTTCAATTCATTAGTGGTGTTTTGTTAAGCAGTTTTTAATTTTGATGAAGT
G
TAACTTATTCATTTTTTATTATGGTTATTGCTTTATGTTTCAGGTCCCAAATTTTGCCTT
CTCACAAATCACAAACATTATCCTATGTTTTCCTTCAAAAATTATATGGTTTTATGTATT
TTCAATCTCAAAATATTCTCTAATTTTTTTGCTGATTTATTTCTAAAGAAATTTGAGGGA
TTTGCTATAATGG
Sequence 164
CCCCGCGGTGGCGGCCGCCCGGGGCAGGTTATTTAATTTCTTAGTGTCTCAATTTCCTCC
TCTATAAAACAGAGATAATAGTATTTAGCCCAGAGGGTTGTGGTGAAGTGTGAATCATTT
CTCCATGTAAAACACATAGGACAGGCTGGGCATGGTGGTGGGCACCTGTAATCCCAGTTA
CTTGAGAGGCTGAGACAGGAGAATCGCTTGAACCCGGGAGACGGAGGTTGCAGTGAGCCG
AGATAGTGCCACTGCACTCCAGCCTGAGTGACAAGAGTGAGAGTCCATCTCAAAAAAAAA
AAAAAAAAAAAAAAGTACCT
Sequence 165
NCCTGGCATCAGCNATTAGNAATCAACCTGTTAATCCAAGGTCTTTAGAAAAACTTGAAA
TTATTCCTGCAAGCCAATTTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAGAAGG
GTGAGGAAAGAAGATGTCTGAATCCAAGAATCCGAAGGGCCGTCAAGAAATTTTACCTGA
AAGGCAGGTTAGGCAAGGGAAAAGGGGTCTAAAAAGATCTCCCTTAAAAACCAGGAGGGG
GGAAGCCAAAAATCCGATGCCAAGTGCTTTCCCAAAGGGGATTGGGGACCACCACCAAGA
GGGCCTGGCCCTTCTTCCCATCACTTTCCCCTTACCATTGGGGAGGTAATTATTGTCAAA
GGCCATTAAATTTGGTTTCTTTAAGTTTTTGGCAGGTTTACCGCCTTAAAAAAGGGTG
GA
CCCAAATGGATTGGGTCCACCCAAAATCNAGGCTTGCTTACTTACTTCCCTGGTAAGGGA
A
Sequence 166
GTGGCGNCCGTNCGGNCAGGTACTTGCTCAGCCTTTCCAGGCCCCTNTGATGAGCTCTCT
AATCAGCAGGACCAAGGTGTGAAGTGGGAATGAACATGGATCCATCCCATTGGATGGAGA
AGAAAGGTGGACAGCCTGTTCGTCTCTCATGTCAGCCTAGGGCTGGGAACAGTTTGTGAG
GACTTATCTGTTGTACCT

Table 1

Sequence 167
GCNGGCCGCCCGGGCAGGTACGCGGGAATGGGCACNNTGNAGCGCAAGTAGGTCTACAAG
ACGCTACTTCCCCTATCATAGAAGAGCTTATCACCTTTCATGATCACGCCCTNGGGNATC
ATTNTCCTTATCTGCTTCCTAGTCCTGGTATGCCCTTTTCCTNAACCACTCACAAACCA
A
AAACTTAACTAAATAACTTAACAATCCTNAGAACGCCTCAAGGNAAANTAAGAAAACCCG
TCNTGAAACTTATTCCTGCCCCGCCCATCATCCCTTAGNTCCCTCAATTCTGGNCCCT
CN
CCAANCCCCTACCGCCAATCCCTTTTTACAATAAAACAGGACCGAAGGGTCCAAACNGAA
TCCCCTCCCCNTTACCCATTCAAAAAATCAAAATTNGGCCCACCCAAATTGGANNACCTT
GAAACCCCTAACCGAAGTTACCCTTCGGGCCCGCTTCTTAAGAAACTAAGGNGGGAATCC
CCCCCNGGGGCCTGGNAANGGAAATTTCGGATAATCAAAGCCTTAATTCCGAATANCCCG
GTCCGAACCCTTCGGAGGGGGGGGGGGCCCCCGGGGTACCCCCANGCTTTTTGGGTTTCC
CTTTTTA
A
Sequence 168
ATNTTCAGGAGACGCTCNGTAGCCCTCGCGCTNTATCCTNCGGNACAGTTCTGCGGAAGA
AGTGGCTCACGCCTTCCAGAGCCACATCATCGCGGNCGAAAGNGAAGCCCAGAGAGAGGT
AGGTGTAGGAGGCCTGCAGGTACCTCGGCCGCTCTAAGAACAANGNGGATCCCCCCGGGC
TGCAAGGGAATTCCCTTANCAAAGCANTANTNAAACCCGTCCGNCCNNNCAGGGGGGGGG
CCCCGNTACCCNAANCTTTTGNNNCCCNTNATAGAGAAGGGNGAAAAAATNANGCCCNCC
TNGGGGCAGNAAAAAAATGGGACAATAAAGCTNTTNNNCNNGGGGGNTNAAAAANTTGT
TAAATCCCCCNACCANNAATTTTCNCNAAACAAAAAAATAAAAAANCNCCGNGGANNGAN
AAAAAAAANNGGNATAAAACACCCCNGGGGGNGGGTCCCCNCAAAGNGGGGGGGGGACCN
CCNCCCNAACAATTAATGTGGGGNGGGNGGANANANAATNGCCCTNNTTTTTNTANNGNG
ANNAAAAANNCTTGGNGCNGNCCCNNACTTCTANNTAAAAAAAAANACCCCCCCNCCCCN
CCCGGGGGNNAGNGNGGNNNGNTTNACTTTANNNGGGCNANNTTTTTCCNCCTTATNNAA
AAAAAAAAAAATACNNGGCACNNGGGAAATTTNGGGGGGGGGGG
Sequence 169
TTTTGAAGCCCNCTTNCCGCGGNGGCGGCCGCCCGGGCAGGTACTTCCACTATTATTGAA
TGTATTCTGTATTATAATTGTATATTTGATTGCCTATCTCCCCTCAACTGCATTATACAT
TTTCATGGGTGAGCCAATGTCTTTTTCACTCTATTTCAGTGCCCTGCACATTTTCTGGC
A
CATAGTAAGCATCCCATGAGTATCTGATGAATAAATGTATTTCCAAATTCAGGTTCAGT
A
TCCTTAATCTGAAAATACAAAATCCGAAATGCCATAAAATTCAAAGCTTTTTGAGGACTG
ACCTCGTGCTCAAAGGAAATGCTCATTGGAGCATTTTGGACTTCAGATTTTCAGATTAGG
GATATTCAACCCGTAAGAATAGTGCCAATATTCCAAAATTCAAAAAAGTCTGAAATCCAA
AACACTTCTGGTCCCAGGTATTTTGGATAAGGGATACTCAACCTGTACCGTAAAATACAT
GCATACTTTCGATAGCACATGTGAAGGTATCTCTCTAAAATTGACCTCATTGGTTTCGT
T
CTCAAGCAAACTGACCTGGGGCCACTCAACATGGCTTTTATCGNGCCTGATGTTAATGCA
TGTCTCTTTTTACAATA
Sequence 170
AAGTCTACATTTTATGTAGTGGTTAATGTTTGCTGTTCATTAGGATGGTTTCACAGTTA
C
CATACAAATGTAGAAGCAACAGGTCCAAAAAGTAGGGCATGATTTTCTCCATGTAATCCA
GGGAGAAAACAAGCCATGACCATTGTTGGTTGGGAGACTGAAGGTGATTGAAGGTTCACC
ATCATCCTCACCAACTTTTGGGCCATAATTCACCCAACCCTTTGGTGGAGCCTGAAAAAA
ATCTGGGCAGAATGTAGGACTTCTTTATTTTGTTTAAAGGGGTAACACAGAGTGCCCTTA
TGAAGGAGTTGGAGATCCTGCAAGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAA

Table 1

ACAATGAGGAACATTTCATTTGACCCAACATCCTTTAGGAGCATAAATGTTGACACTAAG
TTATCCCTTTTGTGCTAAAATGGACAGTATTGGCAAAATGATCCACAACTTCTTATTCT
C
TGGCTCTATATTGCTTTGGAAACACTT
Sequence 171
GGCGGCCGCCGGAGCGGCGCGGAGCATGATGGAAGTCGTAGTAGGAAATGGCGTCGTGGC
ATTGAGGGGGCATCCCTCCTAGAACCTCCAGGAAAAGCTCGCGGAAGACGAGGTTCTGCG
GAGAGAGAGGCTCCAAGCAGTCTGGGAAGTGTAGTCCAGTTGGCTTAGCAGTAGTTTCGT
TGGGGGGGAGCCCGAGGTTCCGGGAAGGGGCTAGGCCGGCTTGAAAAGAGATTATGACTG
TACCTCGGCCGTCGAGCGGCCGCCCGGGCAGGTACAACTTTTATACAACTCAGGAGATTA
AAAAAAAATCTCCACAAGAAGAAGCAACTCANCAGGCCCTGGCATTAAAACATTTCCCAG
AATAAACAGATATGCATTGCATTAAAGGTAATTTTCAAATATTTAAGTTACACCAAGATT
TCCCTCCAATATGTGCCTTTCTCAAACCAATGCAACTAATTCATTGCTAATACTGGGG
CA
TGAATTTTTTGGCAAATGTTTATGGTTTTACTTTCTTCATTAATCAAAAAANT
Sequence 172
CGGGTACANATTTAAGGTAGATGGACTCAGGGTAAGGATAGCTACAGCTGTGTGGGGCTG
AAGGTCTGTGGCACTGAGCTACTGGGGAAGGAGGGCTCTGTTTTCATNGTGACACACTGA
GTTAATAAAGCACTTACTGAGGGAGCCAGAGCCCAAACTCTAAATGTGCTGTAGAAAAAG
GGCCAAGTCATTGACTGCACCACTCCTTCAGCCAGAGGTAGAAAGGATTTACTCTTCAGC
CATCTGGTAGAGCCCCAAGAACAAGTTACATGTGGACAAAGGGAGGGAGAGGTATCATGG
TGATTAATAAATNCAAACAAAGCTGAATGATAAGNACCCCAGGATGGAATACAGTCTGAG
AAAGGCCTGGGCAAAG
Sequence 173
GGGGCCGGGCCCCCGTAGGGGTTACCCNCCGNGGGTTATTAAGGGGTTGGNAAAAAAAAA
AAACCACCTGGCNCANTTTCCAACCCAAANGGTNCAAANGGGGAAACCCCCCAANGGGGG
CCCAGGCCTTGGGGAAAAGTTGTTTGGGGNAAGCCCACCAAACCAATTGGNCTTGGTNGG
GGAGGCCAACCCACCAATGGNCCTTGTTGNGTAAGAAATNTGGGCNAGGGNGGTTGGTTC
CTTGNAAAGGGTATTTGGGTGGTTNCGTTAANTTTGGGGAAAAAGGAAATTTTTTTAAGG
GTTATTTGTTAAGAAAGCCAAAGGGTTTTGGAAAAAAATGGGGAATTTGGGAAGAACCTG
GCCAATTGGGGTTGGGGCCCATTAAAANAATTGGGGAAGGNAAAAAATTTTGGCCCCTTG
GGTNAAGNCCANTCCTTAAGGTTCCTTAACCTTTTGGAAAANGGGGAAAAGGTTGGGGGA
AGGNAACCCANTTAAAAGGGGGNANGGGANGGACCCAAAAAAAAAAACCCAGGGGGGTNT
TTTGGTTNGGNCCCCCAATTAAAAAAAAGGGTTAATTTTTTTTTTTTTTCCAAAAAAAG
G
GAACCCANCCCCCCAAAAAGGGAAATTGGGTTGGGGGGTTNAAAAAAAATTGGGGAAAAA
AAAAAATTTTTAANTTTTTAAGGGTTTTTCCAAACCTTTTTTCCCCCCTTGGCCTTGGG
C
CCCAANTTGGGAAAAAAANCCTTTTTTTGGGCCCCNTTTTTAAAAAGGNAAAAAGGGGGG
TNGGGCCCTTGGGGGNAANTTTTTNCCCCCAAAAAGGGGGGTTTTTTTTGGGTTNAAAAA
AAGGGGGGNCCAANTTTCNTTTCCGGGGGTTTAAAAAAAGGGAACCCTTGGGCTTTTTTT
TT
Sequence 174
GGCGAGCGGCCGCCGGGCAGGTACCCTAGGGTGTTGTTTAAAGGACTTGATAACCAGCTT
GAAGAGGTTCCTACTGACCAGAAATGGAATGAAATTTAAGCATCAATAAGGGTAATAACT
GCAAGAGACTGACATCCACTATGGTTTAAATCCATGAGGTCACAATGATACTTAATTTT
T
CATTATTCTGAAAACCAGTAAATAAAGGCTAAGATTCAACAAGCATTTATCCAGCCTTTC
CTCAATGAAATATATCNTAAGAGAACCGAATAGTTAACATAGAGACATGGCCGGGCAAGG
TGGCTCTCGCCTGTAATCCCAACACTTTGGGAGGCCCGAGGTGGGAAGATTGCTTGAGCC

Table 1

CAAGAGTTCTAGACCAGNCTGGACAACATGGTGAAACCCTGTGCCTACAAAAAAAAAAAA
AACAAAAAAAAAGGTCCCC
Sequence 175
CAGGACCAAAACCTGGGGATTAAGCTAAGAAGTCTGGTGGAGAGACTCTGTGGACGTAAA
GAAGGGAATGAACACAGAGAAACTTTCAGCCAGATTCCTGATNGTCACCTGAACAAGAAA
AGTCAAACTGGAGTGAAACCATGCAAATGCAGCGTGTGTGGGAAAGTCTTCCTCCCGTCA
TTCATTCCTGGACAGGCACATGAGAGCTTCATGCTGGACACAAACCATCTGAGTGTTGGT
GGGGAATGGANAGAGGACNCCCCCCGNAAACAGAAACCAACCATGGGGAAAAGCCTTCAT
TTCCCCCAGTAGTNGGTGCACCGGCTCACCAGTTAACNACCAACTTNGAAAGGAGACCTT
TATGAATTGCAAGGGTGGTGCGGGGAAAGCCCTTTAAATTCTCCCA
Sequence 176
NCNGGNCAGGACGCGGGGGCCGNGAAGAGCTTTGCATTGTGGGAAGTCTTTCCTTTCTCG
TTCCCCGGCCATCTTAGCGGCTGCTGTTGGTTGGGGGCCGTCCCAGCTCCTAAGGCAGGA
AGATGGCGGCCGGANAGAAGACNAAAAAGTCNCTCGGAGTCGATCAACTCTAGGCTCCAA
CTCGNNATGAAAAGTGGGAAGTNCCT
Sequence 177
CCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTATGAATNATTNATTTTCT
T
TNTCAGAAAAGGATGCGCCTCCACTTAGCAAGGCTGGGCAGGATGTGGTCTCTGCATCTC
CCCACAGACAGGGGTGGTTCTAGA
Sequence 178
GGTGGCGGCCGCCCGGGCAGGTACCAAACCATTTTCACTAGTTCAGGATAGGAATATTCA
TCAGATTGTCTCTGTAAAAGTGAATCACAAAAATTCCACCTGTGTAGGTGTGGGACTGGA
CAGCTGAGTGACAGGGCCCTGGGAAGAACAGAAACCACTTTTCCTCTTTCCTCTGAAATA
TCAGAAGTTAAAAATCTACTCTGAGTTATATGTGCATCAATTTTAGACATATTGCTGAT
T
TTATTATGAAAATGAAGTGCTAAAGACAAAGGATATTTCCATTCCTCTGGACAGGCAGCC
ACAGACCAGCACTGCTTGACCCATGTGTATACACATGTGTGCTTTGTACCT
Sequence 179
GGTACTCACAGTCACGCAAATTCACAGTCTGCGTGCACGGCTCTCCATTCTTCTTCTTGG
CTTTACAGGTTCCCAGGTCAAGAGCTTCACCCATAATTAAGACCTTCTGAGGATGATCGA
TAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGGATCC
CTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAGAACA
AGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTC
CACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCACCCAATCT
A
TTTCTTCCAGCTTCTCTCTGGCCATCTTTTCTTGATCTGAGACAGTCTGATCAGTTTTC
G
GCCGCTCTAGAACTAG
Sequence 180
GGCGGCCGAAAACTGATCAGACTGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAGCTG
GAAGAAATACGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTACGCCACAGAGTGT
GAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGACCTGACACAATG
TGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGACGGAGCAGGGGAC
TGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAGGAGGTGTG
TTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGACCTGGGAAC
CTGTAAAGCCAAGAAGAAGAAT
Sequence 181
GTGGCGGCCGAGGTACTACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTG
GCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCT

Table 1

CCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATG
CTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAA
T
GTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTT
Sequence 182
GCGGCCGAGGTACATGGATACGTTCTCTTCTGGGGGCGGTCTCCAGTCCTTTCTCATGAG
GGAGCACACTCCTCTGCCTCATTGCAGTGGCCTCAGGGATATGGAATTAAGATCCACCTG
GTGTGATGAATAAACCCAGACTCTCAGCAACGCAGGAAAAAAAACAAAAACTGGCTGGCG
ATCTGGAGTAAAGGATCCTCACATCCACGTGAACCAGGAAACTCTGTGCCCAAATCGACG
AAAAAAAAACACTGGGAGAGCCGAACTAAAAGTCTTTTAGCACGGGTACCTGCCCG
Sequence 183
TCCCGCGGTGGCGGCCCGAGGTACGCGGGGAGCGGAAAGGGAGACTGTGGGGAACTAGGA
GCAACAGCAGGCATGGACCAAAGCAGTGAAGGATGTATGAAAAAGATTAGCAGTGTGAAT
CTTGACAAACTTATAAATGACTTCTCACAGATAGAAAAGAAAATGGTAGAAACCAATGGA
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GCAAAGGAGGTCTCCATTAAAGAAGAATGTGCTACTCTTCATAATATAATAAAAGGGCTA
CAACAGACCATTGAATATCAACAGAATTTGAAAGGTGAAAATGAACAACTAAAAATAAGT
GCTGATCTTATAAAAGAGAAGTTAAAGTCTCATGAACAGGAATATAAGAATAATATTGCC
AAACTTGTAAGTGAAATGAAAATCAAAGAGGAGGGATATAAGAAAGAAATAAGCCAACTT
TATCAGGGACATGCAGAGAAAAGTTGAATTAAATGAAGAAAAGCCCAAAGAACTTATANA
GAAAAAGGNGATGGGAANTTCANAGGTTAATGCCAAGCTTAGAAGTCAAAAAAAAAAAAA
AAT
Sequence 184
CCGCGGTGGCGGCCGAGGTACATGGATACGTTCTCTTCTGGGGGCGGTCTCCAGTCCTTT
CTCATGAGGGAGCACACTCCTCTGCCTCATTGCAGTGGCCTCAGGGATATGGAATTAAGA
TCCACCTGGTGTGATGAATAAACCCAGACTCTCAGCAACGCAGGAAAAAAAACAAAAACT
GGCTGGCGATCTGGAGTAAAGGATCCTCACATCCACGTGAACCAGGAAACTCTGTGCCCA
AATCGACGAAAAAAAAACACTGGGAGAGCCGAACTAAAAGTCTTTTAGCACGGGTACCTG
CCCG
Sequence 185
CCGGNCGCCCGGCAGGTACGCGGGGGTGTCCGGCGATGGGCACGGGCATTTCTTCGTTTA
TAGCTGTCTGTTTGCATTCTGATTGGGAACACTGGGATCATTTTCATCATGCCGACAGTG
GTGGTAATGGATGTATCCCTTTCCATGACCCGACCTGTGTCTATTGAGGGGTCCGAGGAA
TACCAGCGAAGCACTAAGTAATATGGATGATTATGACAAAACCTGCTTGGAGTCTGCATT
AGTTGGTGTTTGCAATATCGTTCAGCAAGAATGGGGTGGTGCAATTCTTGCCAGGTTGTC
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AAAATTAACNAAAGTGNGAGCACNNGGTTTCCCTACCTTTTCNTTTCCCATCAANTNT
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CNGTTTGTCNTTTCCNCTTTGGGGNGNGGCCATTTTTATNTTGGGGGGNCCCCTTGGGGA
ANAANAAACCCCCCNCCCCTTTANAAAANNGGNCCCCCCCCCGNGNGGGGGGNAATTAAA
AAAAAATTTTNCCCCCCCCCCCCCCGGG
Sequence 186
TCCCGCGGTGGCGGCCGAGGTACTCACACGTCACCGCAAATTCACAGTCTGCGTGCACGG
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A
GACCTTCTGAGGATGATCGATAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCAT
GGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTG
AACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTT
CCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAA

Table 1

C
CCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCTTGATCTG
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Sequence 187
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CTTTGCTTCAGTGCCCTGATCTCTGAACTAACAAACCAGAAAGAAGTGGCAGCATGGACT
TATCATTACAGCACAAAAGCATACTCATGGAATATTTCCCGTAAATCTGCAGAATCGCTA
CACAGACTTAGTGGCCATCCAGAATAAAAATGAAATTGATTACCTCAATAAGGTCCTACC
CTACTACAGCTCCTACTACTGGATTGGGATCCGAAAGAACAATAAGACATGGACATGGGT
GGGAACCAAAAAGGCTCTCACCAACGAGGCTGAGAACTGGGCTGATAATGAACCTAAC
Sequence 188
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TGTGCCATTCCTTGTCAATTTCATGCTGCCTACAGCAACAGCATAATACTGCAAACAGCC
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AGGTCCTCTGTAACAAGCCGTAGAGGCCCAGAAATGTGGTGACAGCGAGACACATTTCTT
AACTCTTACACTTGTTGAAATGAGTAGAAGGNGACATTTGGTTTGGAAATCCCTCCCC
A
Sequence 189
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TCCTCAGTGGAAATATCAACAAGACTCAGCCCACCTGCACCCAGGTGATTAAAAAGCTTT
ATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACATGGACGCGCGCGACATTTGGTGC
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TCCGTGAGAAAGATCCACCTACGACCTCTGGTCCTCAGACCAACCAGCCCAAGGAACATC
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ACTTNAATGTNAAANCCAAAACT
Sequence 190
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AGGAAAGGGGAAAAGTTTGGTCGAGGAGTGATAGCGGGACTCGTTGACATTGGGGAAACT
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GAAGGACAGTTATGAAACGAGTCAGCTGGATGACCAGAGTGCTGAAACCCACAGCCACAA
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TGATAGTCAGGAACTTTCC
Sequence 191
CGCCGGGCAGGTACTCCCTGGAAAGTCCAGCTGAGAAAGCGATCCTGCCCTCTGCTCCTC
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Table 1

TCATTCCCTGCTGGGCTCACTCACCGGCTTCGTATAAGGTCCTTTTTGAGGTTTATTA
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GGAACCTTGGTCATCTTAAAAATCCTTCAGGTTTTAGCCTGTGCCCCCAAGACAAGGATT
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Sequence 192
CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTC
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GGCTTGAAATACAGCTGAAATAACTGAATTTTCTACTTGAAACGTGTGTGCCTCTCCACT
GNGGGGCCAAGGCCCTGGAAATGTAAAGGGCCAATCTTTGTTACAGAGGGGTTCATTGCA
GTGAAGGGCGGGTTCTGCAAAGACAAACAGGTCTCACAGATAGTTGCCCCCGCGTACCT
Sequence 193
NGGCGGCCGAGGTACGCGGGGGGCTGNAGTAGGCTTCGTCTTCGGNTTTTCTCTTCCTTC
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Sequence 194
CGGCCGCAGCGGCAGCTACAACAACCGCGTCGCTCTCCGCTCAATTTCCAAGAGCCAGCT
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Sequence 195
CTTCCCGCGGTGGCGGCCGGTGTGCTGTGCTCAGCTGCCTTCCAAAGGAGGAACAGATCG
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Sequence 196
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TGATGAATCACAATCACCATGGTCGCCGCCTGAGCGCCAACCCCTACCCCGTCGCCTCAT
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Sequence 197
NCGAGGTACCTGCCTNACAGNGCAGGGCGGTATGCCGCCAAACGCTTCCGCAAAGCTCAG
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Sequence 198
TTGCTCAGCCTTTCCAGGCCCCTCTGATGAGCTCTCTAATCAGCAGGACCAAGGTGTGAA
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Sequence 199
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TCGTCTCTCATGTCAGCCTAGGGCTGGGAACAGTTTGTGAGGACTTATCTGTTGTACC
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Sequence 200
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GCCACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGA
CCTGACACAATGTGTGTCCTTGTTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGAC

Table 1

GGAGCAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTC
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Sequence 201
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GCTGCTGACCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCA
NAANCTGATGAGCAACTTGGACAGCAACAGGGACAACGAAGGTGGACTTTCCAAGAAGTA
CCTGCCCGGGCGGCCCGCTCTAGAACTAGT
Sequence 202
TGGGGCACAGAGAGGGTTTCAGAGGATCCTTGNGAAACACTAGTTAAAAGATGACCGAGT
GGGGAGAAGTGCGAGGAAAGAAGGAAATTAGTCTGACTGGCTTTCTGTCCTGCACCATTG
ATTCAATGGAGACTGGGCGGGAGGAAATGGAAGACTAGGGTTGGAGATGGGATGGGTGGG
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TTANATTCTTTAGGGAAGGATTCAAAAGTTCCCTCCAAAACCCTAATTTTTGGATGGTT
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TCTTAAGAACCTAGGTNGGGATCCCCCCGGGGGCCTGCAAGGGAATTTCCGATATTCAAA
GCCTTTATCGGNTACCCGGTCCGACCCTNCGAGGGGGGGGGGCCCCGGGTACCCC
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Sequence 203
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CGGCTGCTGTTGGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAGA
AGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGGA
AGTACC
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Sequence 204
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CACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGTGACC
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AGCAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAG
AGGAGGTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTG
ACCTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAGCCGTGCACGCAGACTGTGAA
Sequence 205
CNCCGCGGTGGCGGCCGAAAACTGATCAGACTGTCTCAGATCAAGGAAAAGATGGCCAGA
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CAGGGGACTGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAG
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CTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAGCCGTGCACGCAGACTGTGAATTTG
CGTGACTGTGAGTACCT
Sequence 206
TCNCCGCGGTGGCGGCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTC
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TGAACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGT
TTCCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATAT
A
ACCCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGAT
C

Table 1

TGAGACAGTCTGATCAGTTTT
Sequence 207
TCCCGCGGTGGCGGCCGCCCGGGCAGGTACATGGTTCTTCCTCAGAAAGTGGTTCTTCCT
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CCACTTTTTCTTCTTCCTCTTCTTCAACTGAATAGGGTAAGTGTAAAGGCACAACAAAT
T
AACACTGTATCAGATCTCATTCCTTCCAAAAACGTTTGAGTCCTAGTTTTTTTCTGTCA
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TCTCATCAACTACCCAATGTTTGTTTTGTTTATTTTATAATTGGGAAGGTTCTCCAAGG
C
CTACCACTAACTTTAACGAATGATATAGATAGAGCTCAGAGCAATCTTCTCACGATCATG
AAGTCATGTATAAAAATCAGGATTAAAACAAAGGTCATCTGATCTCCAATCATTATTGGG
AAGGAAAGTCAATTATATTANGAAATGGTTAAGAGCTTGCACTCTGAAGTCAGACGGCCT
GGGTTTAATCTACCTGCTGCACCCTGAAAAATTGGTATTTACCCTT
Sequence 208
CGCGGTGGCGGCCGCCCGGGCCGGTACATGGTTCTTCCTCAGAAAGTGGTTCTTCCTTAA
TGTGTTTCTTTTTACCCCTTTTCTTCTTCTTCTTCACAGATGTTTCTTCTTCTTCTGCCA
CTTTTTCTTCTTCCTCTTCTTCAACTGAATAGGGTNAGTGTAAAGGCACAACAAATTAA
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ACTGTATCAGATCTCATTCCTTCCAAAAACGTTTGAGTCCTAGTTTTTTTCTGTCATTCT
CATCAACTACCCAATGTTTGTTTTGTTTATTTTATAATTGGGAAGGTTCTCCAAGGCCT
A
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TAATCTACCTGCTGCAACCCTGAAAAATTGTATTTACCCTTGGTGAAGCTCCTATCTAT
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AAACTTAAGAATGTCTTATCTTACTGGACTGGTACTGGATTAAAAAGA
Sequence 209
CACCGCGGCGGCGGNCGAGGTACACGACATAGGCACATGTGCAAACACAAAGAAGGTGGG
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CTTTCCCATTCCTCTGAAGTTGCTGGAAGGACATTTCCCAGGAAGAAACAATTCCTCACT
GCCTATAAACTGTAGTCCCAATGTNGGGATAGTCAANNGAACATGAGAATCANAACCAAT
CTGGGCAAATGGGGNATGGCAAGTAATGGGNGAACACGCACTAACAGGNACAGTATGCCC
AACCT
Sequence 210
GGTGGCGGCCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGG
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TCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCAT
ATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCC
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AATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTNCTTTGATCTGAG
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CAAGTCTGATCAAGTTTTCGG
C
Sequence 211
GCGGTGGCGGCCCGAGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGG
GGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAA
CTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCC
ATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACC
C

Table 1

CAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGA
G
ACAAGTCTGATCAGTTTT
Sequence 212
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GCTGGTGGTCCTTGATACCAGATAAGCCCTCAGTGTGAAGCAGCTCTTATTTTTCCTT
GT
CTTGAGATTGCTCTTGGAATGGAAATTAGGCTTTTTTGAAGGTGTCGACCCTTTTTGG
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CATTTCTTCAGCAGTTACTTTTTATTTTTTTTAAAATGTTTTGACACACAAGTCTTNTGG
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AANAAGGAAACCTTTCCCTGGGGGAAAAACAACTTGNAAAAGGAAAAAATTAAAAGGAAG
GGCCCGGGGCCC
Sequence 213
GCGGNGGCGGCCGTTTGAGAAGCCAGCGCTCACCCACCCGGGGTCTCTGTGCATTGACCT
TTGGGTGCTGACTTGGAGAAAAGCACAAACACGACCAGTCCCCCCGCGTACCTCGGNG
Sequence 214
TCCCCGCGGTGGCGGCCGAGGTACATGCCTACAGATAGTCCCAGCTACTCGGGAGGCTGA
GGCAGGAGAATCGCTTGAACCCAAGAGGCGTAAGTTGCAGTGAGCCGAGATCATGGCACT
GCACTCCAGCCTGGGTGACAGAGAGAGACTCCATAAGAAAAAAAGAAAAAAAAGGGGGGC
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GCTCCTTAAGTAAACAGAAGTAATACCTGATTAATTAGAATTCCCAACCCTCATCAAGTG
TGTGCTTATATAGAAGAAACCCAGTAAATGTTTGTTGATTGAAAGATATTAATACTCTT
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CTTGGATGAGAGTGAGGAAAAAGGTATTAAGTATTGGCTTT
Sequence 215
GNGGCGGCCGAGGTACTTTGGAGTCCCCTGGTTTCTCAAGAATTGCCGTTGACTCTTTCT
TTGGCTTCTGCTGGCACGGTAACCAGACTCCCTACAACTGCACTCTTTGTCTTTGTCA
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GAAGCCGCGAGCGTAGAGGTTCCGCGTGCTCTGCCGGACTTGAGCAGGTCACTGGGTCCT
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CGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCTACTCCAAAGAGGATGCA
ACCAAGGGGAAATTTGCCTTTACCACTGAAGATTATGACATGTTTGAAGTGTGTTTTGAG
AGCAAGGGAACAGGGCGGATACCTGACCAACTCGTGATCCTAGACATGAAGCATGGAGTG
GAGGCGAAAAATTACGAAGAGATTGCAAAAGTTGAGAAAGC
Sequence 216
CCGCGGNGGCGGCCGAGGTACTTTGGAGTCCCCTGGTTTCTCAAGAATTGCCGTTGACTC
TTTCTTTGGCTTCTGCTGGCACGGTAACCAGACTCCCTACAACTGCACTCTTTGTCTT
TG
TCATGGAAGCCGCGAGCGTAGAGGTTCCGCGTGCTCTGCCGGACTGTGAGCAGGTCACTG
GGTCCTTTACACTTGTGAATTCGAAGCTTGCCAGATGTATCCTCAATGCATTGCCACT
TC
TGCCCCGGTTGTTCACAGGCTGTCTGGTACCGAGATCTCCGACCAGTCTGGGGGCGCTGG

Table 1

CGGCCTGCGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCTACTCCAAAGA
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TTTTGAGAGCAAGGGAACAGGGCGGATACCTGACCAACTCGTGATCCTAGACATGAAGCA
TGGAGTGGAGGCGAAAAATTACGA
Sequence 217
CCCGCGGTGGCGGCCGAGGTACTATCAAACAACATGATACAATTTAAATGTGTCATAGCA
ACTACTAGTGGTCACCTGAAATCCATTTTCCCCTCCTTCACAGTAAGAGTTTTAGNTG
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TGAGTGGCCACTCATAGAGAGATTGCATTTCTGGCTTCCCTTGCAGCCATAGGTAGCCAT
GGGACAAAGTTCTAACCCAGGGGGGGTCCAATCTTTTGGCTTCCCTGGGACACACTGGAA
GAAGAAGAATTGTCTTGGGCCACACATAAAATACACTGGCATCAAGGATAGCTGATGAGC
AAAAAAAAAAAAAAAAAAAAAAGTACCTGCC
Sequence 218
CCCGCGGTGGCGGCCGAGGTACCATCCTGTTCNACAGAGCCATTGCCTATTCCTAAATTG
AATCCGACTGGGCGTGCCCCTCCTCGGAACACAACAGTAGACCTTAATAGTGGAAACATC
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CT
CGGCTTCTTAGCATTCACATTCCTGCTCTCTTACCCCCAACGTCCACAGAGCTG
Sequence 219
GTTATTGGTGGTGAAGACCCGNAGCAACAGTGGGCATGTCTTCTCGCGGTCGATCGGNTT
CTCTGGCTCCTTNTTAATTTCCTCCTGGGNAACGCGCGACTCCACCGCCATCTTCCTCCT
ACGGCCTGCGAGACGCTCCCCCGCGTACCTCGGCCGCTCTAGAACTAAGTGGGATCCCCC
GGGCT
Sequence 220
GGCGGCCGAGGTACCATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTG
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TAAGGTCAGCAGCACAGTGGCCATGGAAAAAGAAAAACTCTACAGCATATTTCCGAGGAT
CAAGGACAAGTCCAGAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACTTG
TTGATGCAGAATACACCAAAAACCAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGC
CAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAATTTT
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GAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCTGTGTGGCTCACTTGTTTT
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TCCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGNTACAATTTGTAA
Sequence 221
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TTCTTCAATGTGGTTCCAGCCACGCATAGTCATATAGATACTACATATNCAAAGATAAC
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TACTGAAGCTTGTTCACAGAACCAAGCTTTCTCCTGGATAAGCTCTTCTNTCCCCTAC
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CGCACTTCTTGGGNAAGGTATTACCCCAAAATGCTCTTCAGNGGATTTAAAATAAACAAT
TTTTTAAAAANANGGACACTTAACACTCACAAAAAAATGGGGGAAATTTTGCTCGGGCCA
TTGGACNGCGGAAACCAAATTACCGGGTTTAACTTCCAAGNATGGCTTGTCATTTCAAAA
ACCTGGTATTGGGGGTCCCGTTCGGAAAAAAANANATAGGATATTAACCCATNTTTTTCT
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Table 1

TTTCTTCTTATTTTAGGTCTTCGGGGATAGGTCTTNTANTCCCAATAAATAATTGGGGT
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AGGTATTCAATCCATAATCCTCCCAGGACCCTGGGTTTTCCCTNGGAAGAAACAAGGGAA
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TAAACTTTCTTTTGGGAAGGAACCCCAGGTTTCAAGATATTTTTTTTTGGGGAA
Sequence 222
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AGAGAATGGGACATTTTAGAGACTGAAGAGCATTATAAGAGCCGATGGAGATCTATTAGG
ATTTTATATCTTACTATGTTTCTCANCAGATGTAGGGTTTTCTGTAGATGATGATGTCC
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TATGGCCATATCTCCAAAAGANATGAATCCGACAGCNGATACAAAGTTTTTTGGGCTGGG
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TTCTCATAAANTAAAAATAACCTACCAATGGCCTGGGTTGCNTCCGTNGGGAATTTGNNT
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AGAAA
Sequence 223
GGGCGGCCGGAGTGATGCCATCTGCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGG
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CCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTACACAAAAA
CTTGCGAGTAGAGGGTTTGTTTAGAGTACCT
Sequence 224
CCGCCCGGGCAGGTACTCCCTGATAAAGGGGAATTTCCATGCCGTCTACAGGGATGACCT
GAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAAAGGGTGCAGACGTCTG
GTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCCAGGAGTTCCTCATTCT
GGTGATAAAGATGGGCGTGGCAGCCCACAAAAAAAGCCATGAAGAAAGCCACAAAGAGTA
GCTGAGTTACTGGGCCCAGAGGCTGGGCCCCTGGACATGTACAGACTCTCATTTTATGAT
GTATCCTACTGCATCAGGACATTTGTGTCAATGTCAGGTGACGAGGGGAAATGAAAGTGA
TGAGACGATGAGAGGAGTGAAATACCAAGGACGCCATACTAGGAAACCCAGGTCTATTTG
TTATCAGAGTAAGGATCAAGCCAGATAGCCTGTTATGTAATTTCTCCGATAAAAGATTT
T
GAAAGCAGGTGCTGTGGGCATCTGTATGGGGGAATCGCACTCATAGAATTATTTTCATTT
GTAAATATTTGGTATCAGGCCCAGCAAGGGAAA
Sequence 225
CTCCCCGCGGTGGCGGCCGAGGTACTCACAGTCACGCAAATTCACAGTCTGCGTGCACGG
CTCTCCATTCTTCTTCTTGGCTTTACAGGTTCCCAGGTCAAGAGCTTCACCCATAATTA
A
GACCTTCTGAGGATGATCGATAGATAAACACACCTCCTCTGAACCATCCTTGGGCTTCAT
GGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTG
AACTTCTCCAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTT
CCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAATATAA
C
CCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCT
G
AGACAGTCTGATCAGTTTT

Table 1

Sequence 226
TTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGATGGATAGCCGCTTGCA
GGAGATCCGGGAGCGGCAGAAGTTACGGCGACAGCTCCTCGCGCAGCAGTTGGGAGCTGA
AAGTGCCGACAGCATTGGTGCCGTGTTAAATAGCAAAGATGAGCAGAGAGAAATTGCTGA
AACAAGAGAAACTTGCAGGGCTTCCTATGATACCTCTGCTCCAAATGCAAAACGTAAGTA
TCTGGATGAAGGAGAGACAGATGAGGACAAAATGGAAGAATATAAGGATGAACTAGAAAT
GCAACAGGATGAAGCTTATCATCAATTCATTGTATAAAAATAAAGAGATTTTCCTGAGAG
AACTGATTTCAAATGCTTCTGATGCTTTAGATAAGATAAGGCTAATATCACTGACTGAT
G
AAAAT
Sequence 227
CNCCGCGGTGGCGGCCGCCCGGGCAGGTACGCAAAGTGATTCAGAGAACGCTGGGGCTCA
CAGGCGCTGTAGCAAACGTGCAACTCTTGAGGAACACTTAAGACGCCACCATTCAGAACA
CAAAAAGCTACAGAAGGTCCAGGCTACTGAAAAGCATCAAGACCAAGCTGTTACTAGCTC
TGCGCATCACAGAGGGGGGCATGGTGTTCCACATGGGAAATTGTTAAAACAGAAATCAGA
GGAGCCATCGGTGTCAATACCCTTCCTACAAACTGCATTATTAAGAAGTTCAGGGAGTCT
TGGGCACAGACCAAGCCAGGAGATGGATAAAATGTTAAAAAATCAAGCAACTTCTGCTAC
TTCTGAAAAGGATAATGATGATGACCAAAGTGACAAGGGTACCTCGGCCGCTCTAGAACT
AGTG
Sequence 228
GAGCTCCCTCCTACCCCCTAGCTGAGTAGGCCAGGTTTTGGTGCAAAATCTCCCACATTG
GCAAAGTTCCTGCATATGCTGCGCAGTATGNGCCTTGAATAAAAATCCTGAAGATTAGAT
GGTTCAGGCTGCATCATCCCAAAGCAAAGAGCACCTCTTTGAAGCTCACCTGCCCGGGCG
GCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTCAGTANGNAGCTTTAAAACAGTTACATAT

Sequence 229
TGGCGGCCGAGGTACTACAGGATGATGGCTTTCTCTTCCTCTGGGTCACAGGCANGGGCC
ATGGAGTTGGGGAGAGAATGTCTAAACCTCTGGGGGTATGAACGGTAGATGAAATTATT
TGGGTGAAGACAAATCAACTGCAACGCATCATTCGGACAGGCCGTACCTGCCCGGGCGGT
CGAGCGGCCGCCCGGGCAGGTACTTNNTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTGGGAACCNGNTACATTGNTCAGTTTTTACTTGNAAAAAGT
NTTATAGAANAGTTTTATTGGAATGTTATTTTATTAAGCCNTTTTCATGGGTTATTTTTT
TTTAAAGTTTAAAAAGTTTTTACAACANGCTGGGNGGGGGGGNTTNCACCTGGCATCCCA
GCACTTTTGGAGGNCCCGGCGGGCANAAACCTGANGGCGGGGAGGTTTAAAAAANCNACC
CTGNCCANATTGGNAAACCCNTNTTTTTTCTTAAAATTCCCAAATTAAATTC
C
Sequence 230
GGCGGCCGCCGGGCAGGTACGCGGGGGAGTCAGACCCAGTCAGGACACAGCATGG
Sequence 231
CCACCGCGGTGGCGGNCGAGGTACGACGTTTCCATCAGCTTGTCTGTTTCATTCCCTGAT
GTTACGAGCAATATGACCATCTTCTGTATTCTGGAAACTGACAAGACGCGGCTTTTATCT
TCACCTTTCTCTATAGAGCTTGAGGACCCTCAGCCTCCCCCAGACCACATTCCTTGGATT
ACAGCTGTACCTGCCCGGGCGGCCGCTCTAGAACTAGGTGGATCCCCCGGGCTTGCAGGT
AATNTCGGATATCAAGCCTTATNCGATACCCGTCGACCCTTCGGAGGGGGNGGGCCCCCG
GGTACCCCAGCCTTNTTGTTTCCCCTTTTAGGTGGAGGGGGTTTAAATTTGCCGCCGCNT
TGNGCGGTAAATTCAATGGGTTCATTAGGCTTGTCTTCCCCTGTGGTGNAAAATTNGTTA
ATCNCGGCTCACCAANTTTCCCACCACAAACCAATANCGNAGNCCCGGGGGAGGCCATTA
AAAAGGTNGTAAAAAGCCCTTGGGGGGTTGGCCCTAATGAAGTGGAGCCTAAACTTCACA
ATTAAATTTGCCGTTTGGCGCTTCACTTGCCCCGCTTTTTCCAAGTCCGGGGA

Table 1

Sequence 232
CGGTGGCGGCCGCCCGGGCAGGTACTTTATTTTTTTTTTTTTTTTTTTTTTTTTNCTTTNA
A
AAAAAAAAAANGATATTTTAATATATTCAGATCCNCAAATATGAAATAAAACTAAGNNGA
GCTGGTATTCATTTACACATAATTATCTTATACCGTTNGGAATAAGAATTTGGGGCNC
GT
TAGCAAACCAAAAGGCTCAAAAAGACGTCGNGATATTTAGTTCTTGTCTCCCTCTACAAA
NGGGAAGCACTNTTTTATCCGGCATTCCTAGGGGNGTTCCTATTTTCAA
Sequence 233
CGGTGGCGGCCGNCCGGGCAGGACGCGGGGGCCAGTTCTCTTCGGGGACTAACTGCAACG
GAGAGACTCAAGATGATTCCCTTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGT
T
AACCCTATAAACGCCAACAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGT
CGGGGACCAAGGCCCAAATGTCTGTGCCCTTCAACANGATTTTGGGCACCAAAAAGAAAT
ACTTCAGCCACTTGTAAGAAACTGGGTATAAAANAAGTCCATCTGTGGGACAGNAAAAAC
CGACTGTGGNTATTATGGAANTGTTCGCCCTGGGTTATTATGGAGGAATNGGGAAAGGGA
AATGGAAAAGGGCTGCCCAAGNCANTTTTTTAGCCCATTTGACCCANTGGTTTTATTGGG
CACCTTCTGGGGCCATCCGGTNGGGGGAGGCNCACCCCACCAAACCGGNAAGCCGCCTTA
TTTCCTTGGACCGNCCCTNAAANAAACCTTGAAGGGGGAAGGGGNGGAATCCGGAGGGGG
AAAAGGGGGGA
Sequence 234
CGCGGAGGCGGCCGCCCGGGCAGGTACAGTATAGGTTGGTTTTGCCTGTTTTGACGCTTT
ATATATACGTAGACACACATACACATGTATATATACACACACACATTTTACATATATATA
TGAAACTGTATAATGTGTTCGCTTCAGTGTCTGGCTGCTTTTACTCAACATTGTGAAAT
T
AATTCCTGTTATCGGNATATGGGTATCNAAATTTGNTTTGCCCTAGTTTTTGCCTTCTC
A
TTGCTTTCTGAATTGGGGGCAGCTTTGCCCCTCAAGGGGAAATTTAGCAATGTCTGGAGA
CATTTTTTTTATTTTCATAATTTNGGGAGGGGACATGGGGGGAGGTTTGGTGGCTACAGG
AACCTTAATTAAGGTTCGAGGGACAGGGGTTAGGTGCTTGAACGGTTNCCACANGTAACA
CTTCGGGCNCGCTTNTAAGAAACCTAGGTGGGATTCCCCCCCNGGGTCTGGCNANGGAAA
ATTCCGANTATTNCNAAGCCTTANTCGANTACCCCGGNCGACCCTTNGANNGGGGGGGGG

Sequence 235
CGCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAATAATTTTGT
CATTTTTGTAGAGACAAGGTCTCCCATGTTGCCCAGGCTGGTCTCAAACTCCTAGGCTCA
ACTGATCCTCCTACCTCCACCTNTGCCTCCCAATTATCCCCAATTGAGAGATGAAAATTC
TGACAAGCTCTCAAACGTTAACTGACTTGCCCATAAATGACAGTTCCAAAGTTATAAGGG
CCTAGNAACNTTGAATCCAGGTNCTGTTAGNAAATTCTAGGGTTTGAGAAATCCCATATT
TCTNTCCACTTCCCGCGGTACCCTGCCCCCGGGGCCGGGCCGCCTTCTAGGAACNTAGGT
GGGATCCCCCCCGGGGCTTGCAGGGAATTCCGATATTCAAGCCTTATTCGGATAACCCGT
CCGACCCTCGAAGGGGGGGGGGGCCCCGGGTACCCAAGCTTTTTTGTTCCCTTTTAGTGG
AGGGGGTTTAAATT
Sequence 236
GCGGCCGNCCGGGCAGGNACCTACGCCACAGACAGCCAGAGGGAAAGCGACCCAGACAGC
AGCCCCTCCTCGACAGGCCCACCCTGCAGCTCAGGCACCAAGAAAACAGCCGATACTGGC
AGCCATTGCAGCTCCAAACTGCANNAGGCAAGGCCAATTTTAACTTTTCAATTTACAGTC
GATTTTGAAGAGCTTTCTACATATCCGGTTATGTAAANTTCATATATGTATTTTTTGGAA
ATCAGTTCTTATANAACCAGCCTCCGATTCAAGTCTTTAGGCTAAAATTTTATAGGTCC
T

Table 1

AAGGGTAGGTATGGTTAACAATTTTGGAACCTTTTTGGTCCTTAAAGAAAAAGGTTGGAC
TTGTTTCAANATANTTTCTNTCTTACCTNGTGAAAAGGAAAATCNTTACTTTTTTCCTAA
TTAAAAAGGAATTCTTGTTACCCTTCGGGCTCCGCTTCTTAGGAAACTTAGGTGGGGATC
NCCCCCCGGGGTCTTGNGAAGGNAAATTTTCGAATATTCCAAAGGCTTTTATTCGAATAC
CCCGGCTCGGAACCTCGGNAGGGGGGGGGGGGCCCCGGGGTACCCCCAAGCTTTTTTNGT

Sequence 237
GCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGGTCAGCCCATTATCTTTAATCCT
G
ACTTTTTTGTGGAGAAACTCCGACATGAGAAACCTGAGATTTTCACTGAGTTGGTGGTCA
GCAATATCACAAGGCTCATCGATTTACCTGGAACTGAGTTGGCTCAGCTGATGGGGAAG
TGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATCAGGATTCTTCCGGTCTCTCATGT
CTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTCCCCACTGACGGAGGAAGGCATTG
CCCAGATATACCAACTGATTGAGTATCTACACAAAAACTTGCGAGTAGAGGGTTTGTTTA
GAGTACCT
Sequence 238
CCCGCGGTGGCGGCCGAGGTACGCGGGGATTGTGTGCAAAATCAGAGAGGGGTGCAAGGA
TCCTGATTTTTCAGGAGTTCAAGCGACAATGGCAGCCCAATACGGNAGTATGAGCTTCAA
CCCCAGCACACCAGGGGCCAGTTATGGGCCTGGAAGGCAAGAGCCCAGAAATTCCCAATT
GAGAATTGTGTTAGTGGGTAAAACCGGAGCAGGAAAAAGTGCAACAGGAAACAGCATCCT
TGGCCGGAAAGTGTTTCATTCTGGCACTGCAGCAAAATCCATTACCAAGAAGTGTGAGAA
ACGCAGCAGCTCATGGAAGGAAACAGAACTTGTCCGTAGTTGACACACCAGGCATTTTCG
ACACAGAGGTGCCCAATGC
Sequence 239
CCGCGGTGGCGGCCGAGGTACCAGTTAAGTGAACAGCTCGTCTAGGTCTGCTTTTGTAAC
ACCCAAATACAATTAGCACTTCTCTGCTGGTATTCCCTGGGCCGTCTTAATTATCTAG
AG
GCCAGGAGGCAAAGCCTAGCACGTAACAAAGTATGTGCTTTGTAACTGCTGATTAATTCA
GTTTCTTAACTAGGCAGAGCAGGTCATCAGTGTATCTAATTCACACTATTAATACACTG
T
CTTGCTGAAGAGTCTGACCCTGCCCAGGAACCCCCGTTATGGCCTAGCCCCAGNGGGAAG
NCAGTAAAACCTGCCAANAGCCAGGAGAAAAAAGGGGGGCCAGTCTTAAGAATGAAGGCC
TAGGTGCTTGGCCTGGAGCTCCCAGTTTTAGGGTCCTGGTTACTGTTTCTGGTTTCCAAC
TTATTAAAATCCAGGGGATGGACCTGGTTACCTCAGATTTCAGGTTGCCTTATGGTAGGA
AAAATAGGAATGCCACAGGCCAAAAAACATTAATTTTGGGGGGGATGGACTTGGGCAGNC
ACCCTTTTTTTTTTCCCTTTTC
TT
Sequence 240
GNGGNGGGCCGGCCCGAGGTACTTTTTTTTTTNTTTTTTTGGTATGACTATAGATGGC
TA
GTGNGTCTTTTTATTAGCTATCANCGTTCATTTAACAGACAAAAAATTCAAGTTCAATG
N
NNGGNCATTAAAATACGGAAGAATTAACAATAAGTTCATTAATCAATCTTTCANCTGTT
C
CTATTTTATCACAAATNACTTTTCCTANAATTGGAANAAGGATNCATGGGAAGGGGACAA
GTCTTGGAAAAACGCAAACCGTAATTGTGTTCTTTCAAATTCCATAAAAGACACTTCAGG
NNCAAAAAAATAAATAAACAAGGNAAGGGCCGCNTCATTACCTNTTAGTTTNGGGGNGTN
GGAAATTGAATCATGGCCAAGTGCCTAAGNGCNTTTTTGCTGNTNAGTTAACCCNCCGTG
CCCGCGTCNTAGGAAACCTATGNTGNGGATCCCCCCCGGGGCCTTGCCANGNGGAAATTT
CGAATAATCCAAANGCCTTTATCCGGAATACCCCGTCCGGACCCNCCGAAGGGGGGGGGG
GGG

Table 1

Sequence 241
GCGGTGGCGGCCCGGTGTGCTGTGCTCAGCTGCCTTCCAAAGGAGGAACAAGATCGGCAA
GTGCTCGACGCGTGGCCGAAAATGCTGCCGAAGAAAGAAATAAAAACCCTGAAACATGAC
GAGAGTGTTGTAAAGTGTGGAAATGCCTTCTTAAAGTTTATAAAAGTAAAATCAAATTAC
ATTTTTTTTCCAAAAAAAAAAAAAAAAAGTACCT
Sequence 242
TGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAGCTGGAAGAAATAGATTGGGTGACAT
TTGGGGTTATATTGAAGAAGGTTACGCNACAGAGTGTGAATAGTGGAAAAACCTTCAGCA
TATGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTTATTTGGA
G
AAGTTCACAAAGCGCTCTGGAAGACGGAGCAGGGGACTGTCGTAGGGATCCTCAATGCCA
ACCCCATGAAGCCCAAGGATGGTTCAGAGGAGCGTGACTGTGAGTACCT
Sequence 243
GTACGCGGGGTGCTGGGATTACAGGCACGAGCCAGTGCGCCCAGCTGCCTCTGTTTCTTT
TATTAAGCTGTTCTGGACTGTGGGGCTCCTTGGGCAGATGCTGTATTATGGGGATAAGCC
ACACACTTTTTGAACTGGCCCGGTCAGGGGGGACATAACCATTTNCTGTGCCACCCCATC
AATCCCCACCTATTCTGAGTGTAGGCTCCTCCCCTGCTTGAGTAATGGCCACAGATCTTG
GCTCGGCACTCCTAAGCTGCATGTTGAATTCCTGGGACAACAAGACTGGCTTGTGGTTCC
ATTCTCCAGATCCTTGGGTTGGCTTCTGGGTGCACTAGGAGATCTGAAATGCTCTCAGGC
CACCAGGAAAGTACTGGAAGTAAAGTCTGACTCTAAAGAAGATGAAAATCTAGTAATTAA
TGAAGTAATAAATTCTTCCAAAGGGAAAAAACGCAAGGNAGAACATCAAACAGCTTGTGC
TTGTAGTTCTCAATGCACGCAAGGGTCTGAAAAGTGTNCTCAGAAGACTCTNNAAGAGAC
GAAACGAACCCTGTGCCTGTAACTTTTGAGGNGAAAAGAACAAAAATGGCTCTTAGGNGG
TCCCGAAAAAAN
Sequence 244
TCCACCCACCTCGGCCCTCCAGTGTGCTGGGATTACAGGCATGAGCCACGGCACCCGGCC
CTGGTTTGCTTTCTGAACCATGTCAATACAGTACCACCACAGTTGCTATCTCTTGAAC
AT
CTTTCATTAAAACATCACCGTCTAGTTTGAGAATACTTTTAAGCCTGCTGGCCTCCTTT
G
GGGCATTCTTTTTTCTCTTTTCAGCACGCATCTTTCTTTTCCACTTACTCCGTAAGCTT
T
TAGCCATGTTTTACCTTGAGGGCCGAAGTTAACTTCAGCGGGAGTGAACGACAGGGGTGG
GCTCCACTTTATCCAGTGCACTCGGAAGCCGGAGGGCCCCCACCAAAAAGAGCAAGGGGA
ACCCTC
Sequence 245
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACAATTGCTTGAGTGAGTTCATGGTCCGTAGG
AGGATGACCACTAGCCCACCACCTTCCACTGTTTCTACAGTCCTGGNCAGCAAGTTTGGA
GTTAAGGCTTCAAAATCCTGCAGCACACACATGCCGAAGGTATTGCCCAGGATCTTGTGG
GTCTCGTTGTAGTAGCAGTAGCGAATGTTTGTGGCTGCTATGAAGAGTTCAAAGGGGTCG
TCCTGCTTTATGTTCAGTGTTCCATTCTTTATTTTCTTCTGCAGCTGTCGCA
T
Sequence 246
GCGGCCGTGGGGATCAGCGTAGGTGAGCTGNGGCCTTTTGCGAGGTGCTGCAGCCATAGC
TACGTGCGTTCGCTACCGAGGATTGAGCGTCTCCACCCATCTTCTGCGCNGNCACCATCT
ACATAATGAATCCCAGTATGAAGCAGCAACAAGAAGAAATCAAAAGAAGAATATAAAGAA
ATAGTTCTTGTCCCAAAGGAAGGAAACTCTTGAAGGATTGAATTTCAGCCCTTCTTGCAT
CTTGGGATCTCTTGGTTGGGAAACGGAAGGAAANAAATNGGAAGCCTTGTCCCGCAAGNG
CTTTGTCCANANAAAGGGGAAAACCATTCTGGGGAATGGACCCACCTTTAAACCATCTAC
CAAACCTTCCAAGCCCCTTGGGGGGGTNTATTTGGTCCCCAACACAAAAAAATAGAAGTA

Table 1

TAAAGAAATANAGGTTANCCTTCGGGCCCGCTTCTTANGGAACCTAGNNGGGAATCCCC
CCGGGGCCTTGCCAGGGGAAATTCNGGAATNTTCAAAAGCCTTTATCGGAATACCCCGTC
CGGACCCTTCGGAGGGGGGGGGGGGCCCCGG
Sequence 247
GGCTTGCTTGACTAGATGAGCTGCTATAGTAGCCAATCCTGTTAGACTTGGACCATTGTT
TGTCTGAAGAANGGGAATCTGTCGCTCGCCCTGAGCACTGTATTTATTCCCCTTACTCAA
GNCCCAAGGGACTTCTCCAAGTAGCCGACAAACTCTGCCGGGCCGCCCGCCATCTTCCGG
GCCCGCTCTAGAAACTAAGTTGGGGATCCCCCCGGGGGCTTGCAAGGGGAAATTTCCGAA
TATCAAAAGCTTATCAGAATAACCCGTCCGAACCTTCGGAAGGGGGGGGGGGGCNCCGG
GGTACCCCAAGCTTTTTTGTNTCCCCTTTTAAGTGGAAGGGGGTTTAAATTNGCCGCCGC
NTTGGGCGGTAAANTCANTGGGTCATTAGGCTTGTTTTCCCTGGTNGTCGGAAAAATTTG
NNTTATTCCCGCTCACCAAATTCNCACAACAAACAATAACCGAAGCCCGGGGGGAGGCCA
TTAAAAAGGTTGGTAAAAAGNCNCTTGGGGGGTGGCNCTAAATGGGAAGTNGAGCCTAAA
CTTCACAATTAAATTTGCCGTTTGGCCGCTTCACTGGNCCCGCTTTTTCCAAGT
Sequence 248
CCNCTCCCGCGGTGGCGGCCGAGGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTT
TTTTTTTTTTTTTTTTTTTNCAGAGACNAGGAATTTAATTAGGGNTGTAACAAATGGTTA
ATTNTAGNAAGAAAAACCAAATTGAATAATTTTCTAACTCACTTGGCAGGGGGGGNCTCG
CANCCNTAATGAACATCACATAATGAAGTTNCTCCTTTCCANATCTATAAACAGGCTCAT
GTAACTAACTGATNCTCAGTAAAANGGNNCATAATCCAAATNTNTNTAACAAANGGGGCT
TGCTATAAAATCTCTTACATTTTAANACTTACTCTTAANAAATCATCTATTCTTCCCTC
Sequence 249
AGACTGTCTCAGATCAAGGAAAAGATGGCCAGAGAGAAAGCTGGAAGAAATAAGATTGGG
TGACATTTGGGGTTATATTGAAGAAGGTTACGCCACGGAGTGTGAATAGTGGAAAAACCT
TCAGCATATGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
AT
TTGGAGAAGTTCACAAAGCCGCTCTGGAAGACGGAGCAGGGGACTGTCGTAGGGATCCTC
AATGCCAACCCCATGAAGCCCAAGGATGGTTCAGAGGAGGTGTGTTTATCTATCGATCAT
CCTCAGAAGGTCTTAATTATGGGTGAAGCTCTTGACCTGGGAACCTGTAAAGCCAAGAAG
AAGAATGGAGAGCCCGTGCACGCAGACTGTGAATTTGCGTGACTGTGAGTACCT
Sequence 250
CGGCCGGAGTGATGCCATCTGCAGTTTTGTGATCTGCAATGATTCTTCCCTTCGAGGTCA
GCCCATTATCTTTAATCCGGACTTTTTTGTGGAGAAACTCCGACATGAGAAACCTGAGAT
TTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTCATCGATTTACCTGGAACTGAGTT
GGCTCAGCTGATGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATCAGG
ATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTCCCC
ACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTACACAAAAACTT
GCGAGTAGAGGGTTTGTTTAGAGTACCT
Sequence 251
TGGCGGCCGAGGTACCAGCACAAACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCG
TCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCAGGG
Sequence 252
AGGTACATTTTACTACGCACCCTTACGCATTCTTTTTCTCACCTCTGTGTGTGTGTGTG
C
GTGCACATGCACACACACAAATGGGTGAAACAATTCTCACCATACCAAGAGCCACCGCGC
CCTGCCGAGAATTTGCATTTCTAACAAGTTCCCAGGTGATGCTGACACTGCTGGCTCATG
GAACCACTGCTGTAGTATTTTCCAAATTATCCTGATTCTAAGAACCACCTATGACCTGT
G
CTGTTTTTTCTGTGGTTACTGGCTCATGTCACATAAATTCTTTTAGGATTCAAACATGT
T

Table 1

TGTGATATTACTCAGTATTTACATCTTGCTTTTACTGCAGCATGATGGAAAAATTAACC
A
CAGGTATATCATAACAAAAAGAACATGAGTTACCATTTTTCACAAAGTTCAGATATATT
T
AAATTAGCCTATTTAATCTTTTTTTTGGGT
T
Sequence 253
GGGNGGCCGGGCCCGCCCGGNCAGGGTACTTTTTTTTTTTTTTTTTTTCTACCAGTAG
CC
TATTTCAGATTTATTAAAAAACACATAGGTAACCGAGTCANAGCTTTGGCTAGGAATGAN
TTGGAAAAGAACTGAAGGCATAATTCCACAGGACATTCACAGTTAGTGTGCTAGAAGACA
NGAGAGGGAAGCAGGGAAAAGTGTTTTTAAGAAAGCATTTGCGGGCCGGGACAAATGGGA
AAGGGCCCGGGCTTTCATCGAAATTCCCTTGTTTTGCCTTGGATCCCACAATCTTGCTTG
GGAAAAGGGTGGGGACAAGAAGGAAGNGCCCAAGGGATGGGGAGCCACCCGATCCCAAGA
CCAAGGAAGTANTTTTGCCGCTCCCGGGANGGGGGGGCAAATTGGATCCTTTGGAATCCT
TCAATGGGTGGCCTNGGGGGTAGCTTAAGGGGGCCCGGTGGAATCCTCCTTTCTNGCATT
TCCGGGGGCCGGGCNAAATNGCCCAAGGGGGGTACCCTTCGGGCCCGCTTCTAAGAAACC
TAGGGNGGGGGATTCCCCCCGGGGCTTGCANNGGAAATTTCGGAATATCAAAAGCCTTAA
TCGGATACCCGGCGNACCTTCGAGGGGGGGGGGGGGCCCCCGGTACCCAAGCTTTTTGGG
T
Sequence 254
CTCACCGCGGTGGCGGNCGAGGTACTCATGGNTGCTGNAAATCATGGCACGCCCGTTCTG
CAGGGNTNTGCTTAGCCAGGCTCCTNTGAGATCTGGCTATTNTGNCTTGTGGATNNTCAG
TCCCCGNGTACCTGCCCGGG
Sequence 255
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGATTGTGTGCAAAATCAGAGGGGGGTGCAA
AGATCCTGATTTTTCAGGAGTTCAAGCGACAATGGCAGCCCAATACGGCAGTATGAGCTT
CAACCCCAGCACACCAGGGGCCAGTTATGGGCCTGGAAGGCAAGAGCCCAGAAATTCCCA
ATTGAGAATTGTGTTAGTGGGTAAAACCGGAGCAGGAAAAAGTGCAACAGGAAACAGCAT
CCTTGGCCGGAAAGTGTTTCATTCTGGCACTGCAGCAAAATCCATTACCAAGAAGTGTGA
GAAACGCAGCAGCTCATGGAAGGAAACAGAACTTGTCGTAGTTGACACACCAGGCATTTT

Sequence 256
ANCGCACACCACCACNTCTGATTAATNTTTTGNATTTAAANNTTTAGGTGGGGCTNCACC
ATGTTGCCCAGACTGGTNTTGAACTCCTGAGCTTAAGCAATCCACCTGCCTCGGCCTCCC
AAAGNGTTGGGATCACAGGCGTGAGCCACCGCATCCGGCCTCATGTTCTTTTTCATTAAA
GAGAGAAATCAACTATTCAGGACCGGCCCCCACCTTTCCTCAGGAGTCATTTCTGTTCCG
CACAGGCCTGCTGAACTGGGTGCTTTATATAGGGNANAGGGGGCCTCATTTTTNGTTCCC
CTGNCCCNCAAGCNTTANGGGGCAAAAANAAAACCATNCCAANAATTTGGNAAAGGGNNT
TTTTTTTTTTNAAAATNNGGNNNGGGGGGGGGCCCCCCTCNCTTGNGGTCGGGNGGNTTT
TNCNGGNGNNAAAAAAAAAAAAAAAAA
Sequence 257
AGCTCCCCGCGGTGGCGGCCGAGGTACTCTGACTTGCAGGGCCCAAGACCGGCCTTGCGA
GCGTCGTTGGCTGATGGGAGTAGAAGCCACAGAGAGTCTTCCTCTTGGAGGTACAGTCAA
TTCTGAGGTTTGGGCGTCATAGACTAAACCCAGAAAACAGAACATTGGGAAGTCTTCGGA
ATATTCTCTATCTTCTTCACCAACGAGTAAGACCGTTTTG
Sequence 258
GGCCACGTGACCGACGCCAACATNGCGGCGCCCAGTGGCGTCCACCTGNTTTTCCGCAGA
GGTTCTCATAGAATTTTCTCTTCACCACTCAATCATATCTACTNACACAAGCAGTCAAG
C

Table 1

AGTCAACAAAGAAGAAATTTCTTTTTTCGGAGACAAAGAGATATTTCACACAGTATAGTT
TTGCCGGCTGCAGTTTCTTCAGCTCATCCGGTTCCTAAGCACATAAAGAAGCCAGACTAT
GTGACGACAGGCATTGTACCTGCCCGGGCGGCCG
G
Sequence 259
GGTGGCGGCCGGCGGGAGGCTGACGAGAGCCCGGGAGGCGTTAGCGAAGGAAGAGAAAAA
CCGAAGACGAAGCCACTACAGCCCCGCGTACCT
Sequence 260
GGAGCATAAAGNTGTAAAGCCTGGGTGTGCCCTAATGAGGTGAGCCTAACTTCACATTTA
ATTGCGTTGCGCTCACTTGNACCGCTTTCCAGTCGGGGNAAACCCTGTCCGTGCCCAGNC
TGGNATTAAATGGAAATCNGGCTCAAACGNCGCCGGGGAGAGGAGGGCCGGGTTTTGCCG
GTATTGNGGGCGGCTTCTTTCCGCCTTTTCCTTCGGCTTCAACTTGAACTCCGCTTGC
GC
TTCGGGGTNCGGTTTCNGGGCTTGNCGGGGCGNAGGCCGGGTAATNCAGCCTTCAACTTC
AAAAGGGCNGGGGTAAANTAACNGGGTTTATTCCCCACCAGGAAATTCAAGGGGGGAATA
NACCGCCANGGGGAAAANGAAACCATGNTGGAGCCAAAAAAGG
Sequence 261
TGTGTTGAAAAATTGTTATCNNNCTTCACAAATTCCACACAACATACCGANGCCCGGNNA
GTCATAAAGTGTAAAAGCCCTGGGGTGCCTTAATGTAGTGAGCTAACCTCACATTAATTG
CGTTGNGCTCACATGCCCGCTTTTCCAAGTTCCGG
Sequence 262
GGGCGGCCGAGGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGGAAAAG
ATCTGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTG
CTCACGGAGGCACCCCTGAACCCNAAGGCCAACCGGGAGAAAATGACTTCAAATTATTGT
TTGAGACTTTTCAAATGTCCCANGCCCATGTATGTGGCTTATCCAGGCCGGTCGCCTGTC
TTCTCTTATGCCTCTGGNACGCACATCCTGGCATCTGAGCCTGGACTCTTGGAGATNGGG
TGTTCACTCCACAAATTGTTCCCCCATTCTTATNGAGGGGGGCTATTGCNCTTGGCCCCC
ATGNCCNATCATTGNCNTTCTNGGATTCTGGCCTGGCCCGANGAATCTTCACTTGAACTA
CNCTTCATTGGAAANNATCCCNTGGACCTGGAANGCGTGGGGCCTAATTTCCCTTTCGGT
TTACCTAACCTGGCTTGNAAGCCGNTGGAGGAATTGGTTCNCGGGGGACCAATTCAAAAG
GGAAGAAAANCTGG
Sequence 263
CTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGCAGCCGTTTTT
C
TTACTAGAAGCTAGGCNGAAAGAGTTGTTACTCANATTTCTTGAACTTGAGACGTCAAAG
GTGAGACGCCAGCCAAGGAGAAGGGATGGTCAGGGACCTGCCCG
Sequence 264
CGTGCGGATCTTCTTCTTTTTGNGGCTTCCTTCANGGGGTCAANAAAACCCTTCTNGGCC
TTTAAAGCCTTCGCTTTGGCTTCAGCTTTAGGAGGGGCAGGAGCTTCCNCCTTCGANNTC
GGCGCCATCTTGNGAAAAGCCCCGCGNACCT
Sequence 265
AGCNNCCCGCGGTGGCGNTNGCCNGGGCANCCCGCGGGGGTGGAAACCTCTTCAGCATTN
GCTTNNNNTCAGGGGGCTAAAAAACCCANCAACCGGGACCCCAGCTTTTCAGAACTGCAG
GGNAACAGCCATCATGAGNGAGGGCACCAAGAATTCCCTGGAGAAAATCCTTCCACAGCT
GAAATGCCATTTCACCNGGAACTTATTCAAGGAAGACAGNGGCTNNTNGGGANCGNGGGG
ATAGAGNGCGCAACCAGGGNGAAANNTTAAACACNGAGNNCAAAGNGGNCGNGGGNCCCN
CGGCCGCTCTAGAACCAGGGGACCCCCGGGCCCGCAGGGAANNCCGANANCAAAGCCNAA
NCGAAACCCGGCNACCNNCGAGGGGGGGGCCCCGGACCCCAGCNNNNNGGNCCCCCNNAA
GGGNGGGGNAAANGNGCCGCCNNGGCGGAAANCAAGGGGCAAAGGCNGGNNCCCNGGGGG
NAAANGGGNANNCCGNNCACAANNNCCNCACAACAACCAAGCCCGGGAGGCANAAAAGGG

Table 1

GAAAAGCCCN
Sequence 266
AGGTACTTTTCTAGGTATTGCTGGGCAAGATCCTTGTTGGAGTCCTCCTCTTTTGCTG
CC
CCACTCAGAGGATAGGCAGAGCAGACTGGCAGACACAACAGCACAAGGAATGCAAGATGC
ATCATTCTCACTGCCCTTACCTTCTTTGTCTACTGGGCTTCTCCCCGCGTACCTGCCC
GG
GCGGNCGNTCGAGCCGCCGGGCAGGTACTACCTGNACCAACTTTTTCATTTGGGCATCAC
AAAGACGAGTCTTCTGATGTTCTATAAGCAATATGNTTATATGAAAGNCAGAAGTTTAGC
GAAAATTCGGCCTAAACAGNAATAAATGAAAATGGANTGGAAATCAAAGNNCTTAAATAG
AACANGAAGGCNGGGCACCGGNGGNTCACGCCTNGNANNCCCAGCACT
T
Sequence 267
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTACCTCATTTCCTACCAATCATT
TTAAGAGAATTTGGTTGTATTTCAAAGAACAAAACAACACAATTTCTGTCCTGCTGTTT
A
TTTTAGCGGTGGTCGCGGCCGAGGTACGGATACAATTCCGCTGAGTTAGATTCCAAATTC
TAACCTCTCCATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCTGGATGCTTTGCCA
AGCAATTGACTCCATCACGGTGACCATCCAGCGAAGCAAGGAATGGTTTTGCAAATACTC
GTTCCAGTTTGGTAGCATTTAAAGCTCTTATATATTCTCGTGGGACCTCAAAAGGATG
TA
AAGCAGGATCATAGTTTCTTGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAAT
TGTCCGGATTCCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
Sequence 268
NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTATATGAAAGTCCTCACTTTCAGA
AGCAGAAAAGGAGTAACTAGATGGGCATTTTCTATACCAGCTAAGGCTTTAAACATAACA
ACGTCTACTGAACTATTTTCTACTTACTTTGACTGAATAAGCCAGTGAGATCGTGACTG
C
AAGTGGAAGACCTTCTGGCACTGCGACCACTAAAACTGTAACTCCAATAATGAAGAACTT
CACAAAGTATTGTATATAAATTGGTGTGCACTCAGCAAGCCATGGTCTTTTCTGAACCCA
GAAGGTGTCAATGACAAAATATAATACTAGAATGATAACTGTGATGGCAGGCATCAACAG
ACCTTTCAGAATAGAAATGAAAGAAAAATGTGATTATTAAATTTCCAGACACTAACCCTT
GACAGATATAAATTAAACACTGTAAAGAGTTATAACTTGCTTGATAGTATTGAATTTCT
C
TGAGAAATTACTTCTTTCTTGCACCTTATAACTTGACATTGTCAGATTTAATTTTT
Sequence 269
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATAGTGGAGGCACTGAAAGACCA
GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT
GAACCAACCTCGAGCGGCCGCCCGGGCAGGTACAGATGCACAGGAGGCCATAGGGTTTAG
GCAAAGGGGAGCACAAAAGTTGAAGATGAGGCGCTGCCACCAATGCTGGGACTTCAGGCC
AGGGGCAGGAGCTGAGGAAGCCACAAGGGAGGACATTTTCTGCAGTTGCTGAACCAGTAG
CAACCAGGTCCTGAGAAAGCCCTCTCTTGTGGAAGAATAACAGCCAGGAGGAAAAGCTTT
TCATTCTGCAAAGCTGGGGCAGAAAGTTCTTNTTTGAATCCCGCGTACCTCGGCCCGNTC
TAGAACTANTGGATTCCCCCGGGCTGGAGGAATTC
Sequence 270
GTCTTCGGNTTTTCTCTTCTTTTTCCAGGGCCTCCAANCCCTCGTCAGCCTCCCGC
Sequence 271
GGGAGGCGNNAGCGAAGGAAGAGANTNTTCGANGACGAAGAAAACCCAGCGCCCCCCACG
NACCT
Sequence 272
TTGGAGCTCCCCGCGGTGGCGGCCGAGTCCCACAGTTAGCTGCAGCAAAACGCAGGCTGC

Table 1

CTCAGGGAAAGGAGCCTGGGTTGATTAACTTGTGTGTCAATGTCCCACCCGTCCCAGGTA
ACATTTTGCCCCCTGAGGTCCGGGGTAATTTAATGGCTGCTGGACAAAACCTCCAAAGTT
CTTGAAAGATCAGAAATGATAGCTACCTGGAGTCCAGCTGTACGGCACTTGGCGTAAAGC
CGCTTCCCTCAAGAGTAACTACAATCTTCCCATGCACAAGATGATTAATACAGATCTTAG
CAGAATCTTGAAAAGCCCAGGAGATCCAAAGAGCCCTTCGAGCACCACGCAAGAAGATCC
ATCGCAGAGTCCTAAAGAAGAACCCACTGAAAAACTTGAGAATCATGTTGAAGCTAAACC
CATATTGCAAAGACCATGCGCCGGAACACCATTCTTCGCCAGGCCAGGAATCACAAGCTC
CGGGTGGATAAGGCAGCTGCTGCANCANCGGCACTACAAGCCCAATCAATGAGAAGGCCG
GCGGTTGCAGGCAAGAAGCCCTGTGGTAGGTAANAAGGG
Sequence 273
TNTTAGGGNCAAACACGGCCCCAGCCCGCGNCCCAGNCNGNGCGAANGATTTTTTCAGGG
NGACAAAAACCCAGGNCACCCACCTGCCCG
Sequence 274
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGCGTCGATGCTATGCGCTCAGTTC
TAGTCAGAATAATCTTGCTCATCCTCCAGCTCCCCCTGTTCCACCAAGGCAGAATTCAAG
CCCTCATCTGCCAAAACTACCACCAAAGACTTACAAACGGGAGCTTTCGCACCCCCCATT
GTACGCGGGGGAGGAGCCTGAGGAAGAGGGCGGCGACGGTGGTGGTGACTGAGCGGAGCC
CGGTGACAGGATGTTGGTGTTGGTATTAGGAGATCTGCACATCCCACACCGGTGCAACAG
TTTGCCAGCTAAATTCAAAAAACTCCTGGTGCCAGGAAAAATTCAGCACATTCTCTGCAC
AGGAAACCTTTGCA
Sequence 275
CAGCGAGCACGCGTNTTCCGCAACCCGAAACCNCCTTACAGGAGGTTTAANACNCANCCC
AACGGGGAGAGNGGGGAAACATGANGACAGANNNNGGGGAANGAAAATGGNACCTCGG
CCGCTCTAGAACTA
Sequence 276
AGGTACGTTCTATTCCTGCTCCTATTAGGTCCTTCTCACCGCACCGGCCCTCGGTCGATT
ACGCCTCTCCAGTTCTGCTGGGGACGTTCTAGCCTCGCCCCANCCGCGTCGATCTTTATG
TTATACCGTCACTCCCAGTGCCCTAATGGAACTATCCCTCCACTACTCCCCCTGGTTCTA
CCCGGCTCCAGAGCCTCTCCCGGCCCACTAATTTATTCCCAAATTCTAGGCCCGGCCCCA
TCAAGCCCTCCCCGCGTACCTGCCCG
Sequence 277
GACTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGAGCGGGCCCTACCGTGTGCGCAGAAA
GTGGAGGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACTCANCT
GTTCGNTGCTTCAGGGCCTGCTGATTTTTGGAAATGTGATTATTGGTTGTTGCGGCAT
TG
CCTGCTGCGGAGTGCATCTTCTTTGTATCTGACCAACACAGCCTCTACCCACTGCTTGAA
GCCACCGACAACGATGACATCTATGGGG
Sequence 278
TTCGCCCGGGCAGGTACTTTCATCCATAAAGGCCTGCAGCTGTTTCACTGATCCTTGCAG
TTCATCCATCACCAACTCCATACAGTCAAAGACTTTGCTCTGGTTCTGTAATATTTTCT
G
GTAGTCAGGTTTTGTATTAAGAACTTCATTCTGAGAAGACCCAAGATATGTCATAGGTTC
CACTTTGACCTCAGTAATTTTGGCCTCAGTTGATCCTCTGGACAATATCTCTTTAGCCT
C
CTGCTGGTAGTGAGGCAAGAGCTGATCCCAAGTCTGACGTTCTAAAGAAAACTTTGTTAT
GTATTCCTTCATCTCAGCCACAGATGCTTCCAAAGAAAAATCTGATGCTTTTCCATTTG
A
ATCTTCAAAACATTTTTGNAGAGTTCCATCAGTTTCCAGGCCGTCTGCAAAATGTTTCA
A
TTCTTCAGAAAGAGAAGATGCTTTGGCTCTAAAACTTTCAAGACTGAAGCCCTTAGTGGC

Table 1

CCTTANGAAAGGGT
Sequence 279
CACTGTTCTTTCTTTCTAATAAAACTTTCTTTTTCGAACCTATACTGTCTTCTGTAAATT
CTTCTTACTACCCTATGACCCGTGAGCCAACCACTTTCCGATGCCAGGGTTCTGACACCT
CACCTGGCATAATATAAAGTGTTTTTTTTTTTATACCCTTCCACTTGGAAAGACTACAG
A
GGAATCTTGCNCTGCATAGTTCAAACTAAAAAGAGAAGAGTTAATTACCTGAAAAGCAAG
AGAAAACAAGAAGGGGTAAATTTTGAACCAAGGGAAATCATTTAAGAAGTGTCTGGTATT
TTTCAAATTTCTGTCAGTTGTTACATTTGTCATAAGTAAATGTTTAGGAATAAAGGATG
G
AGACATGCTTATTTTATTTAACTCCCCCAAAATTAAAAANNAAAAAAANAAAAAAAAAA
AGTCCCTGCCCGGGCGGCCGCTCGAGATAAC
Sequence 280
CCGCGGTGGCGGCCGGAGTNATGCCATCTGCAGGTTTTGTGATCTGCAATGATTCTTCCC
TTCGAGGTCAGCCCATTATCTTTAATCCTGACTTTTTTGTGGAGAAACTCCGACATGA
GA
AACCTGAGATTTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTCATCGATTTACCTG
GAACTGAGTTGGCTCAGCTGATGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCTGGCC
CAGCATCAGGATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATAC
TTGGGTCCCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTATCTAC
ACAAAAACTTGCGAGTAGAGGGTTTGTTTAGAGTACCT
Sequence 281
GGGGGGAGACATGTGGAGGTCCCAGCAGAGGCCAACCTGTGTCTCTTCATCTCCCTGGGA
AGGGTGCCCCCGAAGTGAAAGAGATGGCCTGGTGGAAAGCCTGGGAGAATGAATAAACAG
ACTAGGGTGAAATCCATACAATGGGAATGGTAGCAGACAATAAAAAGAAAATGAACTATT
GATGCCCCCTACTGCACAGCAGAAGCTCTGAATCGTGTTCCTGAATGAAAGAAGTCAGAG
ATGAAAAGATGGGCCAGGAGTCCAGTTTCTGGAAGGCCAAGAATCGAAGTAGCAAGCTGC
AAGCCGTTTTCCAGACAAGCNGNGATGTGGGGATGCCACAAGAATTCAGGACTGGAGGGG
Sequence 282
CGCGGTGGCGGCCGAGGTACTTNTNACTGCCAGAGGCTGTGACGNTGTGTATTCNGAGAG
CAGCCTTNCCTGCANTGATNCCATCCCGCAGGAATCNAANTTCTCCCTNGATACNGNGCA
CTCTGCCTGTCTTTCCACNTTTCCCTTTCNCATTTTGCANTACACNGTTCACCACNCT
GC
CCTTAAGGCTTGGAAACTCACNCCACCTTCAAGCNTCCCATGGTTCTCTGCCACTCATGG
GTCNGGGNAACCAGGGTGGACAAGGGGGCCAGAATCAAAGNCGTTCTTTCACCCCCACCC
ATGGGCCAAGGGGAATGGGGGCCCCAGNNNGGGGTTCCCCAAAGGCANCAAGNAAAANNA
ACTTGGANACTTGGAAGTGGANGGGCCATTGGNAGGCAAGNCCTNGAAAANGCCANAAAA
AGGGGAGGGGNCNGNAACCACCNCAAAAAAGGTTTGGANGGCCAGNAAAAGGGANANNGG
GCCCCAGGGGAAAAAACCTTTTGGGCCCCATTTTTTTTCCAATTTTCCAATTGGGCCT
TG
GGCCANTAATTTCAAAGGGGAAGGAATTANCCTTGGGNNAAAGGGGNTNGGGGGGG
Sequence 283
TGGCNGCCGAGGTACAGNATTGGAAATGGATCTGTCTTTGGTAAAGATCAGCCTATAATT
CTTGTGCTGTTGGATATCACCCCCATGATGGGTGTCCTGGACGGTGTCCTAATGGAACTG
CAAGACTGTGTCCTTCCCCTCCTGAAAAGATGTCATCGCCNACCAGATATAAGAAAGACG
GTTTGCCCTTTTCAAAAAGACCCTGGGAATGGTGGGCCCATTTCTTTGGTNGGGNCTTCC
CAATGGCNCAAAGNAAAGGGGAAANGGGCNATTGTGAAGAAGGAAANANAGTATTTTTACC
TNGAAAAAGGCCATAAATGGTGNANANAAATTCTTTCCANAAATTCCNCAAGNGNGGTGG
CANGCCCCTNTAGTANTAAAANTANCGNCCCAAAGGAAAGGNTCANGTTTAAAAGGGGTT
TATTTTGTTTGTTNGGGGTAAAATCNCAAGCCCCAAATACCCCAAACTTGNCCCCTGGAA

Table 1

CTTGGCTTTTCNCAAAGGTTCNAGGCTTTCCNATTCTCAATTCCCCCCCAAAAGGGGAGG
AAACCNTTTCC
Sequence 284
GTGGCGGCCGCCCGGGCAGGTACGCGGGGGCTCTAAGCTGCAGCAAGAGAAACTGTGTGT
GAGGGGAAGAGGCCTGTTTCGCTGTCGGGTCTCTAGTTCTTGCACGCTCTTTAAGAGTCT
GCACTGGAGGAACTCCTGCCATTACCAGCCTNCCCTTTCTTTGCCAGAAAGGGGAGGGGG
GGAAAAACAATNACAATTTTATTTCCATTGGCCCAAGTNCTTGTNTNGCCAATTGNCAAG
TGCTTTTTTTTGGGCCNTTTNTCTTACCCCTTTGCCAAACCAAGAAAACTNAAATNTTG
N
CNACNCAAANCTTCCCTTTAGTTAGNCGCGGAATNTCNCCGCCCCCACAAGTAAGAAAGT
TCNCNTGGNNAAGNCCCACCAAGANCCTTTTTTTTTGGCTTTTTTGCCAATTTGGTGA
AG
GGAAG
Sequence 285
TGGCGGCCGAGGTACTAGGTCCCAAATGTTTCAACCGATTTTACCCTATGTTTTCAAGGG
TATTATAGAAGGGGAGAGGTATCCTGTAGTGATGTCCACGTATCTTGGAGTTATGGGTCG
AGTTCTACTACAAAACACTAGTTTTTTTCTTCACTTACTTAATGAGATGGCCCATAAATT
TAATCAGGAGATGGACCAGCTTTTGGGAAATATGATTGAAATGTGGGTTTGATCGAATGG
ACAACATTACCCAGCCTGAAAGAAGAAAACTTTCAGCTTTGGCTTTGCTCTCTCTTCTGC
CATCTGATAATAGTGTTATCCAAGATAAATTCTGTGGGATTATAAACATTTCAGTAGAA
G
GCCTGCATGATGTCATGACGGGAAGATCCTGAAACAGGAAACTTATAAAGACTGTATGTT
GGATGGTCTCATCTTGAGGGAACCCAAAAGTAACCAGGAAGATGAATGAAACCACCCAC
Sequence 286
GCGGCCGAGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGGAAAAGATC
TGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTGCTC
ACGGAGGCACCCCTGAACCCCAANGGCCCAACCCGGGANGAAAAATGAACTTCAAAATTA
TTGTTTTTGGAGAACTTTTCAAATTGGTCCCCAGGCCCATGGTATTGTGGGCCTTATC
CC
AAGGCCGGGTNGCCTGGTCTTCTCTTATTGCCCTTNCTGGGGACCGCCACAAACNTGGGG
CAATTNGNTGGCCNTGGGAACTTCTTGGGAAAGAATTNGGGTNGGTCCAACCCCCAACAA
AATGGNTCCCCCCCAATTCTTATTGGAAGGGGGGCCTTAATTGGCCCCTTTTGGCCCCCC
CAAATGGCCCCANTCAATTGGNCCGTTCNTTGGGGAATNCCTTGGGCCTTGGGGCCCGGG
AAGNAATTCTTCAACCTTGGAACTTAACCCCTTCAATNGGAAAAGAATTCCCTTGGACCT
TGGAAGGCCGGTGGGGCCTAATTTCCCCTTTTCGGNTTTAACNTAACCTTGGCTTGGNAA
GCCGGTTGGAANGNAAATTTGGTNCCCGGGGGAACCATTTCAAAGGGGGAGGAAAAAANC
TNGGNGGTTTTAATTGTTAAAGCCCTTCTTGGGGNACTTTTTTGAAAAAAA
Sequence 287
CTCCCCGCGGTGGCGGCCGAAAACTGATCAGACTGTCTCAGATCNAGGAAAAGATGGCCA
GAGAGAAGCTGGAAGAAATAGATTGGGTGACATTTGGGGTTATATTGAAGAAGGTTACGC
CACAGAGTGTGAATAGTGGAAAAACCTTCAGCATATGGAAACTGAATGATCTTCGNGACC
TGACACANTGTGTGTCCTTGNTCTTATTTGGAGAAGTTCACANAGCGCTCTGGAAGACGG
AGCAGGGGACTGTCGTATCGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCA
GAGGAGGTGTGTNTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGCTCTT
GACCTGGGAACCTGTAAAGCCAAGAAGAAGAATGGAGAAGCCGTGCACGCAGACTGTGAA
TTTTGCGTGACTGTTGAGTACCTCCGGCCGCTCTAGAACTANTTGGATCCCCCG
Sequence 288
GCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGTGGAGCGCCTCACTAACTCCATGATG
ATGCA
Sequence 289

Table 1

GGACAGACTGGCTCATNGAAGACATTNACTNTGATGGGACCATTTNAANCNGATAATTTT
TCTCATAACCTGAGAGGAGTNATCCCACGAAGTTTNGAATNTTTGTTTTCCTTAATTGA
T
CGTGAAAAAGAAAAGGCTGGAGCTGGAAAGAGTTTCCTTTGTAAGTGTTCCTTTATTGAA
ATCTATAACGAGCAGATATATGATCTACTGGACTCTGCATCGGCTGGA
Sequence 290
TGGCGGCCGCCCGGGCAGGTACGCGGGGCCCGTAGGAGCCTCTCTCCCTACTGCTGCTAC
ACAAAGACCCTGAGACTGACCTGCAGGAACTNAAACCATGAAGAGCCTGATCCTTCTTGC
CNTCCTGGCCGCCTTANCGGAAGTAACTTTGTGTTATGAAATCACATGAAAAGCCATTGG
GAAATCTTTATGGAAACTTAATTCCNCTTTTNATTTAAANCCAGGGNAAGNNAATATGT
N
AAAAATTCCNCTTTTTTATTANNTCCCCCTCTNCAATCCAAGNANGNATGGGGGAAGCNA
GCNTAAAACCNCTNCNNATNANANAGNTNGGGTTTCTAAATAAGNAANCCTTTCTTTCTA
AANANGNNCNTNGNGTTCCCACCGATATCTTTTATATATTNNGGGATTNANCCCCCCNTN
TGNNAGNTTTATNTACTTTNACNNANGCATTTTTTTTTNNGTGNAAAAAACCCCGCNNT
T
AACCNACCCCAANTNGGGGTTTTTATATTGGGGGNANTNACCAAAAATGGCCTNGGCCCT
TNTATNANAAATCNGCGCTTTNNCNTTTATAACNAGGGAAAAAAAGCCCCCCCCCANNGG
GGGNNANNCCCNAAATATNTNTAANATNNTTGGNNGGGGGAAAAAAAAAAAA
Sequence 291
GAGCCCGGGTGGCGGCCGCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTGGGGGAGTTA
AATAAAATAAGCATGTCTCCATCCTTTATTCCTAAACATTTACTTATGACAAATGTANCA
ACTGACAGAAATTTGAAAAATACCAGACACTTCTTAAATGATTTCCCTTGGGTCAAAAT
T
TACCCCTTCTTGTTTTCTCTTGCTTTTCAGGTAATTAACTCTTCTCTTTTTAGTTTGAAC
TATGCAGTGCAAGATTCCTCTGTAGTCTTTCCAAGTGGAAGGGTATAAAAAAAAACACTT
TATATTATGCCAGGTGAGGTGTCAGAACCCTGGCATCGGAAAGTGGTTGGCTCACGGGTC
ATAGGNGTAGTAAGAAGAATTTACCGAAGACAGTATTNGGTTCCGAAAAAGAAAGTTTTA
T
Sequence 292
CGGTGGCGGCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTTGTTTTTATCTTTT
GGCCTTTTGGTGACTTGGTGCTCCTTGGAGTCACTGGAGTTCTACTTTGAATCCCACT
CT
GACATCAATCGACTGCCTTAATTCCTGGTCCAGCTGCCCGACCCTGACTCTCTNCCGCTC
TTTTCCTCAGGTCGAANGTTTNCTTTAAGATCACGCTGACGTCGGACCCACGGCTGCCGT
ACCTGCCCG
Sequence 293
GTGGCGGCCGCCCGGGCCGGACGCGGGGACATTCGAGTGGGGATTAAGAGAAGGAAGGCT
GCCTTGCTGGAGCTGTGTGGTCTTCTCCAAGTGAGAGTCGCAGGCAATAGAACTACTTTG
CTTTTGGAGGAAAAGGAGGAATTCATTTTNAGCAAGACACAAAGAAAAGCAGTTTTTTTT
CANGTGCTGACGGCCACCCACCATCATCTAAAGAAGATAAACTTGGCAAATGACATGCAN
GTTCTTCAAGGCANAATAATTGCAGAAAATCTTCAAAGGACCCTATCTGCAGATGTTCTG
AATACCTCTGAGAATAGAGATTGATTATTCNACCAGGATACCTAATTCAAGAACTCCAGA
AATCAGGAGACGGAGACATTTTGGTCANGNTTTGCAACATTGGACCAAATACA
Sequence 294
GCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAGGCACATTCTTTTCTACGTGAAGAGTTN
TGTAAACTGAACTTTGTTTTCAGNNCCGGCTCCAGCCATCCTCGGGTAGCTTGCCAATAG
ATGAATCCCACTCGTTTGACCCATGACGCTCCTTCTTTGCATNNCTCCCTCTTTCCCC
AC
AGCAGNGCATGTCCACCATACCACCTGAGAGTCTGTGGAATCTAATTTTCTGTNATACTT

Table 1

CTTTCCTTACACTCATTTTCCTGTCTTTATTATGATAGTCTAACTTTTTCTCCTCAAAGG
TATAGCTGCCTTGCTTTCATGAAAACACACTTTCCTATTGTGATTTATCAGAGGCCTTT
C
CATATCTCAGCCACTATGCTATGACAGATTTTATAATTAATA
Sequence 295
CNCGCGGTGGCGGCCGGAAGAGCAACCGAGATGAAGGTGAAGATGCTGAGCCCGGAATCC
GGACAATTATGTCCGCGAAACCAAGTTGGACTTACAGAGAGTTCCAAGAAACTATGATCC
TGCTTTACATCCTTTTGAGGTCCCACGAGAATATATAAAGAGCTTTAAATGCTACCAAAC
TGGAACGAGTATTTGCAAAACCATTCCTTGCTTCGCTGGATGGTCACCGTGATGGAGTCA
ATTGCTTGGCAAAGCATCCAGAGAAGCTGGCTACTGTCCTTTCTGGGGCGTGTGATGGTA
GAGGTTAGAATTTGGAATCTAACTCAGCGGAATTGTATCCGACCCT
Sequence 296
CCGCCGGGCAGGTACGCGGGGCTCCCTTGTGAGTAGACTATGCAAAGAAAAAGTGGGCCA
CCATATCTGGAAACTACAGTCTATGCTTTGAAGCGCAAAAGGGAATAAACATTTAAAGAC
TCCCCCGGGGACCTGGAGGATGGACTTTTCCATGGTGGCCGGAGCAGCAGCTTACAATG
AAAAATCAGAGACTGGTGCTCTTGGAGAAAACTATAGTTGGCAAANTCCCATTAACCACA
ATGACTTCAAAATTTTAAAAA
Sequence 297
GCGGCCGCCGGGCAGGTACGCGGGGGGAGGGCTCCGAAGTCTGGTTTTGGGCGGGAATTG
AAACCGCCGCTGAAGCCAACAAGAATTTGAGAACTGTAAATACCAAGCCTTGAAAGGGAC
CATGGTGCGGCCTGTGAGACATAAGAAAGCCAGTCAAATTCTCACAGTTTGACCACTCTG
ACAGTGATGATGATTTTGTTTCTGCAACTTGTACCTCGGCCGTTCTAGAAACTTANTG
GA
TCCCCCGGGCTNGNAGGGAATTTCCANATTTTNAANCCTTTTTNCGGANCCCCCNCNCCN
CCCCTNAANGGGGGGGGGGNCNCNNGCCCCNCNNTTTTTNNNTGGCCCCNTTTTTTGNNG
GGGGGGNGAATTTANCNNCCCCNCNGNCGGGGNAAANAAAATAGGGGGGNAAAANTNTTT
TTNTTNNGNGGGGGNAANAAAATTTTTTTNTCTCCCCCCCAAAAATAAAAAACNCGNCCC
NCTTTCTNTCCCCGNTGGNNGNAAANNANTATNGNGGTCCCCCCNNGNGGGGGGGGGAN
ANTTTTTTTTTTNNNNAATTTTTTTTT
Sequence 298
GTGGCGGCCGAGGTACTCCCCAGCAAATATTCTTTGTTGGCTTGCTTGACTAGATGAGCT
GCTATAGTAGTCAATCCTGTTAGACTTGGACCATTGTTTGTCTGAAGAACTGGAATCT
GT
CGCTCGCCCTGAGCACTGTATTTATTTCCCCTTACTCANTCCCCAGGGGACTTCTTCCAA
GTAAGCCGACANACTTCTTGCNGGCCCCGCNCGCNCANTCTTTTCCCGGNCCGGCTTCTT
AGTAAACTTAGGTTGGGAATCNCCCCNCGTGGGCCTGGCNAGGGGAAATTTTCGGAATTA
TTCAAAAGGCCTTTATTCNGAATAACCCGGTTCNNACCCCTTTCNCAAGNGGGGGGGGG
CACCCCGNGTTAACCCCCAAGGACNTNTNTTTGGTGTNCCCCCTTTTTAAGTTGGAAGGG
GGGTTTTAAAAATATTGGCCGACCGNCCTTTTGGGTCCGNTTANAAATTCCAATTGGGGG
GNTCAATTAAGGNCCTTGNTTTATTCCCCTTNGTNGTTGGAAAAAATTTNGTTNTAAAT
T
CNCCGNCNTTTCAACNAAAATTTTTCCCNANNCAACCAAAACCNAATTAACCNGAAGNCC
CCCGNGGGGAAGNCCAATTAATAAAAANNTTGGTTAAAAAANGGCCCCTTGNGGGG
Sequence 299
TGGCGGCCGAGGTACTTCTGTCTTCCAGTTTTCCACTTCAAACTTCTATCTTCTCCAA
AT
TGTTTNATCCTACCACTCCCAATTAATCTTTCCATTTTCGTCTGCGTTTAGTAAATGCG
T
TAACTAGGCTTTAAATGACGCAATTCTCCCTGCGTCATGGGATTTTCAAAGGGTCTTT
TT
AATTCACCCTTCCGGGTTTTAAATCCTCTTTTTTTAAAAAGAATCCGTCCTTTCAAAAAT

Table 1

TATNTTTAAATTCACCCTTACCAACCTTTTTAAAACCTAAAAACCTTTAAAGGCTTGTTT
TAAAGGTCCACCCTTTCATTTTTTAAATCTAAAAAAGGCCATTTGGCCCCTTTCTAATT
T
GGGNTAATTNAAATTCCGGGGGCCTCTTGTTAGGTACCCTNTTCTCTTCAAATTTTTAT
C
CTTTTTTTAAAAATTACCATTTTTTTTTTTACCTTCCCATTGAAAGGAAAGGCCTTTNCAT
TCTTTCAAACCCCTTCCCGGTTCAATTGGTTTTTTTAAGGAAAAAACCCCTTTTTTTNAT
TTCTTTTTTTCCCCTTTTCCCCTTCCAATGGCCCTTAANCTTTCTTTTCCTTNAAAGGGT
GCCTTTCCAATTAATTTTTTTTTCCTTCTTTTAAAAAAAAATTCCTTTTA
Sequence 300
CGCGGTGGCGGCCGAGGTACTTAAGGTTGACTGGTAATCAGGGTAACTTCTGATACTTAT
CACACAAGATGGTGCCTCAGCATTTAAATAAATGGAGGTAGGGGAGGGCGTGGTGGTAAC
ATACTTTTAAACCAGCGATTGCACAGCAAACCACAATGCAAGGTATTTCTGACTCCCAAG
ATTGCCCGTTTCCTAAAGAGCAATTCTTCTGCAGGCAACAGCAAACCTACCTTTCCTTGC
TAACTGCTTTCAGTAAATTCTTGATGGCCTTCGATTCTGGATTCAGACATCTCTTCTCA
C
CCTTCTTTTTCATTGTAGCAATGATCTCAACACGTG
GA
Sequence 301
TCCCCGCGGTGGCGGCCGGAGTGATGCCTCTGCAGTTTTGTGATCTGCAATGATTCTTCC
CTTCGAGGTCACGCCCATTATCTTTAATCCTGACTTTTTTGTGGAGAAACTCCGACAT
GA
GAAACCTGAGATTTTCACTGAGTTGGTGGTCAGCAATATCACAAGGCTTCATCNGATTTA
CCTGGAACTGAGTTGGCTCAGCTGATGGGGGAAGTGGACCTTAAGTTGCCTGGCGGGGCT
GGCCCAGCATCAGGATTCTTCCGGTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTG
ATATTTGGGTCCCCACTGACGGAGGAAGGCATTGCCCAGATATACCAACTGATTGAGTAT
CTACACAAAAACTTGCGAGTAGAGGGTTTGTTTAGAGTACCTCGGCCCGCTCTAGAACTA
GGTGGATCCC
Sequence 302
TTGGAGCACCCCGCGGNGGCGTTTTGGGACGCNCGGAACNGCAATGCTTCAGGACCCACA
GGAGCGACTCTTTAAAGGGACCACAAAANCCGCACAGAGCTGCAAACAACTATACATGAT
ATAATATTAGAATGTGTGNACCTGCCCG
Sequence 303
GNGGCGTTTTAGGGCGNAACGGCCCCCCATCATGGCGGACCCTAGAGAAAGGCTCTTAGG
GGGACCNAAACCCGNNGCCCGAACACAAGGAGANCGACGGCCGCTCTTNAACCAGNGGAG
C
Sequence 304
TCGCCCGAGCTTTCTCTTGTCCATCTTCTCCCGCTGCTGAAATTTCAGTTGCGGGCGCTG
TCACCTCAGGACCCCTCCCCCCGCGTACGCTGGATAGCCTCCAGGCCAGAAAGAGAGAGT
AGCGCGAGCACAGCTAAGGCCACGGAGCGAGACATCTCGGCCCGAATGCTGTCAGCTTCA
GGAATCCCCGCGTACCTGCCCG
Sequence 305
NTTAAGAGCAAAGGCTCATGTTTGCCAAGTCTGTCCTTTTGTAACAAAAAACCCAGCAGC
TTTATCAAGCAGAATTCCACCTGTATTTCTTAACTTGCCAGAGCTGAGTCTCATGGCC
AC
CCTTAGCAGGAGTTGGGGAGGTATTTTTAACAAGGCACATTATCATCTCCCCCACCCAAA
GTGGAGCTATTGCTAATGAAAAAGATACAATGAGATGTTTATGAAATTATCTGTAGCTAT
TAATGTCAGGTTTTTGAAATTTACTGACCTGGAAGAATACTCATAATGCAATGTCAAGT
G
AGAAGCAGGACAAAGAACATTTGCAATACAGTTGTATTTATAAAATTTTGTT
Sequence 306

Table 1

NATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGGCAGCGGAAAGCTCAGCCC
ATGTGAGGTGCCTCCTGCCAATCACAGACTACCCTTCCCTGGTCCTGGAGGTTCAAAGAA
TTGCAGGAGGGTAGAAAAGCACCTGGGTCGGGTGCAGACTGCGGAGCGGGCCCTACCGTG
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Sequence 307
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TTCTTCTTTACCAGGGGTCTTACTCTGTTCTGAAACATGGCACCTCAGGCGGCTCCGGCA
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Sequence 308
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Sequence 309
CCCGCGGGGGCTTTNGGGGGCAANCGAACACCNCTTAAAGGGNNCNCCNTCTAAAAATNT
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NGCCCGGG
Sequence 310
CACCGNGGACAAGAGCAGGNGGTNCTTGGGGGGNGNAAAACCCGCNCCGCGANGCAAGAG
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Sequence 311
CCTGAGGAAAAGCTCGCACCAGGNGGACGCGGATNNGGTANGGGGGGTAAAANACCCNCC
CCAACAAGCCGCGGGGCAAAANGNCCNCGTACNTCGGCCGCTCGAGAACTAGCGNACCCN
A
Sequence 312
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Sequence 313
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Table 1

Sequence 314
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GATGGCCAAAGACAACTCAACTGTTCGTTGCTTCCAGGGCCTGCTGATTTTTGGAAATGT
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Sequence 315
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Sequence 316
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Sequence 317
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Table 1

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Sequence 320
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Sequence 321
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GGGGGNGGNGAAGGANCNNAGAAGNNGGANGCCAGGAAANGGGANGAAGACCAAANGGGC
CANGNNNCAGAACAGAGAAGACCCCNGGNAA
Sequence 322
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Sequence 323
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Sequence 325
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Sequence 326
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CTTTATATTATGCCAGGTGAGGNGTCAGAACCCTGGCATCGGAAA
Sequence 327
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Table 1

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GGTGGGGCT
Sequence 329
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GCATTTTTTGGGGGAATTATACCTTCCCACCAATCTTTTTGANTNTATTTTTCCTTTGG
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CCTTAAATCATGAATTTTTTTCAAAATTAANAAGGTTNNAAAGNTTTAAA
Sequence 330
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Sequence 331
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TGCCCG
Sequence 332
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TCACTCGGGGAAGGAGGTATGGTGGCAACACTTTATGCTTAATATTCAATTCTGCTCCAG
TAGAACATGGTACCT
Sequence 333
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Table 1

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CT
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CTCGGCCGCTCTAGAACTAG
Sequence 335
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Sequence 336
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Sequence 337
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Sequence 338
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Table 1

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GGGGCNCNNAAAAAAGGAAGGGGGGGGGGCCGAAAAACNGCCAAAAAAAATANAANNNNG
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AAAA
Sequence 339
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Sequence 340
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Sequence 341
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Sequence 342
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CTTTCCTTGTCCTATTTTTAATAAGACAAAGAACATCACCATATTAAGTTGAAGTACCT
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CCCGGGCGGCCGCTCTAGAACTAGGTGGATCCCCCGGG
Sequence 343
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Table 1

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Sequence 344
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Sequence 346
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Sequence 347
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CTTCAGAGCTACCACCAGGNTTCCGAAACTTTTTCGGNGGGAGGCGCTTTNGCCACCACC

Table 1

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Sequence 348
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TTATGTGAGTGATACATCTTTTCATATCTTCTTGGTGTGTGTGTGTGGTATCATCAGCC
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CAACATCTGAAGCAAATGTTGGGTGGGGGGTACCTCGGCCGCTCTAGAACTAG
Sequence 349
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CCCTGACATAGCCATGCTTTTTGAAGAAGCCTTTGTGCACCTGAAACCC
Sequence 350
CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCGTGCTAAAAGACTTTTAGTTCGGCTCT
CCCAGTGTTTTTTTTTCGTCGATTTGGGCACAGAGTTTCCTGGTTCACGTGGATGTGA
GG
ATCCTTTACTCCAGATCGCCAGCCAGTTTTTGTTTTTTTTCCTGCGTTGCTGAGAGTCT
G
GGTTTATTCATCACACCAGGTGGATCTTAATTCCATATCCCTGAGGCCACTGCAATGAGG
CAGAGGAGTGTGCTCCCTCATGAGAAAGGACTGGAGACCGCCCCCAGAAGAGAACGTATC
CATGTACCT
Sequence 351
CCCCGCGGTGGCGGCCGCCCGNNCTGGTACTTATAATGCCNNNNNTTNCNGGNTGTGAAT
GGATTACANTGTATCTTTTCAGGGAAACCTATTATTATCAATGTGACTCCACNGGGGGAG
TCCATGGTGATGATGATGAGGAGGAGGATGATGATGATGAGACACCTCTAAACTTGGAAC
AAGTTTAAGACTTTATGAGAGAAGAAAAAAAATCACCAACAAGAATTGTTTGAGGAAAAA
TCATAACTATCCTGTGTTCATTTTTTTTTTTATAAACAATAAGAAAAAGTTGTTGGATTT
TTTTTTAATGATTTCTTTTTTGGGGGAGGGAATTTTTGTTGCAGTTTTATGGTGGAAAA
T
GCAAAAACCAGAGCCAGGTGCATAATCTTGTAATCTGTGGATATCCCTGGAGCAGGACTG
ANCCT
Sequence 352
NCCGCGGTGGCGGCCGCCCGGGCAGGTTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGT
AACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAA
CAACGCAGAGTCCAGGGAAGCAGTGGTAACAACGCAGAGTACCCGGGGAAAAAAGGCAAA
TAGAATGAGAACCATATTATGTACCT
Sequence 353
CTCCCGCGGTGGCGGCCGAGGTACACCCAGCTTTGTCTCCTGGCCCCAAATCTCCTTTTC
CTTACTTTGGGCATTAACTGCTGTTGAGGTCTCACAGCCTGATGGTCATTATCCCTGA
AT
GGCATAAATCAACAGGCTGTATGAGCATTGTGTGAGATTCTACATGAGGGAGAGCATTTC

Table 1

AAACCCATGACAGATGAGAGAAGTTAGTACACTCTCACTGAACTGGGGATGTTTGACTTA
AAATGATGGACAATAAGATAGTGAGCAGTAAGTGTGCTCTAGGCTAGGCTACGAGAGGCC
ATGAGCTCCTCATCTCTTCTCTGTTCTGAGCTCTCTGATCCACCGCACTTGGGGCAGGGG
GTGCATTCTCTGTGCCTCTCCTGAGTCTACTTTCTGCATCATTGGGTTCTCCCAGCTC
AC
TTCCATAATGTCCTCCTAGGCTGCATTGGAATTTGTGTGTTGTCTAGACCCATGGCCAAN
ACTGTCATTGCCTGTGAGGGAGACCAAGCTTACCCACCCAAGGGCTTTTG
C
Sequence 354
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTT
GC
CTTTAGAAGGTTAAAATGCCAATATAAAGCTAAAACAGTAATCATCAGAGACAGCTCTAA
TAAGGCTTTGCTACTGTTTTTACTATATAAATCTTTACGTGTTAATGGAAAGAAAATTAA
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G
GGCAGAAAGATCATACAGTTAGGAATGAAGACATCAGAATGTTCCACTAAACAGATATTT
AACTAGATACTATTATACTACTAAGAATAGCAAGAATGTCTCTCAATTCTGGGAATTTC
T
CCTAGCTCACACAAATGAAACGCACATCTCCATGAATGCTTTCTAATAAATGCTTCCAGG
ATAGTATCATAAACAAAGTCAAAATTAAGAAAAATCAC
Sequence 355
GCTCCCGCGGTGGCGGCCGGAACCGCCATCTTCNAGTAATTCGCCAAAATGACGAACACA
AAGGGAAGGAGGAGAGGCACCCGATATATGTTCTCTAGGCCTTTTAGAAAACATGGAGTT
GGTCCTTTGGCCACATATATGCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGA
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TTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTACTGAA
G
AATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGGACTGGTCT
TTCTATCTCTTGTACCT
Sequence 356
GTTGAGCTCCCGCGGTGGCGGCCGAGGTACCTGACTGTGGCTCAGATCTGCGTCGCAGCA
GCGAGAGAAGAAATCACTCCATATCCGATGAGAGGAAGGGTGGCACAGAGATGGTGTCTA
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AA
TTCCATGAGTGACCTACCTTTCCCCAGGAATGGGACTGAGAGGGTAGTCTCCAGCAACTC
AGTCTGCACAGGGCTCCCCGTTCAGGCTGCCTTT
Sequence 357
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CGTTACGTGTGGGGCACAAACGTGGAATATTAGGAGAGAGCTGGTTCCAGCACCAAATCC
AGAGTCACTCGGGGAAGGAGGTATGGTGGCAACACTTTATGCTTAATATTCAATTCTGCT
CCAGTAGAACATGGTACCACCATTCTTCCAAGTTCAAAAATTATCTTTGATTCATTTTG
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TCCCCATTCCTCTAATATGTCACCAATTCTGCTGATACATTCTTTGTAATCTCTCCATC
T
ATTTTAATCTGTTATTCACCTGAGCTACACAAACATTCATCTGCACAAGGAGTATTCCA
C
GTGCTGAAAAGACAGAGGATTAAGCCCTCCTTGTGGAGGCATTCACAGTCTGGTTTTAAT

Table 1

ACACAAACCAACAATTATAATACACAGGGATAAAAAAAGTAGAGGCACTTATTGCATACC
TGTACCT
Sequence 358
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AGCTGAAAACACTGTTTCAGCCCCCTCTCTGGTGACCTCAGCCTTCTCCAGGTGTATCTC
TTGATGATCTTGGAGACCAGCAGCCACAGCTGCTGCTACTCCTGCAGGAGACTGTCAGGC
TGTGGTGGGGGGCAGGGGTGTTGGAGGAGAAGTTGAAAATCCGTGTGTTCTCTGTCCCTC
TGCTCCTCCATCTTAGCTTCTGGAGGAGTTAAGGCACCAAGGGCA
Sequence 359
CGGTGGCGGCCGCCCGGGCAGGTACTGGTGTTGTGATCGGAACGTGTCGATCCCCTCTTC
TCATCACTGCTGCTCCAACTGGATTTATTACTCCGGGAATGGTAGAGAATAAAGATTTGT
AGGAAAGGTGCTGAACTGCCAAGGAAGGCATTTCTTGTGCCGTGTCTGGAACCGTGTATC
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CTGGAGAAAGACACTGAAATTTGGCCATGCAGGTCTACTTCCCGTAGGGGGGATTTTTTT
TTANNAANTGTTTNNGCCCCNTTTGAAAAAAGGGNTTTTAAAANCNAAAANAAAANTTT
T
NTTCCCCCCGGGGGGGNNGGNNTTTTTTTAGGGGGGAAAANGGNGGTTTTANTCCCCCCN
NNGGNAAANCCCCCCCNNTTTTTNTTTTTTGGGGNNGGGAAANATTTTTTNGGGGGTGCN
CNGGNGNNTTTNNNNANAANNNAAAACCCCCCNTTTTNNTTTTTTTAANANACCCNCNNN
AANNGGGGGGTTTTTTTTTTTTTTTAA
Sequence 360
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CCTGTGGAAACTGGTTGAAGTGATTCCTGAGGGAGCAATGCTGAGGCTTGGCATGACAAA
TCCGCCCTATATTTTAGAGCATCTGGAGGAAATGGCANAAATCCTTAATCACCCCAGAGT
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Sequence 361
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AGCACAAACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCCGTCTACCCGGGAATCC
GGGGTCCCTGACCGA
Sequence 362
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GACAACACCTGATCAGTCCTAATATCAGAAAAGAGACAAGTAGACATTATGTGCTTCCTG
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AACCTGTATCTCGTAATGAGGAAACAATCAGTAAAAAAGTCTAGATTGTGGGACATTCCA
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CTGCACATCATACACAAACACCACCCCACCACCCACCACTCAGACACACACAAAAGGGCA
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ATTGGATCCTGGATTTAAAAATAAACAGCTATAAAGGATATTTT
Sequence 363
GCTCCCCGCGGTGGCGGCCGAGGTACTTAAAACCAAATAAAAAGTGACATTTGAATTTCT
TTTAAAAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACCAGCACA
AACCGGGCCAGCCTCCTAAACTGCTCATTTACTGGGCGTCTACCCGGGAATCCGGGGTCC
CTGACCGA
Sequence 364
TNCCGCGGTGGCGGCCGAGGTACAACGCATGAGTCCCGGGAAAGCATGTGGTAACAACGC

Table 1

AGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAG
AGTCCCGGGAAGCAGTGGTAACAACGCAGAGGCTTTCAGCACAGCCCAGGGTGCCCGGGA
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GAAAGCAGAGCCCATTAGTGGGAAAAAGTTGGAGGATGAAGGAATTGAAAAAAAAAAAAA
AAAAAAANGTNCCTGCCCG
Sequence 365
TGACTCCCCGCGGTGGCGGCCGAGGTACCAAGCACTGGGTAAGGCACTTTTGTGGAGCAT
TAGACAGTAACCCTCAAGGAGCTAGAGAACCGGATGGGAGACATGAGCGGTAATTAACTC
ACTTGTTCCCCAGAGTTTCTATTTGTTTTNTTTTCTTTTTCTGTGACTTATTTTCCTATT
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AGTTATCAAGTTATGCTTATATAAGCATTAAAAATTCTCCTCCTTTGACTACACACACA
A
CCACAGTGTGGTTCTAATCNATGGGAGATATCAAGTAATTTTTTAGTAACCTGAATTTT
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Sequence 366
CTCCCCGCGGTGGCGGCCGAGGTACTTTGCATCCTTCAACCCAATCAAGCTGACACTCAG
TATTAACCATCACAAGGCGTGAGGACAGATAGCTGCATCCGCAAAATAGAGAACCAAGAA
ATAGTCCCACACCAAAGTCAGGATCAAATGATTCCTGGACAAGCCACCAAGTCAATTCAA
CTGAGAGAAAGAAGCCTTTGCACCAGTTGGTGCTGGAAGTTCTGGATATGCACCTGGATA
AGTGAACCCCCCTCCGTCACCACACACAAACGTTAATTTGAGATGGATTGCAAACATAAA
AGCTAAAACCATTAACACTTCTTGAAGGTAACATAGAATATTTTGTAATGTTATGATAG
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CAAAAGTCTCTTAGGACACACAAAAAAATTAACCATAAAAGAAGAAAATGGCTGGGTGCA
GTGGCTCACACCTTTAACACCAGCATGTTGGGAG
Sequence 367
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TGAACTGGCTGAATGAAGTGCATGACAACTGAGCAAGCTCTCAGTCCAGGATTACAGCAC
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TGATGAAGTTTTAATAATTCAAGATAAATTGGAAGCCATTAAAGCAAGGTACTGCCAGAT
ACCGAATTGAGCATACCACAAAAAAGTTCTCATTTTGTGTCCTCCCATNCCATTCTCCT
C
ACTAACCAAAG
Sequence 368
CTCCCGCGGTGGCGGCCGCCGGGCTGGTACAATGTGCCTGGCACCTTACAAGACACAAAT
ATGCTCTTATAGGCTGGGGAAATAAGAAAATATGAATGAAGCAACCCAGGTCTTGAGCCA
AAGAATTACCTGGGGTCCGTTGAGTTCAAATCTGAAAATTTCTGTCTTTCAAGGTCAGCA
TCGCCCACAAAC
Sequence 369
CTCCCCGCGGTGGCGGCCGCCCGGGCTGGTACGCGGGGGTTTCCGGTTTGGGTGTGGCCG
CATGGCGTGCTGGGGTGCAGGTGGCCGAAGGGGGCGTTACTGTTGCGACTGGCATCCGCA
TCCGGCAGATGTAGATGGAACCAAAGCCAGAAGTTACGCGTCACCCTTGCTCTACAGCCA
AACATGCAGGACTCTAGTAACCCGCGAAATGATGGGATAGCGTTGCAAATCCTTAAAAGA
GTCTTAACGGAGAAGGAAAAATGTTACATTGTCAAAGTCCCAAAGCCTTTCAGCCTGAAG
CCAGGAACAATTGTTCAAAGTTTCTTTGGAACATCAAGGAAGGAAATCCAGATTTTACTT

Table 1

TAAGTGCAATGGGGGAGTCATTAAGGATTTTGTGTAGATACAGCAAAAGACAACAATCT
TCAAGCCACAATGGCCCTCACCAGAACCCAGC
Sequence 370
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AAGGATTTCCGAGCTCACAGTCAGCTTGCGAGCCATTCTCCCGCGTACCAGCAGAAACCA
GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
CGATTCAGTGGCAGCGGGTCTGG
Sequence 371
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACGATTATTTTCAAACAAGCCTACGTCCCTGA
CTAACCGAGTGGAAGGTGTGAGTGGCACTACAAATTCACAAAAGAACTGTAGCCTCAGAT
AATCAAAGGAGAGAAGGTCAGATGCAATCACTGATGCATGCTAGTAATTCTCAAACCTTC
GTTTTCAGAAACGATTGGATTTTCAGATAGATTTGCAGTAAGAGAATAACAAGTCTTTA
T
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TCCCCACACACTTGCTAATCTACATTTCACAATCTTCTTCACTTTCACTTTGTCTGCAA
A
GGAAATCTACCCTGGGACAGAANAAGCATCTCTTTTTTTTTCCCCCTGACCCTTGGCA
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TTCCTCTCCCTTCAACTT
Sequence 372
GATTGAGCTCCCGNNCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGATGTCTCTTGTC
AGCTGTCTTTCAGAAGACCTGGTGGGGCAAGTCCGTGGGCATCATGTTGACCGAGCTGGA
GAAAGCCTTGAACTCTATCATCGACGTCTACCACAAGTACAAGAGATAGAAAGACCAGTC
CTTGCTGAAAGACAAGTCTGAATGCTCCACTTTTTCAATTCTCTCTCCATTCTTCAGTA
A
GTCAACTTCAATGTCGGATGGATGAAACCCANACACATAGCAATTCAGGAAATTTGACTT
TCCATTC
Sequence 373
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGAAGGAATGGAAACGCCTGGAGAAAGAG
GATGAAATGACGGATGAAGCAGTTGGAGACTCTGCTGAGAAGCCTCCTTCTACTTTTGCC
TCACCTGAGACTGCTCCAGAAGTGGAGACCAGCAGAACTCCACCAGCCTGTGAAACCACG
AACCCTTCAATCAAGAAAAGACCTTTGATCAGGAGAAGACTTCTCGTCTCATTTCTGGGG
ACACATTCAGGATTTCTCCAAAGCAGGTGAAGGTACCTGCCCG
Sequence 374
TCCCGCGGTGGCGGCCGAGGTACGCGCCAGTCACTAGCAGGTCCTTGTGAATCTCCTCAC
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GTGGGAAGGACAGTGACATGGATGATCCCGGACCCTTTGTAGGTCTAGGCTAACGTGGTG
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TNNNNNNNNNNNNTNNAAANNNNGGGGTNCCTTGCCCGGG
Sequence 375
TCCCGCGGTGGCGGCCGAGGTACCTCAGCTGTTGATCTGTGGAGCCTAGGAATCATTTTA
CTGGAAATGTTCTCAGGAATGAAACTGAAACATACAGTCAGATCTCAGGAATGGAAGGCA
AACAGTTCTGCTATTATTGATCACATATTTGCCAGTAAAGCAGTGGTGAATGCCGCAATT
CCAGCCTATCACCTAAGAGACCTTATCAAAAGCATGCTTCATGATGATCCAAGCAGAAGA
ATTCCTGCTGAAATGGCATTGTGCAGCCCATTCTTTAGCATTCCTTTTGCCCCTCATAT

Table 1

T
GAAGATCTGGTCATGCTTCCCACTCCAGTGCTAAGACTGCTGAATGTGCTGGATGATGAT
TATCTTGAGAATGAAGAGGAATATGAAGATTGTTGTTAGAAGATGTAAAAGAGGGAGGTG
TCAAAAATATGGACCAGGTGGTATCTCTACTTTGTTCCAAAG
Sequence 376
GGTCACAGGTCTCGAAAAAGCGGGTGGTGCAATGCTCCATGGGGATGAGGGGAGCACCGC
AGTGGAGCCAGCTCGGTGTGGGAGAGGTACCTCTAAGGTGTTCTTCCTACCTAGCCTAGT
TTTTTTCTACCAACCTAGTTCACCTAGTTTCCTGCCTAACCTCGTTAGATATCACTCTT
C
GCTGCTTCAAGAATACTAAAGCAACACTCCTGATATTAACCTACTACTCAGTTTTTGTG
T
GGCAAAAACAGNAGATCACATCCCATTTGTCTTTTGNGTTCTCTTGGCTGNTTAAGCANC
AANAGTTTAGCACTTTAATTCATTGCTCTACCAAATGGTTTAGTTTGGAAATAGGGGTG
G
ANGTGGACAAGAAGNTTTTGNTTTAATCCCTTCAAAGCCAATTNAACTTGGTTTTTGGT
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TTAGGTNGAGGAAGGGCCANGNANTNGTTCAAAGGTAGGCCTCAATGNAACCGTTTACCC
CCCN
Sequence 377
GCGGTGGCGGCCGGACGGAGGAGACGGTGCTGTGCTGTGTATGAAGACGGCAGTGAATGA
CTCTGCCAACAGAGGCCATGTGGAAGTGTTACATCACCTTTTGCTTGGAAAGATTTACTA
AGAAGTCAAATAGTGGGTTCCTTAGAGGGAAGAGGTTGGAAAGAACCATGACTGTATTCA
GGAAGGCACATGAACTGAAGCTTCTGTCAGAATGCCAATACAAGCAGTTGAGTGTTTCGT
TGCTGTGTTATAAC
T
Sequence 378
TCCGCCCGGGCAGGTACCAGGTGGTGAAACCAACTGCTGAACGCACAGCCTACCTCCTGT
ATTACCGCCGAGTGGACCTGCTGTAAACCCTGTGTGCCGCTGNTGTGTGCGCCCAGTTGC
CCGCTTNGTAGGACACCACCTCACACTCACTTCCCGNCTCTCTTTAGTTGGCNCTTTAGA
GAGAAACTCTTTCTCCCTTTGCAAAAATGGGCTAGAATGAAAAGGAGTATGCCNTTGGGG
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ACAAATTGCTTGANTCCTGGAGATNAAGGAAAGNTGGGATTTNGATTCCCCAAGTCCTCA
TTGCTTAAGTAGGAATAAAATCCTTGCACCCATGCNAACAACCAACTTNGTAAATTTNGG
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Sequence 379
GAGGGACTGCTAGCCAGCCAATAAAATATAAACTCCATTTGTCTTAGTTATATAGAACTG
TGTTTCCAGCTTAGAAAAAGTCAAACCAATGACTTNTAGAACAANCTACTCTCATTTTT
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ATTCAGCCTCTAGAACATGGAAGCTTTAAAAGTGAATTGGCTAAANAGGCAAGACCTTCT
GAAAGTTAACATCTTAATGATTAAAAACAGTAAGTACGCACAACCGAAGCCGTAGAGTCA
CACTTGCAACAAAAGGTTACAANTATTGCTAATGGGGCTCTGTCCGGTNCTGCTTGTCCA
GCTGGACCATCTATTTCATCCCTCCTCCTCTTGAGCTGTCATTTTAATTGC
Sequence 380
NCCGAGGTACGTTAGCTCATTTTCCCTTAAGCGGGTTGTGACGTACGNTGAAATTGCAAA
CGCTCAAACTTCCAACACTTGCGTATACACTTGTAAACCCAGCTTTGNNAAGTGAGACAC
GCATCAAAATCATGATGAACAATTGACCGGCTGCNTNGCAGTCAAGCAGTTGGGTTA
Sequence 381
CCGCGGTGGCGGCCGAGGTACACCATGTGAAGACTGGACTTAAACAGCTACACCACCAGA
AGCCGAGAGAGAGGCTGGAACATAGCCTTCCCTTTGGAGGTAGCCTGGCCCGGNGGGCAC

Table 1

TGTGATCTCAGACTTCCAGCCTTCAGAACTGTGAGACAATATTTTATTGTTTAAGCCAC
T
TATTTTTTGGTACCTGCCCG
Sequence 382
NGGCGGCCGAGGTACTTTTTTTTTTNTNTNTTTTTTTTTTGAGACGGAGTTTCACTCTTG
T
GGCCCAGGCTGGAGTGCAACGACACGATCTCAGCTCACTGCAGGGCTNTGCCTCCTAGGT
TCAAGCTATTCTCCCTCCTCAGCCTCCCAAGTAGCTGGGATCACAGGCATGCACCACCAC
CNCCCNGGCAAATGTTTTTTTTGGATGTTTAAGNCNGACGTGGAGTTTCTCCATGTTGGC
CAAGGCTGGTCTCAAACTCCCTGACCTCAAGGGNGATCCACCNTGTCTCAGCCTTCCAAA
GNGCNTGGGGATTTATAGGCNATGGAACCAATNAACGCCCGGGCCGGCAATAAATTTGTT
ATACANNACTACCATGNAGTTAAATCTGCNANTANNATTGGGACCGAATGGTNTAATCCC
TTCNTACTTCTTTAAATTNTTCCCAANNGGACCTTCAATTAATAATAATAAAAATTNGGA
TCCTNTTTTTTTAAAATGA
Sequence 383
CTGCCGAGGTACTCACAGTCACNCAAATTCNGNGGGTGGNTACACGGCTCTCCATTCTTC
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GCCTTTGGTGNAACCTTCNTCCCCAAAATAAANAAACCAAGGGACAACAACATTTGNGGT
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TTTTTCCCTTTTGAANCCTGGAAGAACAAGGTCTTGGAATCCAANTTTTTTCCGGGGN
CN
NCTCCTAAAAAACTAANNNNGGAATNCCCCCCCCGGGCCTGCAAGGGGAAATTTCCNNTA
NTCAAAAGCTTTAATCTNATTACCCCNTCCAACCCTTCCAAAGG
Sequence 384
AGACTGCAGGAGATGTGGGCCGTGCCAAAGAGATGGATGAGACTGTTGCTGAGTTCATCA
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TTTTGTCTGAAAATCAACTGCAGACTGTAAATTTCCGACAGAGAAAGGAATCTGTAGTTC
AGCACTTGATCCATCTGTGTGAGGAAAAGCGTGCAAGTATCAGTGATGCTGCCCTGTTAG
ACATCATTTATATGCAATTTCATCAGCACCAGAAAGTTTGGGATGTTTTTCAGATGAGT
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AAGGACCAGGTGAAGATGTTTGACCTTTTTGATATGAAACAATTTAAAA
Sequence 385
GTACTCCGTCTCAGAGGANGGGATGCAAATCTTCGTGAAGACACTCACTGGCAAGACCAT
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AAGATGGGNGCCGCCACCCTGTGCTTGNACNTANCAACAATCCCATGAAAGGAGGTCTAC
NCCTGGCACCCTTGG
Sequence 386
CTTTTGAAGGCCCCGNTCGCCCGGGCAGGTACTCCCTGATAAAGGGGAATTTCCATGCCG
TCTACAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCCTCAGTATATCAGGAAAA
AGGGTGCAGACGTCTGGTTCAAAGAGTTGGATATCAACACTGATGGTGCAGTTAACTTCA
GGAGTCCTCATTCTGGTGATAAAGATGGGCCGTGGCAGCCCACAAAAAAAGCCATGAAGA
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Table 1

AACCATTTTTCAGATATAAAGAGAATTACTTCAAATTNGAGTAATTCAGAAAAAACTCA
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GAATTTAAGTTAAAAAGTGGTTTGGACTTGGGAACAGGACTTTTATACCTCTTTTACTG
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AACAAGTACCTCGGCCCGCTCTAGAACTAGTG
Sequence 387
TCCTGTATTGCCTTTTTAATCTTGCTTGTTTAAGNACNTTTCAGGGATTGTCATCATTG
A
TCATCTGTAAAATTGTCAAGNACTAAGGTCCTAAACCTTAATC
Sequence 388
CCTTCCCNCCCNGCGAGNCCGCNGGGGAGATAAAAATATCACCAACATAATATANCACGG
ACTAACCCCTAAACCTTCTGCNTAATGAATTAACNAGAAATANGGGGGCAAGGAGNGCC
ANAGCTAANACCCCCTNAACCAGACGAGCTACNTAAGAACAGGTA
Sequence 389
CACGCCTGTAATCTCAGCACTTTGGGAGGCTGAAGCNGGCCGGATCACGAGGTCAGGAG
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CAGGGCAAGACTCTGTCTCCAAAAAAAAAGAAAAAAGGAAAAAAGCCTTTCTTGATGCTG
TTCCCCATTTCTCCACTAAAACGCCTGCTTTTCTTAACTCCACACCGAACCAACCTGA
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GCCGCTCTAGAACTAGTGGATCCCCCCGGGCTGCAGGGAATTTCGATATCAAAGCTTAT
CGATACCCGTCCGACCTCGAGGGGGGGCCCGGTACCCCAGCTTTTTGGTCC
Sequence 390
AGTACNCGGGGCTTTTCTCAGGCGGNGGCATGGCGGGACAGGAGGATCCGGTGCANCGGN
AGATTCACCAGGACTGGGCTAACCGGGAGTCGGCCGCTCTAGGGGN
Sequence 391
CGCCGAGGTACGCGGGATGGGATTTCTGACCATTTGCCCTGCCTCTTGCAAAATAGGTCT
AATGGCAGGATGGTGTCATAATTAAGGCTACCAAGACTGCCCATTGTTCCAGGCTGGGCA
GTTCATAATGGGGGCAGACAATAGTGCAAAAAAATTTTACATTTTATCTTTAGAGTGTC
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GGGTCAAATTGATTTCCATGGTTGAGGATGTAGCCAAGTGTGGAATCAGGTGGAATAGGT
GGAGAGTTGCCCATAGTGGTTTGGAAAAGAGAAGAGGACTTTGAAAAGTGGAGGGCTCAT
TAGGTGACCCAAATTTTACCTGGGGCATCCCCCCTTTAGGGCCCCAACTTAGTCTGTCAG
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CAATAATAAATTCCTTTTCATGAATTCCCTTCA
Sequence 392
AGCGCGGGGAGAGGCCGGTTTGCAGTATTGGGCGCTCTTCCGCTTTCCTCGCTCACTTGA
CTCGCTGCGCTCGGGTCGTTCGGCCTGCCGGCCGAGNCGGTNATTCAGCTTCACTCAAAA
GGGCGGTAATTACCGGTTTATTCCACCAGGAATCAAGGNNGGATAAACGCAGGGAAAAGA
ACATGTNTAGTCAAAANAGGCCAAGCNNAAAGGCCAAGGNAACCCGTTAAAAAGGCCCG
CGTTGCTTGGCGGTTTTTTCCATAAGGGCTCC
Sequence 393
NATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGGACACAGGCACTCCTTTG
TCTGGTAGAGAGGAGGAGGGGAAATGGAGCTATTCCAGGATACAAGGGATGGCACTGAGG
GATGCATAAGTCCCCTGCCTCCCTTGTCTCAACATGTTCTCCTCTGCCAGCCCAGTCAGC

Table 1

TTGGGGAGCTAGGTATCAGAAACCTGAAGGATCCAGCCCGCTTTGTCCTACTAGTGTCTA
TAAGTCTCTGTCCTGAGATCCTGGGGCTCCTCCTATTTCTAGAAGGGATGAGGTGCCATC
AAAAATAACTTGGCTGGTGTAACAGTTTAGAGAAGGAAGTCACACCTGTAGCCTGGCTGG
CAGGCAGGTGGACATGAGGCTGAGAAGGGAAGCCAGATGTCAGAACATACTAGGCTAGCA
TGCCTG
C
Sequence 394
GTGGCGGCCGAGGTACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAA
AACTATCTCCCACTCTTTTGGCCCAGGCAATGTCAACGACTTCCACATTCCCTGGCCCAC
TTGCTGAGCAACCCCAGGTTCGGCTCTGTATAAGGACCCTCCCCTNCCAACCCCAACCCC
AGAGTGCAGTGCAAATCAACCAACAATTTACTGGTGGAATGGCAATCAAAGGAAACAGTT
AAACACCAAACAATTNCTTAAAGCCAAAAAATATTTTTCATGGAGTTGAACATTTTTCG
A
GTGTGTTTTTTTCAAGTGTAAAAGCAGTGACATTTTGTTCAAACAGAAGCAGCATCTAGG
AATTCTGGCACTTGGGGTTCTAAGGGGGTTACAGGTATGCCATCATGGATTCTTCTCC
C
Sequence 395
NGGGGCCGGGCCCCCGGNGGGGTTANCCTTTCCATTTTTNANCAACCTTTTAAAAGCCCT
TGGGGAGGGNGGGGTTTAANGGGGAATCCCTTTNAAAATTTTTTAAATNTTNAAAAAGGG
CCCCCATTAAGNAATTTCCCAAGGTTTTTNAAGCCTTTTTTAAACCCCTNAAGNACCAGG
GNAAAAAGGTNGGAAAAAAGGGCCANTTTTTTTTACCAAAGGGNGGGGGGAGNGGAAGGG
CCAAANTGGGAAGGAAAAATTAAAANGGGCAAAACCAAGGAATTANATTACCGTTCCAAA
AAAGCNTGGGGAAACCAAGGGGGGCAGGAAAATTCAAGNAAACCGTTGGTCCTTGGGCCT
TATTCAAGCCTTTTTTGGTTTTTTTTTGGACCTTACCTTAAAAGGGCCCCAAACCCCTT
T
TTTTTAATTTCCCTCCTTGGGAATNGGGGTTCCTGGCCAAGNACCCCAAAAGGTTTCCAA
GGGAAAATTTTTTAAGGGCCCAAAAAAAGGGGAATTTTTCCCCCAAAAAATNGGGGNATT
CCCCCCTTAATTAACCAATTCTTTCNAAAGGAAAAGGGAATTANCCAAGGGGGTTTTGGG
AAGGNAAAAGGGAAAANGGCCCCCNNCCAAGNAAAGGGGNCCTTTTGGGTGGGAATTGGG
AAAACCCCCAAAAAAAAGGAAAAATTCCNTTTTTTAAAAAAAGGGAAAAANGGGGGGTTN
TTNCCTTTCNAAAAAAATTGGCCCAATTTNGGTTCCCAAGGGTNAAGGNAATTTTTTTG
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GGGGNAAG
Sequence 396
TGGGGGCCGGGCCCCCGAANGGTTACCCCCGCGGGGGGGGAGGCCTTTTNTTNCCCTTTG
GGCCCAGGGTNTTNCNTTTCCCCAAGNCAANGGAAACCCCCTTTCTTTTNCTTTGGGTTT
TTTGGAAAAAANGGAATGGGGTTCCCGGGCTTGGCNTTTTTTGGGGTTANGGGCCACCGC
TTCAAGTTCCTTGAAATGGTTCCCGGCNCATGCTTTCCCCGGGGCCCGGCTTCNTAAGNA
AACCTAAGTGGGGAATCCCCCGGGGGCCTTGCAAGGGAAATTCCGATAATCAAAAGCTTA
ATCCGGATAACCCCGGTCCGAACCCCTCGGAAAGGGGGGGGGGGGGGCCCCCNGGGGTAC
CCCCAAGCTTTTTTTGGTTTTTCCCCTTTTTAAAGTNGGANGGGGGGTTTTNAAAATTT
T
GGCCCGGCCCGCCTTTTGGGGCCGGTTAAAATCCAATTGGGGGTTCAANTAAGGGCCTTG
GGTTNTTTCCCCTTGGTGGGTGGGNAAAAAATTTGGGTNTTAANTTCCCCGGCNTTCCAA
CCAAAANTTTNCNCCAACCAACCAAAACCCAATTTANCCGGAAAGGCCCCNGGGGGGNAA
GGCCCAANTTAAAAAAAAGGGTTGGGTTAAAAAAAGGGCCCCCTTGGGGGGGGGGGTTGG
GCCCCCNTNAAAAATTGGGAAAGGGTTGGGAAAGGNCCCTTTAAAAAACCCTTTCCAAAC
CAAATTTTTAAAAAANTTTTNGGCCCGGGTTTTTTGGACCCGGCCCNTTTCNAACCCT
TT
GGGGCCCCCCCCGGGCCTTTTTTTTTCCCCCAAAAGGGTTTNCCGGGGGGGGGGNAAAAA

Table 1

AA
Sequence 397
GTGGGGGGCCGGGGCCCGGGAGGGGTACCCCGCCGGGGGNGGCCTTTNTTTCCTTTGGCC
AGGTTNTCTTCCCNAACAAGGGGAACCCCTTNTTTCNTTGGGTATTTTGGAAAAAGGAAT
GGGTTCNGGGCCTGGCTTTNTTGGGGTTAGGGGCACCGCCTCAAGTCCTGGAAATGGGTC
CCCGCCAATGGNGTGGCCNGGCCCCGCATCTTANGGAAACCTANGTGGGGAATCCCCCCC
GGGGGCTTGCAAAGGGAAATTTCNGAATATTCAAAAGCTTAATCGGAATNACCCCGGTCC
GNACCCCTCNGGAGGGGGGGGGGGGCCCCCGGGGTAACCCCAANCNTTTTTTTTGGTTTC
CCCCTTTTTAAAGTNGGAAGGGGGGTTTTAAAATTTGGGCCNGCCCGCCTTTTGGGGCCG
GTTAAAATTCAATTNGGGGTTCCAATAAAGGCCTTGGTTTTTTCCCCTTGGGTGGGTTGG
AAAAAAATTTNGGNGTNATTNCCCGGCNTTTCAACCAAAANTTTGCCCCAACCCAACCAA
AANCNCAATTTAACCCGGNAANGNCCCCCGGGGGGGGAAAGGCCCAATTTAAAAAAANGG
TTGGGTNNAAAAAAANGGNCCCCTTGGGGGGGGGGGGTNGGCCCCCTTNAAAAATNGGGA
AAGGGTTGGGGAANGGCCCTTTAAAAACCTTTCCAAACCCAANTTTTTAAAANTTTTTGG
GCCCGGTTTTTGGNCCCGGNCCNTTTCNAACCCTTTGGGCCCCCCCCGGGCNTTTTTNTT
NCCCCAAAANGTTTCCTGGGGGGGGGGAAAAAAA
Sequence 398
GCGGCCGGGTACAAAATTTAGAGGTTTCCCCTTTATCAACAAGAGACCCAGGTGCCAGCA
TGTTACTACCAGATCCAGTTCTTCTTAGGACAGTGTGGCTCAAAGGGATGAGACCTTCCA
GACACTGGTATCTGAGCATCTGTGGCCTGCCCCTGAGTTGTCAAGATAATTTCTTATCTC
TGAAGGAGTCCAGACAGGAATGCTTCCACTGCTGGGTGGGTGCTCGCCCCTCTTGCTCCT
TAAGCGCCCGGCTCACCCCCTTGCTAGCACAGGGTGTCTTACACAGTTTATGGACTTTT
CTGTGAACTACCTGAGGGCAAGAACCATGTNCCACTCCCTGCTTGCTCCTCAAATATTTT
A
Sequence 399
CNGCCGAGGTACNCGGGGAGAGAGGAAAAGAACACAGATCTCGCATGGTTCAGATTTTTC
TTTTTAGGTCCAGGAGTAAGATATATCATACNGAAAATGAAAATTATAATTCTTCTTGG
A
TTCCTGGGAGCCACATTGTCAGCCCCACTTATCCCACAGCGTCTCATGTCTGCCAGCAAT
AGCAATTGAGCTTACTTCTTAATCTTTAATAATGGGTCAACTTTTGCCACTACAAACTT
C
AGGGGCCCACTTAATTCATGGANTCCACCTTTCTCTGGGAATTTTACAACAGCAGCAGCA
GGCTCAAATTCCAGGACTCTCCCAGTTCTCTTTATCAGCTCTAGACCAGTTTGCCTGGAA
CTGCTCCCAAAATCAGAATACCCTTAACCAGGGAAGAGGCCAGTTTTGGNCCCAAAGGGA
GCCCCAAGGCAAGGGCCAAGGTTNGAATCCCNTTAACNGNNTTTAAAAACAACCCGCCTT
TAAGAACACAAACCCAGGNCCCCANGACACCGTTGAATGCCCCTTATTGTTATTTCTTC
CC
Sequence 400
GACAGACAGTGCTTGATGTTCATAAAAAATACAATGCCCTGGTAATGTCTGCATTCAACA
ATGACGCTGGCTTTGTGGCTGCTCTTGATAAGGCTTGTGGTCGCTTCATAAACAACAACG
CGGTTACCAAGATGGCCCAATCATCCAGTAAATCCCCTGAGTTGCTGGCTCGATACTGTG
ACTCCTTGTTGAAGAAAAGTTCCAAGAACCCAGAGGAGGCAAGAACTAGAAGACACACTC
AATCAAGTGATGGTTGTCTTCAAGTACCTGCCCGGGCGGTCGAGCGGCNCGCCCGGGCAG
GTACGCGGGGGCTAACCAGGCCAGTGACAGAAATGGATTCGAAATACCAGTGTGTGAAGC
TGAATGATGGTCACTTCATGCCTGTCCTGGGATTTGGCACCTATGCGCCTGCAGAGGTTC
CTAAAAAG
Sequence 401
CGGTGGCGGCCGGTTGCCTTGTATGTCACGAGCAATTAGGAGAGTCACGAGGATGAAATA
GATGAACCCGACCATGCAGTTAATCACCAACATCAACTACTAGCCAGACGGGATGAACCA

Table 1

CAGCGTCACACAATACAGTGTTCCTGTTGTAAGTGTAACAACACACTGCAGCTGGTAGTA
GAAGCCTCACGGGATACTCTGCGACAACTACAGCAGCTGTTTATGGACTCACTAGGATTT
GTGTGTCTCGTGGTGTGCAACTGCAAACCAGTAACCTGCTATGGCCAATTGTGAAGAGAT
GGGAGTCTCCCCGTATTGCCCAGGCCGGTCTCAAACTCCTGGGCTCAAGCAATCTTCCCC
GCCCACTTCCCGAAGCCCTAGGATTACGGGAGTGAGCCACCGCACCCAGCCAGAAAAACG
TTTAAAAATTTGGAAAACCTTACTTTTTTTAATGAGCATTTTTGCATCAAGGGGGTTAC
A
GGGACATTAGGCTTTTTTTTTT
Sequence 402
ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACATATCCTCTGTGGGAAAAA
CTGCTCTCAGAGTGTGCACTCTCCCCACAAGCCAGCGCTCAAACTGGAAAAAGTATCTCA
ATGTCCTGAATGTGGGAAAACCTTTAGCCGAAGTTCTTATCTTGTTCGGCATCAAAGAAT
CCACACAGGCGAGAAGCCTCACAAGTGCAGTGAGTGCGGGAAGGGCTTTAGTGAGCGCTC
CAACCTCACTGCCCACCTACGAACTCACACAGGGGAGAGGCCCTATCAGTGTGGGCAATG
TGGGAAAAGCTTCAACCAGAGTTCCAGCCTCATTGTCCACCAGAGGACCCATACCGGGGA
AAAGCCTTACCAGTGCATTGTCTGTGGAAAGAGATTCAACAACAGTTCCCAGTTCAGTGC
TCACCGGC
Sequence 403
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAAATTAAGTATTAAAATGAGGATTGAA
CTGGGGCAAACAGGTTATTGTGAAAACAGTCAATATGTAAGCTCCTTCAAGGGAAATCAA
CTACTGTTCCTCAAGATTAGAAGATGTNCACACTCTTTGCATTACCTCCCTAAAGGAGGA
AACACCCATTAATTTTCCCTTATGGAATCAATATGGAGTGGAAATATGAAATGAGGAGAT
GTTTTAGAAAGCAGGACANATCTACCTACCATTACTGGAATTAAAATGTATCCTCTGGGC
CCACTCCATTGATTCCGATCTGAGGTGAGGAGGACTAAAAGCAGCAGCAGGTTACAGAAA
GACTGAATAAGATGAAAGTATGCTACGTATGTCTAGCTGGGGAAGGGGGGATCTGGAAAA
A
Sequence 404
CCGCCCGGGCAGGTACGGACGCCCAGGGATCCGCGCCGAAGCTAGCACGCANCCTACCCA
ACAGTCTACACAGCNCGACCAAAGCCCCCGCGTACCCAGAGGAGTCGCTGGTGATNGGGG
AGCTCAACCCTGTTNAGTAGCTCTGCTCATCAAGTGTCTGGAGAAGGAGGTTGCGGCATT
GTGCAGATACACACCCCGNAGGAACATCCCTCCTTATTTTGTGGCTTTGGTGCCACAGGA
AGAAGAGTTGGATTGACCAGGAAAATTNAGGTGACTTCTCCANGGCTTTCCAGCTTGGTC
TTTTT
Sequence 405
CCGCGGTGGCGGCCGAGGTACGCGGGGGGCGGCGGCGGAGAGAGCTGGCTCAGGGCGTCC
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ACTTCAGCTACAGTGTTAGCTAAGTTTGGAAAGAAGGAAAAAAGAAAATCCCTGGGCCCC
TTTTCTTTTGTTCTTTGCCAAAGTCGTCGTTGTAGTCTTTTTGCCCAAGGCTGTTGTGT
T
TTTAGAGGTGCTATCTCCAGTTCCTTGCACTCCTGTTAACAAGCACCTCAGCGAGAGCAG
CAGCAGCGATAGCAGCCGCAGAAGAGCCAGCGGGGTCGCCTAGTGTCATGACCAGGGCGG
GAGATCACAACCGCCAGAGAGGATGCTGTGGATCCTTGGCCGACTACCTGACCTCTGCAA
AATTCCTTCTCTACCTTGGTCATTCTCTCTCTACTTGGGGAGATCGGATGTGGCACTT
TG
CGGGGTNTGTGTTTCTTGGTAAGAACTCNATGGAAACAGGCCTCCTT
Sequence 406
TCCCCGCGGTGGCGGCCGAGGTACAGTTCACAGTGCTTGATGATAATAAATGGTTATTTT
ACTGGTTCATGTATTTACTATATCATACTTTTTTTCATTAGAGTGTGCTCCTTCTACTTA
TGTAAAAAAAAAGTTACCTCAGGGAGGTCCTTCCTGAGGTCTTCCAGCACACGGCATTGT
TATCATAGAAAATGACAGCTCCATGTGTGTTACTGGCCATTACCACCTTCCAGTGGGAAG

Table 1

GATGTGGAGGTGGAAAGCATACTGATGATTTTGTCCCCGTGGAGGCCTAAGCTAATGTGT
GTGTTTGTGTCTTAGCTTTCAACAAAAAAAAGTTTAAAAAGCAAAAAAAAAAAAAAAAA
A
Sequence 407
GTGGCGGCCGGTGTGCTCATCGTAGCCTCGGGTCGGGGGATGCGTCTCCGCTTTAGCGCC
AAGATAGAACTTCCTCAGACCACCGCCGCCGCCCCCGCGTACCT
Sequence 408
GTACCTCCCTGGCTGAAGTCTCTACATAGCTCTCAGGAACCTTCGGAAAGGCATCCAACT
CTTTTACCAAACTTAAAGTTTTTTTCCGATTCAGTCGCCTCATCTTCAGGAAAACCTTC
C
TCTTCCTTCATATAGTCATGCTTGTGTTATGGTCCCAGCCTACCGCCATGTTTTACAGA
A
GCCCGGGTCGCCGGGGCTCCCGCGTACCTGCCCGGGCGGCCGCTCGAGGCAGGTACTGAA
TGACACATTACCTCCACACTCTCCCGGACTAGG, NGTCAACAGGGCCACAGGGTTGCTTT
CTGTCTTTGGTGGGGCAGGGGAGTTGACAGGGATGAGGGTCCAAGGAATTAAGCATGGAA
TGACAAGAAAACANGGGAAAGAGTTACCCTGTCACATAGTAGGTTAACTTTTTTAAGGGT
TTGCAAGTAAGAGGNNTTTCGACCCTTTCNCTTGGCTGAGCCANATCNCGGGAACTTGAG
AGCTTTTACTGGGATTTTCAATNNAAAAAATTAACAACAATGTCAAACTNGGGTTTGGA
T
NATTGGNTTAAAGCCTTTTTAAGATTCTTTTTTAAATAACATTTTTCCCCGAAAAAAAAA
AAAAA
Sequence 409
TTTTNGGGGGGAGTTAAATAAAATAAGCATGTCTNCATCCTTTATTCCTAAACATTTAC
T
TATGACAAATGTAANNACTGACAGAAATTTGAAAAATACCANGACACTTCTTAAATGATT
TCCCTTGGTTCAAAATTTACCCCTTCTTGGGTTTCTNTTGCTTTTCAAGGGTAATNTAA
A
CTCTTCTCTTTTTANGTTTGAACTATGCAAGTGCCAAAGGATTCCNCTGTAGTCTTTCC
A
AAGGGGGGGAAAGGGGGTNTATANAAAAAAAAAAAAACACCTT
Sequence 410
GGGCAGGTACTGTGCAGTAGTAACCCATAATTCTAAATGAGGATTATGGATTTTTCTGGA
AGATTCTTTTTTCCTGTGGAACATGATGAGAAATGTTTAGGAGAGGGGACATAGCCATTT
TTGTATGAAGACCAATTCAAGAAAAAAATATATGTATGTGTGTGGGTGTATATGTGTGTA
TATATGTATAT
Sequence 411
GGTACGCGGGGTGCTGGGATNCAGGCACGAGCCAGTGCGCCCAGCTGCCTNTGTTTNTTT
TATTAGCTGNTCTGGACTGNGGGGCTCCTTGGGCAGATGCTGTATTATGGGGATAAGCCA
CACACTTTNTGAACTGGCCCGGTCAGGGGGGACATANCCATTTCCTGTGCCCCCCATCAA
NACCCACCTATTCTGAGNGTNNGCTCCTCCCCTGCTTGAGTNATGGCCACANATCTTGGC
TCGGNNCTCCTAAGCTGCATGNTGAATTCCTGGGACAACAAGACTGGCTTGTGGTTCCAT
TCTCCAGATCCTTGGGT
Sequence 412
GCCGGGCAGGTACTTAGAGTTTTCCAAGTATGTTCTAAGCACAGAAGTTTCTAAATGGGG
CCAAAATTCAGACTTGAGTATGTTCTTTGAATACCTTAAGAAGTTACAATTAGCCGGGCA
TGGTGGCCCGTGCCCGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCACTTCAA
CCCAGGAGGTGGAGGTTACAGTGAGCAGAGATCGTGCCACTGCACTCCAGCCTGGGTGAC
AAGAGAGACTTGTCTCCAAAAAAAAAAGTTACACCTAGGTGTGAATTTTGGCACAAAGGAG
TGACAAACTTATAGTTAAAAGCTGAATAACTTCAGTGTGGTATAAAACCGTGGTTTTTA
G
GCTATGTTTGTGATTGCTGAAAAGAATTCTAGTTTACCTCAAAATCCTTCTCTTTCCCC

Table 1

A
AATTAAGTGCCTGGCCAGCTGTCATAAATTACATATTCCTTTTGGG
Sequence 413
GCGAGGTACCTAGTCTANATGAGTTTGATGCTTACAGTCAAGGCTATTAGCAAATATTCA
GGAAAAGTAAAGCCTAAAGAAGAAAAGAGGGAATGAATAGTTTGTCTAGAGATAATAAAA
GGAAGGTGAATTTTTAAAAAGACAAAAATAANGCTAGAAAAGACTGAGTGGAGAAAGCCT
ACAGAATTTCAGAAAGCTAAAGAAATTGGAAATTAGATTGAATATAGATAGAAATGGGAG
GACAATGCAGCCAATGAAAGACTGTGGGACTAATAAAGGGAGAGCCCTGTGGTTTGGAA
AGTGTCCCTTAATCAGCCTGCAGTGCTGCAAAACAGAAACCCAGAG
Sequence 414
GGTGGCGGCAGGTACGCGGGATCCAAGATGAATGTGCAGAGAAAATAAAGAATCCAAAGT
CATAGTCATGAGGACAGAATAAAGACATTTTATGCCTTTTTGTTTTGTTTTGTTTTCCTT
TTTGTGGAGAACAGGGTCTCTCTATATTGCCCAGGCAGGTCTTGAACTCCTGGGCTCATA
CTGTCCTCCTGCTTCTGCCTCCCTAAGAGCTGGGATTACAGATGTGAGCCACCATGCCCG
GCCAGAATAAAGACATTTTAAAACTAAAAAAAAAAAAAAAAAGAGTTTGCTTTGCATTAA
TCTTTTTTTTCTTTTTTTTCGTTTTTATTTTTTAGTTTTTATTTTTTTTGAGACGGAGTC
TCACTCTGTCACCCAGGCTGGAGAGCAATGGCATGGTCTCGGCTCACCGCAACCTCTGCC
TCCTGGGTTCAAGTGATTATCCTGCCTCAGCCTCCTAAAGTAGCTGGGATTACANGTGTG
AGCCACCACGCCTGGCCAGAATAAAAGACATTTTAAAACTTANGGAAAANAAAANAAAAN
NNTNGNNNCNNCCCCCCNNNAAAAAAAAAAAAAAAA
Sequence 415
ACCGAAGACGAANGCCACTACATGCCCCCGCGTACCTGCCCGGGCGGGCCAAAGGCCAAC
AAGGGNAGTGGGGNCGGGCTGCANGAATTTCGATATCAAGCTTATNGATACANGTTGACC
TCNAG
Sequence 416
CCCCGCGGTGGCGGCCGAGGTACGCGGGGCTGCGGAGGACCGTGGGCACGCCAGGGTCGG
TGAAGGATCCCAAAATGGCTGGGCGAAAACTTGCTCTAAAAACCATTGACTGGGTAGCTT
TTGCAGAGATCATACCCCAGAACCAAAAGGCCATTGCTAGTTCCCTGAAATCCTGGAATG
AGACCCTCACCTCCAGGTTGGCTGCTTTACCTGAGAATCCACCAGCTATCGACTGGGCTT
ACTACAAGGCCAATGTGGCCAAGGCTGGCTTGGTGGATGACTTTGAGAAGAAGTTTAATG
CGCTGAAGGTTCCCGTGCCAGAGGATAAATATACTGCCCAGGTGGATGCCCGAAGAAAAA
GAAGATGTGAAATCTTGTGCTGAGTGGGGTGTCTCTCTCAAAGGCCAGGATTGTAGAATA
TGAGAAAGAGATGGGGAAAGATGAAGAACTTAATTCCATTTTGATCAGATGACCATTGAG
GGACTTGAATGAAGCTTTCCCAGAAACCCAATTAGACAAGAAAAAAGTNTTCCTATTGGG
CCTANCCACCCATTGAGAATTATTAAATTTGAGTNCAGGANGGAACTTCTGGCCCTTTGT
ATTACCCATTCTGGGCCTTTAAAATATTATTTTTCCAAAAAAGGAAAAAAAAAAAAAAAA
AAG
Sequence 417
GGCGGNCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAGGGAGTTTTGCTCTTTTTGCCC
GGGCTGGAGTGCAATGGCACGATCTCGGGTCACTGCCACCTCTGCCTCCTGGGTTCAAGT
GATTCTCCTGCCTTAGCCTCTTGGGTAGCTGGGATTACAGGCGCCCACCACCATGCCTGC
CCAATTTTGTATTTTTAGTAGAGATGTGGTTTCACCATGTTGGTCAGACTGGTCTNGAA
C
TCCTGACCTCAAGTGATCCACCCNCCTTGGCCTCCCAAAGTGTTGGGATTACAGGTGTAA
GCCACCGTGCCCGGCCATCAGTTGTATTTNTATATAGTAGCANATGAACAATCAAAATGN
GATTAAANAAAATGCCNTTTTTAATAGCCTTAAAAAAAAAAAANTTNTTANTGAATAAAN
TTTAANCCAAAGGAGGGGNCAAACCTTTTCCNTGGGAAATTCCAAAACNCNTNTTTGGNA
NGAATTCAAAGNAGGNTGAAANCCCNNCCCCTTTTTNCGGNGTTNANAAAAAANANATTT
TTTANNGGGGGNCCCCNCCCAAANNATANTTCCNCNGTGGGGGGCCCTCTAAAAAANAN

Table 1

TTTTTTTTTTTTTTNTAAAAAAAAAANNTTNTTTTTTTGGGNG
Sequence 418
CGCGGTGGCGGCCCGAGGTACGCGGGATTTTGAATGAATTCTCAACAAAATGTGCTAGCC
ACTGGGGACGCAAAACAAGTAAGATCCCTGTTGCAAGAAATTCATTTTATNGNGAGGGAG
GTTGGCATGGAGACTAAAATTCTCAGGAAAATGAGATCCGTGTTAGATTAGAAGTCCTGA
TGTGAAATGGGAGGACTCAGGAAGGAGGATCGTCTTTACCTGAGGATTTCTAGCCAGAGG
TCCCAGATGCCTGGGCTGAGAACCCAGCGATAAGGGGGCGTTCCCAAAGCAGACACAGGG
ATAAGAACAGAGGAGGCAGCAGCATTGCACAAGCCCCAGGCACAGTGGCAGTTAGGATGG
CTGGAGAGTAGGATAGTTCTATGGGTTGCCCAAAAAATGTGATGTGCTTCATGTTTTCTC
TGACTCATGGATCTGGTAGAGACCATAGACATGATATAGGACTAACTTGCCCATTTTTCA
CANAGAGGAAACCATCCTTATGACTTACCTTAAAGTTTTTTGTTCTGTTTTGAAAGGAA
A
CCATGTGCTTCATGAAACCTACAGTTGGCCAGAAGAATGNTCCTGCCCCGGCCGGCCGCT
CTAAAACTAGGGGGATCCCCCGGCTGCAAGGAATTCGATTTCAAAGCTTATNGATTCCCG
NCACCTCGAGGGGG
Sequence 419
CCGCGGTGGCGGCCCGAGGTACAGTATATTGACCTTAAAAATCAGTAAAGCAGTCATGGA
AATAACAGGTCGTGTATTATTCATGGCACAAACTGACTCATGGCTGGGGAAGAAGCAGC
CACCTTAGACCAGATGGACAAGCCAGATACTGCAGAGAAGTTTCTGGGCTTTTCGGGGAG
CTCTAGATTCAATTCTGTAAAGTTATGATGCAGTTTTCTCCTTCCTCTCCTCTCACCTN
C
TNTGAGCACAGCTTTCAACAAAAACTTTGCATACCCCGCGTACCTGCCCGGGCGGCCGCT
CGAGGTACTTCTCTGAGCATTGGCCTCTGGCTGGGATTATGCTTCAACAGTCTTGAAATG
AGGTCCCTGGCTCCCTCTGTTACAAAGTCAGGGAATGTGAATTCAACCCGTGATATTCTT
TTGTAGGTCTCTTGGTATGTGTTTGCCTCAAAAGGAGGCTTCCCAACTAAAAATTCATAG
CAAAGAACTCCAAGGCTCCAAGAGATCCACCTTCTCATCATGCATCCACCTTCAATCATT
TCANGGGGCANGGAGTCCAAGGTGCCACAAAGAGNGGTCCTTCTGGGAAGATGGAGCATG
TACCTCGGGCCCTCTAGNACTAGTGGAT
Sequence 420
GAGGTACGCGGGGGTCGGCGCCATTTTGTCTCGGCAGCGGTGGCCCGTAGCTCCATCGCA
TTTTATGTTTCTGGCGAGAAGGGAACGGAGTTTTCATCAGGTAGATTGGTTTTTGT
Sequence 421
GGGGCGGCCGCCGCCTNCCCGTGAAAGACCTCCTGCTGGAAGACCTCCAGGATGGAGAAG
TGAGGCTGGGTGGCTCCCTGCGAGGGGCATTCAGCAACAATGAGAGAATTAAAAACTTCT
TCAGAGTCAGTTTCAAAAATGGATCCCAAAGTCAGACCCACTCGCTACAAGCCAATGACA
CTTTCAACAAACAGCAGNGGCTTAACTGTATTCGTCAAGCCAAAGAAACAGTTTTGTGTG
CTGCCGGGCAAGCTGGGGTGCTTGACTCCGAGGGATCGTTCCTAAATCCCACCACCGGGA
GCAGAGAGCTACAGGGAGAAACAAAACTTGAGCAGATGGACCAATCGGACAGTGAGTCAG
ACTGTAGTATGGACACNAGTGAGGTCAGCCTCGACTGTGAGCGCATGGAACAGACAGACT
CTTTCTGTGGAAACAGCAGGCACGGTGAAAGTAACCGTCTGACAGAAAGCATGTGCACTT
CNGGAAGCAGGCCTGCATCTTACCTGTACCTGCCC
N
Sequence 422
ACTTCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAACTGGGGAATTCTGGCCCTAC
GTGCATTCACAGGCAATGATGGGTTTGTGTGTATGGTGTCATGAGATCCTCTACCTCATA
ACAAAAGGACAGTGGGTAGACTAAGGCAGTAGCTCAAAGGGCTTTGCAAAATTTTAATAT
ATTAAAACAAGAGGCATCTGCTAGAAAACATTCTATTGTATACATACTGAAAACCCTATA
AGGTCCTGGATAATTTTTGTTTGATTATTCATTGAAGAAACATTTATTTCCAATTGTGT
GAAGTTTTTGACTGTTAATAAAAGAATCTGTCAACCATCAAAAAAAAAAAAAAAAAAAA
AGTACC

Table 1

T
Sequence 423
NCCCGCGGTGGCGGCCCGAGGTACGCGGGAGAAGGAGATTACCTCAACATAAGAACCGTA
TGTGAAAAGCCCACAGCTAACATCATACTCAATGGTGAAAGACTGAAAGCTTTTCCCCTA
AGCTCATGAAGAAGACAAGGAGGCTTGGTTTTGTGGCTTCTATTTAACATGGTAATGGGA
AGTTCTAGCCAAAGGAAGTAAGCAAAAAAAAAAATCGAAATTAGACAGGGGGAAGTAAAA
TTATCTTTTTGCAGATGATATGACTTATATGTATTATAGAAAACCCTGGGCCAGGTGCA
A
TGGCTCTTGGCTGTAATCCTAGCACTTTGGGAGGCCGAGGTGGGTAGATTGCCTGAGCTC
ANAAGTTTGAGACCAGCCTGGGCAACACGGTGAAACCCCCCTCTACTAAAATCCAAAAAA
AAAAAAAAAAAATTAGCCCGGGCGTGGCGCATGCTAANGCANGGAGAATTGCGTGGAATC
TGGGANGGTGGANGNTGCANTGAGCTTGAAGATCTCCCCCTGNACTTCCAGCCTNGGGGG
ACAGANCCAAGACTNTTTTNTTCCAAAAAAAAAAAAACCGGGGGGNGGACCCCTCAAGAA
TTCNCCCCNCCCCCCCCCGAANCCCTGGTTTGAAATTAATAAATGGGGTTCCGCCAAANA
AAGTNCCNGCTTNTTCAATCAACAGGCCAAAAATTCCTTGTTTTTAAANCCCTGCCCTT
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AAAANTTTTAAAAAGGAAACTTNGNATTCCCGTTTCTTTTTTATTGCCTCCAAAAAAAAA
AAAAAAA
Sequence 424
CCGCGGTGGCGGCCGAGGTACTGCCGAGCCGCTCCTCCCGCAGCTGTGCCGCCTCCTTGT
CCTCCTCCTCATTGTCACTGCCAAACAGGTCAATGTCATCATCCTCGTCATCCTCTGC
TG
GTGTGGCTGGCTTCCAAGCTGGTGCCCGTGGGCTACGGTATCCGGAAGCTACAGATTCAG
TGTGTGGTGGAGGACGACAAGGTGGGGACAGACTTGCTGGAGGAGGAGATCACCAAGTTT
GAGGAGCACGTGCAGAGTGTCGATATCGCAGCTTTCAACAAGATCTGAAGCCTGAGTGTG
GGTACCTGCCCG
Sequence 425
CCTCCCGCGGTGGCGGCCGAGGTACTAAGTGGTTAAGGATGGAAAAGAGCTAACAAGTGA
CAACAAATACAAAATAAGCTTCTTCAACAAAGTATCCGGCCTTAAGATCATCAATGTAGC
GCCGAGTGACAGTGGGGTATACAGTTTTGAGGTGCAGAACCCTGTTGGCAAAGACAGCTG
CACAGCTTCATTGCAGGTTTCAGGTTGGTTGATTTCTTGGGCTTTTCCTTCATCATTAT
A
ATAATGTAGTTCCTGATTTTCATAAATGTATATGGGTTGTTACATCTTCTATAGGATAAC
ATGAGTCCGACATCTTCTGAATCAGCAAATTCAGAGGCAATACCATCTCAAGAAGCCACC
Sequence 426
CTNCCGCGGTGGCCGGCCGCCCGGGCAGGTACTGAATGTGGGAAAGCCTTTTGCCAGAAA
CCACACCTGACCAACCATCAGCGAACACATACAGGAGAAAAACCCTATGAATGTAAGCAA
TGTGGAAAAACATTCTGTGTGAAGTCAAACCTCACTGAACATCAGAGAACACACACAGGG
GAGAAGCCCTATGAATGTAATGCATGTGGGAAATCCTTCTGCCACAGATCAGCCCTCACT
GTGCATCAGAGAAGACACACAGGGGAGAAACCTTTTGGATGTAATGAATGTGGGAAAACC
TTCCGTCAGAAGTCGGCCCTAATTGTTCACCAGAGAACTCATATAAGACAGAAACCCTAT
GGGATGTAATCAATGTGGAAAATCTTCTGTGTGAAGTCAAAACTCATTGCACATCATAGA
ACACACACAGGGGAGAAACCCTATGA
Sequence 427
CCCGNGGTGGCGGCCGGGTACCTTACTTAGCAGAGCACTTTGCAAACATATTACTTATTA
GCAGAGCTCTTTGTAGACCTTCCACATCTGGCTGTCAGATCTTAAGGTTGTGAATTTAGG
CTCCAGTTATATTCACTGGAGAGCATAATCCCACACGGGTTATTTATAAATACAGAGCCT
CTGATTGGACGGTCTCCTGCCAAGAACTAGTAATACCCTTGTTTTAAAATCTTCACAAGG
TAAAACTTAAAAAGCCAACCAAACAAATTGCTCTCCATTCTACTTTTAATTGGGCCAAAC
AGCATATGCTACAGTAGTAACATGTTTTTCGGAGAGTGTAAAAAACTCTGTTTACATTT

Table 1

G
CCTCCTCGTGGGTTGATCGAAAATGTATAAAACTGACTGCTTCTCGCCAGCCTCAGACAA
GAAAGAGTGAGCTGCTGGTACCTGCCCGGGCGGGCCGTCTAAAACTAGGNGGGAT
Sequence 428
GGCCAAATGCAGAAACGTCCCACATGCCCACCAGGAGCAAGCTTCAAAATGTTCAGCTTG
CGGGGCANTNNGCAGAGAAATNCCAGGGATGTTCCTGAAGGCCTNGATGATACCANTATC
CTCATTATAAGATGAATGCACGGGGCCCNTTGCGCTGGATACCGGCNAACCGGNTTCTNA
TTNTGCCTNTGNCAGCTCTCATTCGCTGAGAGGCATAGACCTTTTTGANGATCATTCCAA
NGCTATAAGTCNTCTTAAGGAGCAAAAACCAGCTTCCTTGGTCTNTCTTGAAGNCCTTCA
ACTTTATCTTTCAACTACCAAAGGGAAGGTNCAGGAAACTTTCCTCAATAACCGANGGAC
CTTTAGGACATGAACCAGGTGNCTGGNTAGGGGCTGGAGGCCAGCCCAGGGCAAGAAACA
NAATGGCCGATANCCGTTTTTGGGGTTCCCGCGGTACCNTTGNCCCGGGNCGGGCCGGCT
TCTAANAAACCAAAGTGGGAANCCC
Sequence 429
CGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTGTGATCTCAACTGCTTTT
A
GCAAGTTGTGAATATACTTGGGCTTTCTGTCTTTCCCCAAAAGCAATTTGGGATTATTT
T
CCTCCTTTTTTTTTCTGCATTTCATCATAAATACTGTCATATTCATACACAGTAGCATCTT
CTGCAAGGGCCTTCTGGATTTCCAGTTTGGTCTGTTTCATGGCCTGCTTCTTAGCAGC
TT
CCCTCTGAAGGCTTTCACTCACAGAGGTCTCATCATCATCATCAGAATCATTCCCAAACA
CTGATGGTTTTTGCAAAACAGGGTGCAACTGCTGTGTTTTCTTTGGCAAAATAAGCCCAT
ACTACCTGCCCG
Sequence 430
GTGGCGGCCGAGGTACAGACAAAACTACAGACTTAGTCTGGTGGACTGGACTAATTACTT
GAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAAATAAAACAAA
TAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGCTGTGTC
AATGGAGATGGCCTCTGCTGACCCAGATGAAGACCCAAGGCATAAGGTTGGGAAAACACC
TCATTTGACCTTGCCAGCTGACCTTCAAACCCTGCATTTGAACCGACCAACATTAAGTCC
AGAGAGTAAACTTGAATGGAATAACGACATTCCAGAAGTTAATCATTTGAATTCTGAACA
CTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCTGGAAACCGATTT
CAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAGGCTGCAGCCCATTCG
CAGGCACCCGAAAGAACTTCCCCAGTATGGTGGTCCTGGAAAGGAC
Sequence 431
GGTGGCGGCCGAGGTACCAAAACAACAGCCCTCCAAACAATGATGACCAGTGGAAAAACA
ATGGAGTCACCAAAACCTGGGACAGGCTCATGCTCCAGGACAATTGCTGTGGCGTAAATG
GTCCATCAGACTGGCAAAAATACACATCTGCCTTCCGGACTGAGAATAATGATGCTGACT
ATCCCTGGCCTCGTCAATGCTGTGTTATGAACAATCTTCGAGCGGCCGCCCGGGCAGGAC
GCGGGAGTTCAAGAAGCTGGTGGTCAAGGAGGAGGAGGTGGAGGTGGCAGTGGAGGAATT
GCAGAAGCTGGAAGTGGTCATATGAACTACATTCAAGTAACACCTCAGGAAAAAAAAGCT
ATAGAAAGGTTAAAGGCATTAGGATTTCCTGAAGGACTTGTGATACAAGCGTATTTTGCT
TGTGAGAAGAATGAGAATTTGGCTGCCAATTTTCTTCTACAGCAGAACTTTGATGAAGAT
TGA
Sequence 432
GCGGCCGAGGTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTC
TGCGTTGTTACCACTGCTTACTGCGTTCCCAGCATTTCTTTTCTCTTCTCGTTTCCTGT
A
GATTCCGGCTAATGGTTTCCCCTGGCATTTGACTTCGTGATGTGTAACTGAGTCTCTT
CC

Table 1

TGAAGGGGGAAACGCATTCCAGAGCATTTGTTCGGGCTCATGTAGGAATAGATCTTTGAC
TGCCCGGTAAATCCCGCGTACCTGCCCG
Sequence 433
GNGGTGGCGGCCGCCCGGGCAGGTACAAATCTACCTCCCCACCAAATGTCCTTAGAGGGC
CAAAGATGGCCTTTGTTTCTTCATGATAACATCGCCTTTCTTTTTTTTTTTGAGACAC
G
GTTTCATTCTGTCACCCAGGCTGGAGTGCAGTTGTGCATTCATGGCTCACCACAGCTTGA
ACCCCCAGGCTCAGGTGATCCTCTCACCTCAGCCTCCCCAGTAGCTGGGACTACAGGGGC
ACACCATCAAGCCCCGGGTAATTTTTGAAATTTTTATAGAGACAGGATTTTACCATGTT
T
CCCAGGCTGGTCTTGAATTCCTGGGCTCTAGTGATTCCTCTGCCTTGGCCTCCCAAAGTG
CTGGGATTACAGGCATGAGCCACCACACCCCACCTGTCTATTTTACAATTTTCCTTTGAG
CTCTTTTTTCCAGCAGTCATGAAGCTGGCAAATGGCAGAACTGGAGCTAGAAACTGCTGA
CTCCCTTTATCTTTTCCATAGCACCCCAAGC
Sequence 434
NCGCGGTGGCGGCCGAGGTACTTTTCTAAAAGCTCATCCACTCTATCATTTAGATATCCA
ATTTTCAGAATGTGCTCAACATTGGCCACTCCATCTGCCATTCTTAAGTCTCCTTGGG
AG
TCTCCCAGAAGAATTATGTTACTATTGTCTTTTAGTTGATTGAAATATTCTGTATTCCTC
AAGGCACCATCATGTTTGTTAAATACATGAATTAGTTCTCCTTTAAATCCTTTGAGCAC
C
CCCTATGAAAAATATAAATCTTTTGAACAGGCTTTAAAAATTCTATTTGTTGGATTTTCA
TATTTTGGAGCTCTTAATTGATGTCACTATTATTTCATCATATTTGTAAATACATCTTTG
ATACTAGAGATCTCAAAGCACTTAAGTCCATCACATTCACCATAGCTAAGAAGGGCTCGG
AGAAGTAAATGATTTTTTAGATACTATTTTAAA
Sequence 435
CCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGGGTTGCTCAAACCGAGTTCTGGAGAAC
GCCATCAGCTCGCTGCTTAAAATTAAACCACAGGTTCCATTATGGGTCGACTTGATGGGA
AAGTCATCATCCTGA
Sequence 436
GTGGCGGCCGAGGTACGCGGGGGAACACCACCCAGTGTGGAGCAGCCCAGCCAAGCACTG
TCAGGAATCCTGGGAAGCACCTCCAAGTGACTGCAGATCTGGAATAATAAGTGNGGGGTA
GATCTGCCCATAGAGCTCACTTTAGACCGGCCTATACTCCTACAAGGAATTGNGGTAGGG
ATCTTNTACTCATCCTTGGCACAATAAGAATGGCCAATGCCCTTTCTAGTTGTTTGGGGG
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GTAACGCCANGGTTTTTTGGGGGTTNAATTTGCAAAAATCCCCTTTTTNGNGGGNTANNA
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TTTTTAACCGGGGTTGGGGGGGGGGCAAAATTTTTTGGGCCANNTTGGCAATTCNCNGGG
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TCNCCCCCCNGTTTNTTTTTTTGGANCCCTTAAAAAAAACCATTTTTTTGG
GG
Sequence 437
GGCCGAGGTACCTTTTTAGAAGAGAAAAGAATCTTGAATTGTATATATTTATTTTGCTT
T
ACAGAAAAAAATGGTTTCGTAAATAATTTGCCTATTTTGGTTAACATAGCACATGGAGAT
AATCATCTGAAAGTTATAGGGCACTGCCACTGCTGAATCAAGAGCATGCCCAATATTTGA
GGTGGCTCTGATTTCCTGGCAGCTGAACTCGGGTAGTCCAGTGGCCTAGCTGGTCCTGCC
CG
Sequence 438
CGGGCAGGTACGCGGGGAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCC

Table 1

AGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGA
GGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAAGTGAGAGAGCAATGCGAGC
AGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGAGCCGTGTATCC
TCTCCGATCACATACAGAAGAGGATTGCACCGGAGGGAGCTCTTTGGACTTCCTTGGCAT
GCCGAGGGGACCCATTTGCGTGGGCCCACAAACNTCTTTAAACAACCTTGGAAATAAAAT
GTGTGGGACTTTAAATTTCACCCCAANGTTCTTTCANTNAATTCCTGGGGGGCATTCAAG
AAATAATTTTCTCTTTTATTGGGGTTNTTTGGGGAATNNTAACCCCTTCGGGGCCCGG
CT
TCTTAAGAAACCTTGNTGGGGGANTCCCCCNCGGGGNCTTGNCAAGGGAAATTTTTGGAT
ATTCTAAGGCCTTTAATTCNGATTACCCCGNTTCTAANCCTTNGAANGGGGGGGGGNC
Sequence 439
CGAGGTACTCTGTGATTTCACCTAGATTTGGAGAAGGTGAGGGAGGAAAGGCTGTCCTNT
TTGATCCCATACCATGCAGGGGCAAATGGCTGCCAGCATAACAAAATAAGAAGGAAAGAA
AGAAAAGTGGGCCAGGCGCAGTGGCTCACTCCTGTAATCCTAGCACTTTGGGAGGCCGAG
GTGGGCAGATTACTTGAGGTCAGGAGTTCAAAACCAACCTGGCCATCATGGTTGAAACCC
CGCCCCACCAAAAATACAAAAAATTAGTGGGGCGTGGATGGTGTATGCCCTGTAATCCCA
GTCTACTTTGGGAGGCTGAGGCCAGGGAGAAATCNGCTTTGAACCCAAGTAGGCAGNAGG
GGTNGNCATGTTGAGCACGAGTATCGTTGCCCACTTGCACTCCAACCTGGCCGACAGNA
GTCAAGTACTCTGGGNNAAANAAAAANATAAACCAGGAAAAAAAAGNGAAGGNAAGGGAA
GGGGGGAAAAGAAA
Sequence 440
GGGGCGGCCGAGGTACGCGGGATGTCTAAAATATCTTGTAAAAAGTGTTAAAATAAACAA
ACCCAGTCAATTAAAAATTTTGACTGTTATTGAGAAAACTCCAATGAGGGAAATAATAAG
ATCTATAAAGGTCTTAAGAAAAATATAATTTGAAAAAAACATGTGGCTGAGTGTGGTGGC
TCACGCCTATAATCCCAGCACTTTGGGTGGCCTAGGTGGGCAGATTGCTCGAGTCCAGGA
GTTTAAGACCAGCCTGGGCAACATGGCAAAACCCTGTCTCTACAAAAAATTAGCCAGGTG
TGGTGGGACACGCCT
Sequence 441
GCGGTGGCGGCCGAGGTACATTGTAGCTTTGAACTCAGTGTTTAAAAATTCAATCTGGTT
ACACACTCTATCTTCTAGATCCCTTGAGACACTGTCTTCCTTGAANAAGNNCCAGGTGAA
ATGGCATTTCAGCTGTGGAAGGATTTTCTCCAGGGAATTCTTGGTGACCTCACTCATGAC
TGCCCTCTGTGTCTCTGCTGTTCCGAAAAGCTGGTGACCAGGCTGATTTGTTCTTCAGAA
GTCTTCCTGTCTGCCCCCGCGTACTGTTCCTGCAGGTTAAGGCAGGACTGGAACTCCTCC
ACAGCTTGCACATAGTTTTCAGATTCAACACTAACTTCTCCGAGTTTAAGATGTGCCTGG
GCAGCATAAAGCTGTGCTTCTTTTGTTTCTTGCCTTTTAAAAATGATCTTTGCTAAATC
C
AGCATATCCCAGGCAAGCTCTAGGTTCCCAATCTCCTCCTCCTCATTTTCTTGAAGAGAC
TTGGTTTCAAGGACTGAATCATTTGGCAT
T
Sequence 442
TGGCGGCCCGCCCGGGCACGTACTTTTGCTGCTGAGGAATGGGAATCAAAAGAACGTAGT
CTCCTGGTAACCACCTCAGATCTCTATTATTAGGCTAGATGTNGNGCNNGTACTCCCCCA
GCTTCTTGCTCNNNACCCTGCACTGTAAGTTGCCCTTCTATTAGCAGCCAAGGAAAAGGG
AAACATGAGCTTATCCAGAACGGTGGCAGAGTCTCCTTGGCAATCAACCAACGTTGCTAT
GAAATATGCCTCACACTGTATAGCTCATTATAGGACGTCAGGTTTGTTGAAAAAAAGTGN
GGCAAGACATGATTAATGAATCAGAATCCTGTTTCATTGGGTGACTTGGATAAAAGACTT
TTTACTTTTANAAAAAAAAANTGTCAANAAANANGTTCCCTNGGCNCGGCTCTAAGAACT
AGTGGGATCCCCCGGGGCTGCAGGGAAATTCCGNATATTCAAAGCTTATCCGATACCCGG
NNGAACCCTCCGAGGGGGGGGGCCCCGGGNAN
Sequence 443

Table 1

CCCGCGGTGGCGGCCGAGGTACATGAGAGACACTTTAAGCAGGCTCACAGGAATAGAGTG
AGTGCGGACTCAGATTGTTTAAGCTATCTCTGAACCCATTCCTACTGCGTTTAACTATT
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A
GCGTTGTGGTCCGGGTTCATCGCCATCCTGCTCCACGCTGTCATAATCCTCACGCATCCG
CGCTCGGGACCCCTCTTCTATAAGGGACATACACGAGATCACCGAAAACTCCTCCTTTCT
CCCATTGTTCCTATGAGGTGGGTGGGGACTCCAAAACCCGTAGCTCCTGCCCTACTAGGC
CACTCTACCCCATT
Sequence 444
CCACCGCGGTGGCGGCCGAGGTACCCAGCCCCACCCAGGCAAACAGCTCCGACATGTTTC
GTAAGTGAGACAAGCCAGTGCAAGTTTTTTTTTTTCCTTTNNTTTTGNGCTTACCTTCT
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GCTTAATGGAATTGTTATGGCTAAGCACATAGAAGGCCAAAAAAGGAGTTTTTCAAACCC
AGCAAATCAAGTGCTTGGATTCTGAACTGCCAAAAGAAAACTGCACTTCCCCTCTTAAGT
AAAACCGAAATGAGTTTTCTTAGGTAAATGTATTCATCAAGCCCAGNATATAGAAAATAA
AACCCAGGTTANTGGTGNAGCCGTTTAGGTCACCTGCATCATTTTCCAGGGAAAGATTCA
AACCAAAAATACCAGTNCCCAGNCCAGGACTCACAATGTGTTGGANTAATATTATTATTA
AAAGCAAAAGGAGGCCCCNCCCCCACCAAAGCCCAAGCAGCTGGGNTGGAAAATAATCAA
GGCCTGGTCCCACNCCCGTNGGGTAATGCCCAAATTCCGGGGGGAAAAATATACCTNCCC
TTTGGNAAAAAAACCTTGGGAAAGAAATTCTTACCCTTNGCCTTGGGGAAAAAAAA
Sequence 445
TCCCCGCGGTGGCGGCCGCCGGGCAGGTACTTTACTAAAATGACTGCATTCTTTGGATTC
CTTCAGTCTATGGTTCAAGTCACTAAAGATTCATTTTTGTTGAGTCCTTATGAGAAACA
G
NAGTATGAATCTTGACGGTTTCTGCCCGTCCTAATGGCAGAGCTCTCTGACTTGGGTGTA
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A
CCCAGTGGGTCAAGTCTGGGACCTAGGTGGTGAGCTATCCCATAAGTTCATTCTCAAACC
GTCTTTACTGCACTGTTTAGGGTCAGATACNCATTATATATACNACTTTGGGTGAGCT
CA
GGAGTTTATAAGCTTTATGGGCTTTGGTGTTTTGATTTATAAACAGGAGTTTATNGAAC
T
TTATGGGGTTTGCTTCCTCTTTCTGCCCAGGTTCCTTGGG
Sequence 446
GGTGGCGGCCGAGGTACGCGGGGAGACACAACTTCCTGGGCTTAGATATTTCAGAATATC
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GCACTTTGGGAGGCTGAGGCAGGCAGATTGACTGAGCTCAGGAGTTCAAAACCAGCCTGG
GCAACATGGCGTAACCTCGTCTCTACAAAAAATGCAAACATTTGCTGGGCTTGGTGATGT
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TGTAGGCTGCAGTGAGTCATGTTTGCACCACTGCAGTCCAGCCTGGGTGACAGTGTGTAT
TAGTTTGTTTTCATGCTGCTGATAAAGACATACCTGAAACTGGGAACAGAAAGAGGTCTA
ATTGGNCTTACAG
Sequence 447
CGGCCGAGGTACGTTTTGTGACAGGCAATAAAATTTTAAGAATTCTTAAGTCTAAGGGAC
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AAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCGTCTGATTCTAATAGNA
GAGCCCGGGCTTCACCNGTTTTGGGCTTCCGATATTAATAAGACCAAGCTGAGTCCTCCC
TCCCAATTGGAAATATGAATCATCTACAGCCTTCTGCCCTGGTCGCATAAAATTATGT
CT

Table 1

GGTGTTCTCAAGGCAATTAATAATGATTGTTTTAACACCAACAANAAAGAAAACTATTA
T
CACNAAAANTAAGGTNCCCTGCCCCGNGGCNGGNCCGCTTNCTANGAACTTAGGTGGGAT
CCNCCCCGGGNCTGCAAGGGAAATTANGNATTATCCAAAGCCTTATTCGAATAACCCGTC
CGAACCCTCANAAGGGGGGNGGCCCCCGGTATACNCCAAGCTTTTTTGGTTCCCCTTTTA
AGTGGAGGGGTTAAANTGGCCGCCGCTTGGGCGTAAAATAAATGGGACNAATAAGCCTGG
TTTTCCCTGNGGNGGANAAATTGGTTNTTCCCGCCTCACCAAATTCCCACCACNAAACAT
TACCGAAGCCCGGGGGAGCCAATAAAAAGTTGGTANAAAGCCCTGGGG
Sequence 448
CGGNGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGTTAGTGTTTTCTGATGTCTTTT
CTAACAAATCTTTGCCTGCCCAAAAGTCTCAAAAACATTCTCACGTTTCTAGATTTTTA
G
CTTTAGCTTTTGTGTTTGGGACTATGATCCATATTTAGTGAATTTATTTTTGGGGGGGC
A
GAGTCCATGTTGCCCAAACTGGTCTGGAACCACCACACCCAGCTAATTTTTGTGAATTGC
GGGTACCAGCACACCGGCGCCGTCCTGGACTGCGCCTTCTACGATCCAACGCATGCCTGG
AGTGGAGGACTAGATCATCAATTGAAAATGCATGATTTGAACACTGATCAAGAAAATCTT
GTTGGGACCCATGATGCCCCTATCAGATGTGTTGAATACTGTCCAGAAGTGAATATGATG
GTCACTGG
Sequence 449
CGGCGGCCGAGGTACAAAAAGCAGGGGCCCAGCCCCAGCTGTTGGCTACATGAGTATTTA
GAGGAAGTAAGGTAGCAGGCAGTCCAGCCCTGATGTGGAGACACATGGGATTTTGGAAAT
CAGCTTCTGGAGGAATGCATGTCACAGGCGGGACTTTTTCANAGAGTGGTGCAGCGCCAG
ACATTTTGCACATAAGGCACCAAACAGCCCAGGACTGCCGAGACTCTGGCCGCCCGAAGG
AGCCTGCTTTGGTACCTGCCCGGGCGGCCGTCGATCTCCTTGTGTTCAAGCAACTTCTTG
CGGTAGTCCTGAAGCGCCTTATCTCTAGGGTCCGCCATGATGAGAACCCCGCGTACCTGC
CCG
Sequence 450
NGGTGGCGGCCGAGGTACTCCCTACGGCACTAGTCTACAGGGGGAAGGACGCTCTGTGCT
GGCAGCGGTGGCTCACATGGCCTGTCTGCACTGTAACCACAGGCTGGGATGTAGCCAGGA
CTTGGTCTCCTTCCCGCGTCAAGAGATAGAAAGACCAGTCCTTGTGAAAGACAAGTCTGA
ATGCTCCACTTTTTCAATTCTCTCTCCATTCTTCAGTAAGTCAACTTCAATGTCGGATG
G
ATGAAACCCAGACACATAGCAATTCAGGAAATTTGACTTTCCATTCTCTGCTGGATGACG
TGAGTAAACCTGAATCTTTGGAGTACCTGCCCG
Sequence 451
CGAGCGGCCCGCCCGGGCNGGTACAAATGCGTTTANGAAATGTTAGTATAAGGCTGATCT
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TATTGAAAAAAAATTTTTTTCCTGATTTTCTTTTTCCTGAAGGTTTTTTTGTAGAAACCA
TGGTAAAAAGGGAAAAGAAACCTTTGACTGGCGGGGGCAGGGGGAATACAAAAAAAAAT
CCCTTGATTTTTAAAATATACTTGAATATCAAACTCAGAAAGAGTTATTTTTGTGAAAGA
GGCAAAATTGGTCTTGAGCTGCTTCAGTCTATGTCTGAAGGTTTTACTGAAATTATGG
TC
CAGTTTTAGGAGAAAAATTCACAGAAAAGTCAGATTGTAGATTTTGAGAAGGAAACTCTG
AGGTGGTGATTTTCTCCAAGGTCATGGTTATGAAGCTCAATGAGGGCCTGAATTGCTTCT
TCCACAGATCCCAATTGAATGAGCGCCATTTTGCGATCTTTCTGAAAGAATTTAAAA
Sequence 452
GGGGCGGCCGCTAATGTNAGAAGTTAAGTNAGAACCTATATTGTACGAGGAACAAAAGCC
AATCAGTGTCCTTTTTGTCTTTTTTTACATAAACTTTTACTACAAAAATTNATATATGGA
TTTTGAATTTCCAGTCAAACCAAATTGTAAAACTGTTTCATTTGGTTCTATATTATGTAT

Table 1

ACATAATTTATCTATTATATATTTACATTAAAATATATGCATATATAATGGATTTAATTT
CCTTTNGGNACCCCCATATNTAGAAGNNTCTTCATAANTTAATAAATAATCTAGGGCCAG
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T
TTCTTGGACTTGAAACTGCCTANAGCGTCAGCCTCTCTGTTATTTNTNTCTATTTNCTT
T
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T
AAGAGTAAAAGGGGAAGGAG
Sequence 453
ACGGATACCCTGTTCCGCCTTTCTCCCTTCGGGAAAGCCGTGGCGCNTTTCTCATAGGCT
CACGGCTGNAAGGTAATCTCAGNTTCCGGTGTAAGGTTCGTTCGGCTCCAAGNCTGGGCC
TGTTGTGGCACCGAACCCCCCCGGTTTCAAGCNCCGAACCCGGCNTGCGGCCCTTATCCC
GGGTAACCTATACGTCTTTGAGGTCCCAACCCCGG
Sequence 454
NGAAGGCGGACGCCCGGNCAGGTACGCGGGGACCTTTNACGGCGGGGGGAGCTGAGGCT
CCTGNCGNTATCTNTGATCCTTGCACCCTGGCAGGAAGNTGGTAGGGGGNACTNTAACGG
GAGGNCTNCACATATTGCAGAAAAGAAACCACTTTGGNGNGTAAGACTTGGAAGAAAGTA
ACCGGTCACTTTGGAAAACAGGGGTGGGAAGAAGCTGCCTCTCTTTTGAACCTNTTCCN
AGGGACCAANTCTAACCCAGGTGAGGNNAACCNTGGTNGATGTAAAGCCGGTGGCTTTGG
AGGACAGAATCATCTAAGTGGGAANAAGATACACTAGGAAGGGNGCTGGGGGGANTACCA
TCAAGAGGGAGGNGGGGATNACCTTCAGGCCGGGGGCTTNCGGNGGGGATGAAAGAAGGA
ATGGGNCCGGACAGGTTTGNGGGTNGGAGGGTATGAAGGCTTGGCNAAATGGTGGGGAAT
TTTGGTAACNTTCGGGCCGGGTTTTTAGAANCTNAGGGGGGANTCCCCCGGGGCTTNGGA
AGGGGAAATTTTCGANTAATGCAAGGCTTAATANGAATTACNCGGGGGGACACTTCGGAG
GGGGGGGG
Sequence 455
CCCGCGGTGGCGGCCGCCCGGGCAGGTNCGCGGGGAGGATCTCTGTCTTTTGTTCCCTCA
CCTGTCTGCCTGTCTCCTCTCCTTTCCTGCCTGGGGGGACTGTCCAGAAGACATCATCGT
CCAGTTCCTCTGCATTTGAACAGCTGTNCCCCCACCCCTCAATACCGTTTAGAGCAGAAG
CCAGCAAATACTAATCGGTCAGGGACACGATAGAAACTATTTTCGGCTTCATGGGCCACA
CAGGNCTTCATTGCAAGCTCCTCAAATNTGCTGTTTGTAGCTAAGGAAAGAANCCATTAT
ACCNTGTGTNAANCAAAAATGAAATATTGGCNTGTGTGCCAATAAAAAACCTTATTNACA
AACATTAATNGAGTNGGGCNTGGATATGACTTCACNANTACTGGTTAGTTTTGACAACCC
CCCTGGNTNCTAGNAGTTAAAAATCCCAAAAACTNCTTATTAGTCCCTCCC
Sequence 456
CGGCCGAGNACAACATGACATTTTTAACCAATCCAATCTAAAAATGTTGCCAGAATCCAC
CTGTGGCCCNGAATCGNGTNTTGGTTCCTCTTTCTACTCCNCTGCAGANGACCAAACCTG
TCCCGCTGCCACTTTCCTCACTGATATTGGGAGGAGGGCAAGGCCCAGCCGAAGTTCCAC
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GCTTTCTGTTTTTTTCTTTTCCCCGACAGCACAAAGAANGTAAAGGGGCAGTTAATTGGAC
AGAGTGTTATTTTAAAACATCTCTAATTGTAAATGNAATGTGGTTGGTTTGGGTTTCTA
C
TGCAATTGGTGNGAAGCCATGCCGGNGGGGAAAGAAGAAACNTGACCCCAAGGNTAATTG
AAAATNGGGAGNCCCCCTTTC
Sequence 457
NCGATATTACTGTGCGAGAGGTAAAGGATATAGTGGCTACGATTACNGCCTCTCT
Sequence 458
CCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGACAAAACTACAGACTTAGTCTGGTGGA
CTGGACTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGA

Table 1

GCAAAATAAAACAAATAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGC
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ACCAACATTAAGTCCAGAGAGTAAACTTGAATGGAATAACCGACATTCCAGAAGTTAATC
ATTTGAATTCTGAACACTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATC
ATCTGGAAACCGATTTTCAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAG
Sequence 459
GGCGGCCGCCGGGCNGGTACGCGGGTCGTGNGCTGGTTAGTGAAGGCTTTGTAGCTGAGC
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AATACAAGGGTCAACTGTATTTGTTGGTAACGGACCAGGGGTTTCTTACTGAAGAGAAAG
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AGGATTATCTTATGGCATTATCTCTACAACAAGAACAGCAGAGCCAAGAGATCAATTGGG
AACAAATCCCGGAAGGAATCAAGTGATTTGGAACTAGCAAAGAAACT
Sequence 460
GGCGGCCGGGTACGAATGTGCAAATTAAAGCATGGTAAACTGATATTTACATAAATATCA
AACCAACAATTAGTTTATACATTGTCAATGACCTTCTAAGATATGTCATGAGTGGATCC
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GAAAGAAACATGATTCCCCTCAAGCCACAAAGGATTTTCTCATCAAGTGTTTTCACCTCT
GCATTAGATTTGGACACAAGAAGAGGAGAGCATTTACTCAGGTAAAAATAGTTCTCTTAG
TCTCTTCCTCTAGTTACTAATTTTTAATTTAAAAATACAATTAACTGATCTAGCTGATAA
AAGTCACAAGACAGAAATAAGCTAAGTTCTCTCTTNCTTTAGGGAACGCTGGTGGCAATT
CACCA
Sequence 461
GAGTTTGAGAAAGCTGCAGAGGAGGTTAGGCACCTTAAGACCAAGCCATCGGATGAGGAG
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GGCCCCGGGGATGTTGGACNTCACGGGGCAANGGCCAAGANTTGGANGCCTGGGAANGAG
CTGAAAGGGACTTCCAAGGAAAGNANGCCATGGAAAAGGCTNTACATCAACCAAAGTATG
NAAGAAGCCTAAAAGAAAAAAAATACNGGGANTAATGAGAGCACNTGGATTTTGGGNTAC
NTGTGCCCCATGTGTTTTATTCCTAAACTGGAGNACAATTGCCTNGNNTTTTTTCTAAN
N
ACCCGNTGGAATGGTTGGGGAAATCTCTGGGGAAAAATAANCCAGNTAAAACCAGCTACC
TCAAGGGCNTGCTCACCCATACCG
Sequence 462
AGCCCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATATTGTTCCTGATTTGCCTGATGTG
TGGACGGATCACCAAGCGAGTGACACGAGAGCTCAAGGACAGGCTACAATACAGGTCAGA
GACAATGGCTTATAAAGGTTTAGTGTGGTCTCAGGATGTGACAGGCAGTCCAGCCTGACC
TTTCTGCACACTCCAGACAAACTTCCCAGACAAGCTCCTTTGTGCCTCTACGTGGAGAGG
GCGTGGAAAGTTATCACATTAAAAGATGGAGGATTTAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAGTACCTGCCCG
Sequence 463
GCGATNCCCCCTGGGAAGCTCCCTCGTGCGCTCNTCCTGNNCCGACCCTGCCGCTTACCC
GGATACCTGTCCGCCTATTCTCCCTTCGGGAAAGCCGTGGGCGCTTTCTTCATAAGCCTC
ACCGCTGTAGGNATCCTCAAGNTCGGGTGTAAGGNNCGTTCGCTCCAAGGCNGGGGCTGG
NGGNGCACNGAACCCCCCCGNNCAAGACCCGACCCGGTGGCGCCTTAAACCCGGAAAACT

Table 1

AATNCGNCNTGGAGGTCCCAAACCCCGGGGNAGGACACCGACTTATCCGGCCACCTGGGC
AGGCAGCCAACTGGGGTAAACAAGGGATTAAGCAG
Sequence 464
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T
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAACNGCNGCCNCCNCCATGAAAGAGGG
GCCNCCACATNTTTATTGCATACNCAGGGGAATAACTTATTNTACAANGAACNCTCCTCC
ATTNGGAGACCATGCCCACTTACAGAATGCANCCGNAAATGCGGTAAATNTATTTACAGA
GGNTGGGGNGCAAGATGAGANAAGTTTCANCCCCAGGAATTTGAAGNGAGAATGATCTAC
AAATTNTCCTGACAAGGNGCAACCGGGCTTGNGCTAGNGNGGNCTGAAANAATTCCTGGC
AAANCGTAGGGGGAGATTAAATCTCGGAATTGACAGCAAGTTTGGGGACAGNGCAAAAAN
AGAGGGGTGACCCTGTGAAATTTGGTGCCTGGGGGAACTTCTTGANGCCCCAATGNGGGG
GCACCNCTTNGAGANGATNGGGNTAAATTTANGGGGGGATNTTTTAACCCCTNTCCNNCC
CCAACCAAAAAAGGG
Sequence 465
GGCGGCCGAACGCAGAGAAGGTNGANGATTGCACCATGCCGATTCGTCGAACTGTGAATT
CTACCCGGGAAACTCCTCCCAAAAGCAAGCTTGCTGAAGGGGAGGAAGAAAAGCCAGAAC
CAGACATAAGTTCAGAGGAATCTGTCTCCACTGTAGAAGAACAAGAGAATGAAACTCCAC
CTGCTACTTCNAGTGAGGCAGAGCAGCCAAAGGGGGAACCTGAGAATGAAGAGAAGGAAG
AAAATAAGTCTTCTGAGGAAACCAAAAAGGATGAGAAAGATCAGTCTAAAGGAANAAAAN
TTTTATNNNATTAAAAGTACCTCGGCCCGCTCTAGAACTAGTGGGATCCCCCGGGCT
Sequence 466
TGGCGGCCCGAGGTACGCGGGGAGGTCGGTGCGCGCTTCTCCCGAGGTGGAACGGGCGGC
AGTCAAGCGCCGGCGTTCTCTGCCGTCACCCTTTCCTTGC
Sequence 467
GCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAG
AG
TCTTGCTCCATCACCCATGCTAGAGTGCAGTGGAGTGATCTCGGCTCACTGCAACTTCCG
CCTTCTGGGTTCAAGCTATTCTCCTGCCTCAGCCTTCCAAGTAACTGGGATTACAGGCAC
ATGCCACCACGCCCAACTAATTTTGTATTTTTAATANAGACAGGGTTTGACCATGTTAG
C
CAGGCTGGTCTTGAACTTCCATCAGGNGATCTGCCCTCCTCAGCCTCCCAAGTGCTGAGA
TTACAGGCATGAGCCACCGCGCCTGGCTGATTGNGTTCCTTTCTCACAGATTTTGTTT
CT
GTTTTTGTTTTCCTGAACACTCAGCTGGACTGCATTTCCCAGCTTCCCTTGCAGTTAA
GT
CACAAGTAGCGCTGTGACTGGGTTCTGCCCGGTAGGAAGGTAAGCAGAAGTGAATGTGTA
TCACTTCTAATGGTGTGGGNCTCCCNAAACCTTCTAAAGGGGTATGTTCCCCCTTTTT
TT
T
Sequence 468
TTGGAGCTCCCCGCGGTGGCGNTCGGTGTGCTGNGCTCAGCTGCCTTCCNANGGAGGANC
NGATCGGCNAGTGCTCTGACTGCGTGGCCGACAANNGCTGNCGNAGAAAGAAATNAAANC
CCTGAAACATGACAGNGAGTGNTGNAAAGTGTGGAAATGCCTTCTTAAAGTTNATNAANG
TNAANTCAAANNACATTTTTTTTTCAAAAANATAAATTTAGAACTAANTGNACCTT
Sequence 469
CGGAGGAGAATGGTATCACTCAGGCTCTCAGAGTGACACTGAAGCAAGACACTCATGGGG
TAGGACATGACCCTGCCAAGGAGTTCACAAACCACTGGTGGAATGAGCTCTTCAACAAGA
CTGCGGCCAACTTGGTAGTGGAAACTGGGCAGGATGGAGTACCTTCAGGATTGGCCTGTT
ATCTTCTTTAGAACTAAGTTCATCTTAAAAATTTAAGAAGGTGGACATTTCAACACCAT
C

Table 1

AAGTGCATTTAGGTGACATGTTTAAGTTAACTTGACTTCCTTGAATGACCTAGTTAGTA
A
ACTAGTCACTAGTAATTCGGTCACCAAGCAAATCAAGCCTGCAAGAAAGGAAGCCAATAT
TCAAAATGCCATGTTACCATCTAAACC
Sequence 470
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGATTTTATTGTCTACCTCTCTGGACTTG
CTCCCAGCATCCGGACCAAAACCATCAGTGCCACAGCCACGACAGAAGCCGAACCGGAAG
TTGACAACCTTCTGGTTTCAGATGCCACCCCAGACGGTTTCCAGTCTGTCCTGGACAGCT
GATGAAGGGGTCTTCGACAATTTTGTTCTCAAAATCAGAGATACCAAAAAGCAGTCTGAG
CCACTGGAAATAACCCTACTTGCCCCCGAACGTACCTGCCCG
Sequence 471
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGGGAAGA
CA
CAAAGATTCAGACCACAGCCTACAGGGAGAGAGGATTTCTGAGGATGGTGGTGCACTGTG
AGTCCACGCAGGCCTCCTGGGCATAGGATGGAGCAATTCTATCTCACCTCAGGCCTAGCA
CAAAGGGCTTCAGTAAACCACTGGAGTTTCCTTCATTAGGATTCCATCCCAGGATATCCA
GAGGACAAGAGGCTGGCCAACTGCAGGATTAGCCTATGCTCCCGTGCTGGATATAGGCTA
CACGCAAGAGAAAGCTTGGGTGGGATCTCCTGATCCCGCGTACCTGCCC
G
Sequence 472
GCCGGGCAGGTACTATGGGTGTAGTGNTACTATTACAGTTAATNCNTCCTTTGTAGTGCG
CTGNTAAATGCAGTGAGGATTGGAGCACTGTCCACTGAGTCTCTGTGC
Sequence 473
CAAAATAATTATAATGTATTAACTCATACTGCCTGTCTTTTATAGGGGAAAAAAATAAC
C
TNTTTTATTTTAAAGTTATAAGGGGGNTTACCTTNTAGNGTGCTTGGATGACAGGGAA
AT
TAGCCTACCCCATTTTGGTCTGGAACAGAAGACTTTCAAATTTAATATGGNCCAAGTGTC
TTNACTANTTAAGGCAAGATCATGCTTNTGTCAGTTNACCCCANTGNTTGGAATACCGTG
NACACCGATCGTGGCTCGNCTACAGCCTCCATGTNCCCAGGCTTCGAGCAGGT
Sequence 474
GGCGGCCGCCCGGGCAGGTACGCGGGGGAGCTGAGCCGGTGGGTGAAGCGGCGGCCACGG
CATCCTGTGCTGTGGGGGCTACGAGGAAAGATCTAATTATCATGGACCTGCGACAGTTTC
TTATGTGCCTGTCCCTGTGCACAGCCTTTGCCTTGAGCAAACCCACAGAAAAGAAGGACC
GTGTACTTCTAAAATTGCACTTTATGTTTTGTAGGCTTGGAGCTTCTTGATTATGGGTT
T
TTTCGTTACAAAATTCAACAACAGAATCAATACTTTGCATAAACATTATGGATGCTTTTT
CTGTTTGTACCTCGGCCGCTCTAAAACTAAGTGGATCCCCCNGGCTTGCAGGAATTTCGA
TATTAAAGCNTTATCGATACCGGCGAACTCGAAGGGGGGGGGNCCCGGGACCCANCTTTT
GGT
Sequence 475
TTGANGCCCTCCCCGCGGTGGCGACAGGGTTACATTGGTAAGGGTGACAGTTAGAAGGGG
AAGTCCTTTTAGTGAAATAGATGAGAGGTTTTAGATCTGCACAAACCTTTTTCATGGAAG
TCCAACTTTGCTCCTGGGTAGTTTAAAGGACGTAGTCCCATGTACCT
Sequence 476
NGGCTACACGCTAGGAACCTTGCAGCTTACAGTGACAGAGCTCCCATTCACGAGGCCACC
ACTCATCTCGATTTCTGGATCTCTAGGGAATGAGTAGAGCTCCACCTGGATTCCCTTT
TC
CAGTTTCTTATGTCCACAAGTCACTGTGCACAGATAAGAGTGTTCGTTCTCAAAACTCAC
AGGGCTCAGGGTCATGCGTGGAAATTGGGTCCCCTTCACTCCTCACCTTTCCCCGCTTCA
GAGGGCTGTCTATCTGGGTTCTCCAGGGAGAAAGATGGGGAATTCACAGCCCATGGACAC

Table 1

TACCATGTCAACAATGACTGAAGTCTTCCAATCTGAGCCAGGCAAATTCCNGGNGGGTCC
AGGGGGGAGAATCTCAAACAGNTAAAATGGGTTTTCTCTTGGAACAAATTAAATTTCCCA
CCTCTTTTTTNTTGNTTTTTTCCCC
Sequence 477
NGGNGGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGCAAAA
A
TATTTATTAAAATGATTTTTTTAAGTTTGAACTTTATTGGAAGGAGTCCCTCTAATTCAC
ACTTTCATCCTAGATAAATGGGTAAGAACCACATATGGAATATAAAGCATTGATTTTTT
A
AAAACCACATAGTAGCACAGTTGAAAGAAATGCAATTCTCCAGGGTCTTAGAGAATTCAA
AGGNGGCATCTTAGGGNGGGTCCTAAGGAAACCCAAATTACCAGGTCTCATGGGTTTTCC
TTTTGGGTTCAAGGATTAGAAAGGAGTCAGNGGTTACCCACCTACCCTGGTTTTTTAGGA
GGGGTAGGAATATTGAAACCTTTCCTACTTAGTCCANCAGGTTTTACCTGGTTCAAGGGT
GGGNCCCCCAACCAAGGTTCTTTTTTTATCTTTCAAGCCCCCATTCTTTGGCCCTCTT
AA
GNGGGGGGTGG
Sequence 478
TCCCCGCGGTGGCGGCCGAGGTACCTGCATCAGGGATAAGAACCCATTCCCCTCCCTTGT
TCCGGTGTGCTCTCGCCATTGCACCATCCATGAGACGCACTCTTGTATAGAAGTAAAATT
GCCTTGCTGAGAAAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCG
Sequence 479
CTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGGTGTGGCCTGCATCTCAGCTGGCCGCCA
TCAGNGTAAATAGAGCTTAAAGTCATGGTTTGGCTGCATAAAAATTTTCTAACTTGGGT
T
NAATATTTGTAGNTGAAGTATCTGCTTTCATTTTTTTCACGTTATAAATAAAAATACTAT
GCTGGNCGGGCGCGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAATGTGGGT
GGATCATGAGGTNAGGAGTTCAAGACCAGCCTAGCCAAGATGGTGAAACCCCGTCTCTAG
TAAAGATAAACAAAAAATTAGCTGGGC
Sequence 480
GCGGTGGCGGCCGCCCGGNCAGGTACAGATGCAAACGGAGGTGTAGACTGNGCAGCTGCC
AAAGTGGTGACAAGCAATCCAGAGGACCATGAAAGGATCTTAATGCAAGTCATGAACTTG
AATGTGCCGATGAGGCCTGGCATTCTTGTCCAGAGACAGAGTAAGGAAGTGTTGGCCACA
CCCTTAGAAAACAGAAGGGACATGGAGGCAGAAAAAAAAAAAAAAAAAAAAAAAACGTAC
CTN
Sequence 481
ATGTTTTGTGGCCAAGGTGAGGGCTGCAAGTGTTTTCTAAGGGTTGAAACATCANAATAA
AGGTATGGTGGCAAGTCCTCCTTCTGCTAGGCTGGCTGGCAAGGCCCTATGTCTTGACCT
AGGTGGTAGTTACAAGGGTATTTTATTTTGCCTTATAATAATTCACTAAACTATGTTATT
TGAGTNAGATTTTTATGTNGTGNGNCNTTTTAATTTACACAAAATTAAANCAAAAAGNA
A
CNAAANGTTGCNCTCNGNCTCGGNTTNTAAGTAAACCTAAGGTGGGA
Sequence 482
CTGAGAGATCCCCTCATAATTTCCCCAAAGCGTAACCATGTGTGAATAAATTTTGAGCTA
GTAGGGTTGCAGCCACGAGTAAGTCTTCCCTTGTTATTGTGTAGCCAGAATGCCGCAAAA
CTTCCATGCCTAAGCGAACTGTTGAGAGTACGTTTCGATTTCTGACTGTGTTAGCCTGGA
AGTGCTTGTCCCAACCTTGTTTCTGAGCATGAACGCCCGCAAGCCAACATGTTAGTTGAA
GCATCAGGGCGATTAGCAGCATGATATCAAAACGCTCTGAGCTGCTCGTTCGGCTATGGC
GTAGGCCTAGTCCGTAGGCAGGGACTTTTCAAGTCTCGGAAGGTTTCTTCAATCTGCATT
CGCTTCGAA
Sequence 483

Table 1

GCGGTGGCGGCCGAGGTACTCTTCAAAATTGTCAAGGTCATGAAAGACAGCAAAAAGTGA
AGAATTCTTACAAACTAGAGGAGACAAAGATTGGAGAAGAAACAATGACTGGCNGGGCAC
GGTGGCTCATGCCTGTAATCCACTTTGGGAGCACTTTGGGAGGCCGAAGAGGACAGATCA
TCTTAGGTTGGGAGTTGGAGACGAGCCTGACCAACGTGGAGAAACCCCATCCCTACTAAA
AATACAGAATTAGCTGGGTGTGGTGGTGCATGCCTATAATCCCAGCTACTTGGAAGGCCT
CGGCAGGAGAATCACTTGAACCCGGGAGGCANAAGGNTTGTGGTGAGCCAAAATTGCGCC
ATTGCACTCCAGCCTGGGCAACAAGAAGCCGAAATTTCTGTCTCAAANAATAAANAACAA
AAAAAATAAGTACCTGCCCGGACCGGCCCGCTTCTANAACTAGTGGATCCCCCCGGGCC
TGCAGGGAATTTCGATATTCAAGCTTATCGGATTCCGTNCGACCTTCGANGGGGGGGCC
CGGNTCCCCAAGCTTTTTGGTTC
Sequence 484
GATGTGAACAAATGTGTCATTGCTCTCCAAGAGAAAGGATGTGGATGGCCTGGACCGCAC
AGCTGGNGCAATTCGAGGCCGGGCAGCCCGGGTCATTCACGTAGTCACCTCAGAGATGGA
CATCGAGCGGCCGCCCGGGCAGGTCACAAGCTTTATTGGGCAACAGCAACGAGCCACGCT
GGCAAACAATGAAAGTAGAGTCGCTCAGAAACACGAAAGATCATATGTGTGTCATCACAG
CATCGAGAATTTAAATCATCTGGAAGTTCCTGCTAAATTAAAGCATACTGTGCCNNAGCT
CCCCTCTAATCAAAAAACGCTTGTCCTGGNGAAAAATTTGCATGNGGGNTTACAGAGAGA
GAGATCAACCAGGTGAGGAAATCACAAGACTCTTACATGAGTTTACAGTTAACCCCCCTG
CACCAAAAAAATAAATTAGCCATAATTTGGTT
Sequence 485
TCCCGNGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGGGGAGGATACT
T
TCATTTTTATTTTATATCGTGAGGTATTGTTTGGATTGTTACAATGAACTTGCATTTCTT
TTGTAATGAAGAAAATAATACAGAGGAAATAACAACAACTAAACCTTTGGCCTGGGATTA
TCATCCGGGCTGGGAAATTCATGTTGGGATGGCAAGGTTTTTATTGATAACAAGGTTATT
TTTTGGGGTTTATTATTGCAAAAAAAAAATTGTTCATTGGGAATTGCCCTCCTATTTGG
G
CTTGGGCACCTTGCCCTAAGGGCCACTTTTCACCAAGGGTATTTTCATCCCTTAAATCCC
TCACCAAACCAGGCCCTATTGGAAGGGGTAAATCAATTGGGGTCCCCAAGGTTTTACCAA
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AATTTTGGCCCACCACCATTTTTTTTGGTTGGGGCAAAGGACCGGTTTCCGGTAATCCGG
GCTTGGGTGGATTTCACCTTGGGTCAAAAGGAAGCTTCTCATTGGGGCCAAGGGAGGTTT
CCCTAATTTGGTTGGCTTGGNAAAGGGAATTTCAAAATAATTCAAAAAATACTTAAGAAA
TTTTTTNCCCCCCA
Sequence 486
TGGCGGCCGCCCGGGCAGGTACGCGGGAGTGTGGATNGAACAGAAAATTGGAAATCATAG
TCAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACTTGACTGGGGTTTTTTCT
G
CTTAAAAATTTCAATTCTCGTGGTAACAACCGCAGAGTAGAAGGAGAGGGTGACTTTACC
GAACTGACAGCCATTGGGGAGGCAGATGCNGGTGTGGAGGTGTGGGCTGAAGGTAGNNGA
CTGTTTGATTTTAAAAAGTGTGACTGTCAAGNTTGTATCTGTTGCTTTTNTCAATGATT
C
AANGNGATACAAAATGGGGCTTCTNTCANTCATTTAAAAAGGAAAAACGCCGACCATCCT
TTCTAAGGATTCTCTGTGGGAAAAATGGACTGTCAATTAAAATGGCGGGGTTTT
Sequence 487
CCCCAGGGTTCAGTCCTCAAGGGGCCATCCTGTCCCACCATGCAGTGCCCCTAGCTTAGA
GNCTCCCTCAATTCCCCCTGGCCACCACCCCCCACTCTGTGCCTGACCTTGAGGAGTCTT
TGTGTGCATTGCTGTGAANTAGCTCACTTGGTGATATGTCCTATATTGGCTAAATTGA
AA
CCTGGAATTGTGGGGGCAATCTATTAATAAGCTGCCTTAAAGTTCAGTAACTTACCCTTA

Table 1

GGGAGGGCCTGGGGGGAAAAGGGTTAGAATTTTGTATTCAGGGGTTTTTTTGGTGTACCC
TGCCCGGGGCCGGCCCGCTCTAAGAACTAGTGGATCNCCCNCGGGCTGCAGGGAATTCG
ATNTCNAAGGCTTAATCGATACCCGTTCCGACCTCGAAGGGGGGGGGCCCGGTACCCCAA
NCTTTTTGGTTCCCCTTTTAAGTGGAGGGGTTA
Sequence 488
CNCGNGGTGGCGGCCGAGGNACTTTGTTTTTTTTTNTTTTTTTTGAGGGTGGCTTTAT
TT
TCAATATTTGTCTTATTAATATTTTTCTTATTTTATAATGCAATTACAACNGNTTTAGGA
GACAAAACAATATAAACAAAAGAATGTTAAATAGGTTTTTTTTAAAAAATAAGCTTGGTT
GGCTTTGCAANGGAAAGTCCATAATAANTCTTATTCCCCCCCAAATATTAAGTTTTATT
A
CTTTNGCCACNTAGAGACCCAAAAAATAGCTTATTGGGGAAAAAAATTANGTTATTTAAA
AATANGCCTTAAAAACCACCAAGGAAAAACCCTTACCAGGGCNTATTAAAAATTAAACCA
ATTAAAAAATTACCAAGGGTTTAAAACTTTTTAAATGGGNGGGATNGGCCTTTAAAAACC
AAA
Sequence 489
NGCCGACCGAAACCTGGTGAAGCCCTTTGGGCGATTGGTGATCACCCCTAGATCCGTGAA
AGCTGGCTGCCCCCCCATCCGGGCAAGCAGGGCCAAGGTGGCATCTTNACATTCCTGGAA
CCCACCCAGTAACAGCAGCAGGTATTTCTTCTGGGTAAATGAAGAGCCTTTCGAAAAAAC
TTTCTTGCCCTCAAAGTATTTACCATAAATTCTCTTTAAAAGTGGACATGGTTCAAGAA
T
CAAGNGGGCTCAAGAAGTTTNGAAAGTAAAAGNAGGTCATTTTCCTTAAGTTTCAAGCTT
TTCAAGTTTTGNTATAACTTTTCAAGCCCTCTGGCCCCTTTTTCAAAAAGAATTTTCTT
G
GGAGGAGGTCCAAATTTTTTTTTCTTTTNGTTTNCCAATACNTTTCTTTTTTT
Sequence 490
NCCGCGGTGGCGGCCGAGGTACCTGATTTTATTTCNAGTTTTCATCCGAATCCACTGGGG
AATGGGACGATTTTGCTTTTGTTTCTTGGCCAGGAATCGCTTAATCCTGAAAGTCTTG
TG
AGAAGACATGGCGAGCAGCGGAGTCAAGAACACACCACGATGGCGGAGAAAGGAAGAGGA
GGCCCCGCGTCCTGCCCG
Sequence 491
ACTCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAAAAATAAAAAGGAGGCTGGTGGGAG
AACTGCTTGAGCCCCAGAGTTTGAGGTTACAGTGAGCTATGATCACATCACTGCATCCCA
GGCCTGGGCGATGGAGCGAAACTGTCTCTTAAAAAATGGCAGGGAGTTGGGGAGCTGGGC
AGGTGCAGTGGCTCATGTCTGTAATNCCAATACCTCTGGGAGGCCCAGATGGGAGGGATC
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ATTTTTAAAAAANTAGTCATTNCTTAGTGGGTGCNTTCCCTGTNGTNCCCCACTTCTTT
G
GANGGTTTNNGGNCCAAGGATTTCTTTTNGCCCCTGGANGGACAAAGGCTTTCANTGAGC
CTTTTTNATTTTTACCCCTTGGCTTTTAAACCTTGGGCCATATNAATTAGAANCCCTTN
T
CTTTTAAAAAAAAAAAAAAAANGGGGGGNGGGGCNCNCCCCCTNTTTTTTTTTTGGCCCA
ANCNCCCCNNATTTTTTTTTTT
N
Sequence 492
TCCCGCGGTGGCGGCCGAGGTACATGAGAGATAATGTTATGACAAGAATAGTTTCTGCAA
CATTAAGTATGGGTCAAAAAAAGAAGAAATGGGCCAGGCGCGGTGGCTCATCCCTTTGGG
AGGCTGAGGCAGGTGTATCACAAGGTCAGGAGTTCGAGACCAGCCTGACCAATATGGTGA
AAACCCATCTCTACTAAAAAAAACACAAAACTTAGCCAGGCATGGTGGTGCACGCCTGTA
ATCCCAGATACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTG

Table 1

CAGTGAGCCCGAGATCACGCCACTGCATTCCAGCCTGGGCAACAGAGCAAGACTCCATCT
CCCAAAAAACAAAGAAATGACTTTAGACAAATGGCTTGAATGAAATTACAAAGAGGAGGT
GCATTAAAAAATCCCAGCAGTAAAANCTTTTGAAGAATTAAAATGACAGGCTAAAAATAA
ATAATAAATGTTCTTTTT
Sequence 493
CCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGTGGCGGCGTTGGGTTGAGCGGGCT
TTTTGGAAGTTTGTGGCGGAGTTCTGTGATATGAGCAACAATGGACCAGAAGATTTTATC
TCTAGCAGCAGAAAAAACAGCAGACAAACTGCAAGAATTTCTTGGGCAGGGCCTGGGGAA
TGCTTTTTTATCTCATATTAGTGCCTGTGATGGCATCTTTCATCTAACACGTGCTTTTG
A
AGATGATGATATCACGCACGTTGAAGGAAGTGTAGATCCTATTCGAGATATAGAAATAAT
ACATGAAGAGCTTCAGCTTAAAGATGAGGAAATGATTGGGCCCATTATAGATAANCTAGA
AAAGGTGNCTGTGAGAGGAGGAGATAAAAAACTAA
Sequence 494
CGCGGTGGCGGCCGAGGTACTCATGGTTGCTGTAAATTAAGGCAGCCGTTCTGCAGGGTT
TTGCTTAGCCAGGCTCCTCTGAGATCTGGCTATTCTGTCTTGTGGATTTTCAGTCCCC
GC
GTACCTGCCCGGGCGGTTCG
Sequence 495
AGATCTCAAGATCTGGACTTCTGTTGAAAAATTTTCCCGTGAGGNTNACTTATGTCTG
TA
AAGATGGGAAAAAAATACAAGAACATTGTTCTACTAAAAGGATTAGAGGTCATCAATGAT
TATCATTTTAGAATGGTTAAGTCCTTACTGAGCAACGATTTAAAACTTAATTTAAAAATG
AGAGAAGAGTATGACAAAATTCAGATTGCTGNCTTGATGGAAGAAAAGTTCCGAGGTGAT
NCTGNTTTGGGCCAANCTAATAAAAAATTTTCGAAGAATNNCCCCCNCTNGNAANCNCC
CNGNCTTGAAANCNTTTTAAAAAAAAAAGAAAANGGTTTAAAANNGTAAAAGGGGNCCCC
CNCCCTTTTTTTAAAAAAAGNNGAAAAAAAGGGGNGGGGGGG
T
Sequence 496
CGCGGTGGCGGGCCGGCCGGGCAGGTACCGTGAAAAGGGCACTTCTCCTTGAGAAGGCCT
GACAGTGTCGTTAATGTCCTGCTGGCGCATGGTGAAAATTTCAGGGCAACAGTAAAGCAC
CCTCTTTAATTTCCCTTCTCCAAGCCCAAGCTTTTGCAGGTAACTGGAGCGCTTCCTC
AT
TTGCATAATAGGCAGTTTCAATAACTGGGGAC
Sequence 497
CCGCGGGTGGGGCCGGCCGAGGGTACNNNGGAGGCCTCATAANGGCNGGGNATCNTCGAG
GNTGGTATNGNACTGNTNANAAAGCCNNCATGGTGGTANCNCACCAAAANCTCACAAGAA
CAATTGNNGCNGCGAAACAGGCAACAGANTCTGNCATTATATAATAAGGGCGTGGTACGG
TTGGGGAACCCCGNANGANTCNNTATGGTCCTTGNTTNGCAAGCNNTGCATTTTAAATCA
GACGACCGTNAATTTGTTANCCCCAANCCTTNTTANAATAAATCGGCAATCGCGCAATAT
CTCATCATTNANCNACTGTGGACGACTTGACAATCTTAGTGGCTTNATGGACTTATTGCA
AAACTCGAGAAAGAACAAACCTAGGGGTGCGCCCTGACCTTCGGAATAATTCGTAAGCTA
TATGTGAGAAACTAGCAACAGGGCGTTTCATTTATGNGNAANGGGACGCGAANTGGANGA
TAATTATGTAANAAGNGGGCCCCTACGANTTTGGCCCCTAGACGCCCAGGGAAACCGCGG
GGCNCCATGCATNACNCANACTTANGGNAGGGGTANTTCTCCNCACACNCNTCNTTTTCG
ATTTGGANAATANGCTGGGAATNAATCCTACATGACCTGTCATTTTCGGAGTTATCGCNG
GCCGGTACNGNNCCCCCCCGGGGGGGGGGGGGGGNCCCCCCGGGNTTANCCCCCCAAGCT
TTTTTTTGGTTTCCCCCTTTTTNAGGTTGGAAGGGGGGGTTTNAAATTTTGNCCGGCC
GC
CTTTTGGGGCCCGGTTAAAAT

Table 1

Sequence 498
TGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGGGCCTTCCACTTCAGCTGACT
GAATTTAGGCAGTTCTGGCCACTTCAGTTTCCGCACCCAGGCCTCCTGACCCATGGTATC
TACGATGAGATCC
Sequence 499
GTGGCGGCCGAGGTACCTCAATTGATGATTTCTGGTATGACCTAGCAAATACACTGCTTT
CACTGAAATTTCAGTCTTGCAATCTGCTTTGGGTTCCCCAATCTAAGACAGAAACATACT
CATTTTCCCATCACTGGACTTCCAGGTTGTTTTCAATTTTTCACTGTTACAAACAAGGT
G
GCAACATTTATCTACAAACCTCTTGGATATTACACCGTAGGNAAGCTTTCTGGGTTATT
T
CCACCTAGTGAAACCTTGCTCAAGTTTGAAGGGGGTANTGTTGGGATNCTTTCATCTT
TT
TAATTAAAATTATTTACCAACCATGTTGAAAAAGCCCCGACCAATGGTCAAGGGACTGNG
CAAAGGAGGTGCCCACCAATGTTGAATGGGGGNTGGTGGGAAATGGGCAANGCTTCACTG
NTANACAAGGGTGGCTTGGGGGGACCTCAAGTTTTGGGGGTTCTTTGGGAGNAAAGCCAC
TTTAGNTTTATTAGCCAAGGAANTGTTCTTCATAAAAATTGGGTNTTCTTGGATTTAGG
A
AGACCAANGAAGTTAGGTTNGGGGGAAAT
Sequence 500
CGAGCCGGGAGCCATTNANAGTTGTTAAAAGCCTNGGGGGTGCCCTAAATGAGTGAGCCT
AACCTCACATTTAATTTGCCGTTTGCGCCTCAACTTGCGCCCGCTTTTCCAGNTCGGGGA
AAAACCTTGTCCNTTGCNCAGCTTGCATTAAATGGAATCGGNCCCAACNGCCGCCGGGGG
GAGGAGNGCTGGATTTTGCCGTTATTTGGGGCGGCTTNTTTCCCGGCTNTCCTTCCGCTT
CAACTTGNACTT
Sequence 501
ACATACTAGCNNGGGTAGCATAAAAGNTGTTAAAGCCTGGGGGTGCCTAATGAGTGGAGC
TTAAACTTCACAATTAAATTGCCGNTTGCTGCTCCACCTGCACCTGCTTTNCCAAGAT
CT
GGGGANAACACNTGNCGTGCCCAGGCCTGNNATTAAATGCAATTCNANNNCAACCGCCGC
NGGTGGGAGNAGGGACGGTNATTGCCGTTAATATGGGGGCCGCTACTTTTTCCCGC
Sequence 502
NACAAACATTACGAGCCGGGTAGTCATAANAGCTGTAAAGCCTGGGGGTGCCNTAATGAG
Sequence 503
GCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTATGAATTATTTATTTTCTT
TCTCAGAAAAGGATGCGCCTCCACTTAGCAAGGCTGGGCAGGATGTGGNTTNTGNATCTG
CCCACAGACGGGGTGGTTCTAGACGGCCGCTCTNNAAC
Sequence 504
ACATACTTANCCCGGNAGCATTAAAGTGTAAAGCTCTGGGNNTGCCTAATGAGGTGAGCT
AACTCACATTAATTTGCGTTGCTGCTCACTGCCCCGCTTTCCAGTCGGGAAAACNCTTGG
TCNGTGCCCANGCATGCATNTAAATGNANATCGGCCCAA
Sequence 505
CACAACATACGAGCCCGGGAGCATAAAGTGTATAAGCNCTGGGGTGCCTAAN
Sequence 506
CGGTGGCGGCCGCCCGGGCAGGTACTCGTCTTGGTGAGAGCGTGAGCTGCTGAGATTTGG
GAGTCTGCGCTAGGCCCGCTTGGAGTTCTGAGCCGATGGAAGAGTTCACTCATGTTTGCA
CCCGCGGTTGATGCGTGCTTTTCGCAAGAACAAGACTTTCGGCTATGGAAGTCCCCATGT
TGATGGATCCTGAGGCTTGAAAAAAAACTGAAAGAGAATAAAATATCTTTAGAGTTCGGA
ATTATTGAGAAAAATCAAANACTCCCNAGTTTTGATGACCTGNGAAGGAATATTTCNGAG
GGACNCCANGCCCTTTGGGGNAAGGANTCCTTGACTCTATCTTTTCAAAGGGAATGNAAA

Table 1

ATTCCTAGTAACAGGCCCTNTAAAGACTNAANACCAAACTTTGGACTTCTTGCTTGGATT
TTCNTTTTTATTCCCTTTTTTTTTTATTNTTTTTTTAAAAATAAANAAAATAATTTAATT
TTAAACTTGGNACCTTTTCCTTAAATAATATTACCTTTCTNATTCAAAAGGTGGGAAAA
N
GGGAAAATTTCC
Sequence 507
GGCGGCGCCGGGCAGGTACGCGGAAATCCCCTAACTTCCTTGCTATCTTCCCATNCCATA
TTTAGGTTAGATNGAGAAGTGTGTATGTGTGTGTGTGTGTGTTGCTCNGCACAGTNGA
TGAACTGTAAACATAAATTGAAGATATTGGAAAANTACATNAANTTATGGACCAACATGA
CAATTTTCATTAGGACTTCCTATTCANAGAGTATCAGTTTNACANNTTGGGTATTAGNT
A
CTAGTATNAAACATTTCAGATACTTGCACTGATTTTCTGGTGGANTAAAAGCAANGGCTT
NTACAAGTTNTAAGCATGTCTTNTANGNCTATGCTTTGGAATACCAGCTAATAACCAAT
C
AACAAGNCCAGNAGCCTTAANGTGGTATTTTTTTGGTTGACCCTAAAAAACATGGAACCT
NAANGGGTTTCTNCAAAAANTTGCCTTAACCAAATGGAAANTAGGTGGGGGGAAG
Sequence 508
TATCCGCTTCACAATTCCACACAACNATACGAAGCNCNGTTAGCATTAAAGTGTAANAGC
CCTGGGGTTGCCCTAATGAGTTGAGGCTAACCTCACATTAATTTGCNTTTGCCGCTTNAC
NTGGCCCCGCATTTTCCAGTTCGGGGGAAAACCNTGATCGTTGGCNCAGGCNTGCCATTT
ANATNGGAATTCGNGCCCAACCNCNCCGGTTGTAGGAGGGNCGGGTTTTGCGGNAATTTG
GGNGCGCTTCTTTCCCGCTT
Sequence 509
CCNANGTACACTCCCACCACCACCNCATGGTCTCTTTCATATNNCTCAANNNTCAACNTG
NTCCTGNGGCTTCATAATTNTCCTNTTNCATCTTTTTCACTTCNNANGCAAACACCGC
CT
CNNCTNANGCTNTNNANTCAATNCANTTNNCCTTAATNNAAATCACAAANTNTCCTCC
AT
TACNCANNAANNTNTNNNCATTCANNNCCACAATCCNGGTNNTGGTCTNNCTNNNCCACA
TCANCAAAAATCACATCCACCATTNCNATCCCNCNTACCTTCCCNNNCCNCCCCTCTAAA
ACTANTNNATCCCCCNNNCTNCAANAATTCNATATCAANCTTATCNATACCCTCNACC
TC
NAANNNNNNCCCNTACCCAACTTTTNTTCCCTT
Sequence 510
CGGCCGCCCGGGCAGGTACTCTCTGAGCCAAGGACATTCTCATTTAAACAGTTTAAANAG
GCTGGGNGCNGGATCGGGAAAAAAAAGAAATATACCCTGGCAGCCGCCTGCCCGGCCGGA
AAGCGGANAGGGACNCTAANATCAGCAAATTCNCCAGTTTGGATCCTTGTCCTTTTCCGC
CCTTTTCCCCCCATTAAATCCANAACCCGTCACATGATAATTAANAAAANGGTTCAGTTC
CTCCTCCTCAAACCACTTCCNGTAAGAGGATCCCCCNCNTACCTCNGCCCCTCTAAAACT
AGTGGATCCCCCCGGCCTGCANGAATTCNATATCAACCTTATCCATACCCNTCACCCTCA
AGGGGGGGCCCCGGTACCCAACTTTTTTGTTC
Sequence 511
GGGGGAGGGCAGNAAANCAAACCACAGCNCACNGCANGGGCACACANCACAATCCCCAGC
AAAAAAAAAAAATNNNTNNTNCCAAACANAAAGAGCCTGGCCAGGGGGCCCANACGGGCC
NNAAAGCCCNGGAACCAATTTTTTNTGGGGGCGGGGGCCCCCCAAAGGGCGGGAAAAACA
GCCACGACCCACGGCNCCAAGCNCGAACAGAGAGCNGGGGGAGACGCNGCCAAAAGCAAA
ACGGCGGCCAAANCNNAGGGAGCAANNNGGGGCGAAAAGNNNAACGGAACCANNANGAAA
NAAAANCAAAANAAAACCGGACCANA
Sequence 512
AGCANCACCGCGGNGGCGTTTGCGGGAGAAACNGNGGACCCCCCGGGCTGCAGGAANNCG

Table 1

ANANNCNATTTAGGGNGACNNAAACCCC
Sequence 513
NAGNCACCGACGAGACCAGATTANACNTNGGGGGCNGNAAAACCCCAGCCCCCCCCGGNC
ACAGCCCNAAAGGCCAACCCTTTTTGGAGGNGCNNGGGGANGCAAACNGAAAAANAGCNG
GAAAAAGNAGGAGNNGAAGCCAAACAGCCAAANNCNGCCANNAGGAAGNGNGNAAGGGTT
TTGCNANTTTTTTNANGGGGGGGGNANCACACCCCCNGAANAAAGNCCGGGCNGNCGNCC
CNGAACGAGGGGGGGGGGGGGGGGGGCNGCAAGAANNGGGNGANCAAAGCNNNANCGANAC
CGGNGACCNNGNAGGGGG
Sequence 514
ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTCCGAAATCTTACCTTCAGT
CTTCTCTGCCACCCAGTCATTTATATGCTTCCTGCACTCTTCAGTGTCTTCAGCAAAG
GA
CAACTCCTCCAGCTCTGCCTGATAGAACTTCTGACAGTATTCTTTAAAGTCTGGAAGGAA
ATCACACGTCTTTTCTCCAAAGAGTCTGTTGGCAGTTCTAAGCAAGTACGCGGGGTAAGC
AGGAAGTGAAACCACAGAGCTTCAAAAAAAGAGCGGGACAGGGACAAGCGTATCTAAGAG
GCTGAACATGAATCCACAGATCAGAAATCCGATGGAGCGGATGTATCGAGACACATTCTA
CGACAACTTTGAAAACGAACCCATCCTCTATGGTCGGAGCTACACTTGGCTGTGCTATGA
AGTGAAAATAAAGAGGGGCCGCTCAAATCTCCTTTGGGACACAGGGGGTCTTTTCGAGGC
CAGGTGTATTTTCGAGCCTCAGTACCTCGGGCCGGTTCTAGAACTAGGGGGATCCCCCC
Sequence 515
TTCGCCCACCGGAATGATCACCAAGACACACAAAGTAGACCTTGGGCTCCCAGAGAAGAA
AAAGAAGAAGAAAGTGGTCAAAGAACCAGAGACTCGATACTCAGTTTTAAACAATGATGA
TTACTTTGCTGATGTTTCTCCTTTAAGAGCTACATCCCCCTCTAAGAGTGTGGCCCAT
GG
GCAGGCACCTGAGATGCCTCTAGTGAAGAAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCG
GGCGGCCGCTCGACGTGGTCGCGGCCGAGGTACAACTGCAGTAAGAGGGACGGTTAATTC
ACAGCTTCCAGCTCTTGGCGCCAGAGTCCGATGCACTCCTGCAGATAACGGTCATTTCCA
TTTCCGGGAGAACCTCTTTCGAAAAACAACCCGGATGAGACTATCTGGCAAATTGCAGCC
CTTGGCGGGCTTT
Sequence 516
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ATCTCAGATCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTTTCCTGCTTCATCTT
CC
CAGGTAGCTGGGATTACAGGCATGTGCCACAACGCCTGGCTAATTTTGTATTTTTAGTAG
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CGCCTCGGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGCCCAGCTATACTG
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GTGGATTTCCCCCTTAATTAGGGATGCATGGTTGATTAAACCTCNAGATACAGCTTTT
TT
GCAGTAATGGGGGGGNTGGGT
Sequence 517
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGTGTTGATCCAGTTCTTGCTT
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ATGCCAGTCAATTGGATTTCGTTAAAACACCGAAAATCAAAAAGCATGGATTTAGTAGCT
GACGAGACTAAACTCAATACAGTGGATGACTAGAAAGCAGGTTCTCCCAGCAGAGATGTG
GGTCCTTCCCTGGGTCTGAAGAAGTCAAGCTCATTGGAGAGTCTGCAGACCGCAGTTGCC
GAGGTGACTTTGAATGGGGATATTCCTTTCCATCGTCCA
Sequence 518

Table 1

AAACCCCACCCCCCAGGGGGAAGGGNNGAAGGGAGGGGCTTGGAGGGCNGAGGGGGAAGC
CCCCGGAAAANGACNNCCCCAACCAGGGGANAANAGACCCGGNAGGGACAGGCNAAGGA
GAGGGAACAGGGGAACCANCACTTTTNTNTTTTTGGGGGGCACNNGGGCNGGGACCCCCC
NACAAAAAAAANANCCCCCGCCAGGANGGGGGGGGGGNNAAAGGGNAAAAAAAAAACA
AGACCCAAAGAAAAAAAAC
Sequence 519
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TAATGTTTGTCATAATTTTAAATAAAGTGTCTGGGTTTCAGAATAAAAAAAAAAAAAAA
AAAAANCAAAAAAAAAAGTACCT
Sequence 520
GGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATGTTGAATAAATGTTTTTTTCC
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G
CAGTGAGCTATGGTCATGTTACTGCGCTCCAGCCTGAGTGATGGAGTGAGAACCTGCCTC
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TAGCAAGACCTTGGTATCTTCCCAAAAACCTTTAAAAATTAGGTTGTGTGTGGTGNTGCC
TGGCTGAGATGAGAGGATTTGCTNGAATCCAGGAANGTGGAGGCTGNAGTTGAGCTATGA
TTNGGGCCNCAGCANTTCCAGGCCTGGGGNACNCCAGGGGATACCCTGGTCTTTAAAAAA
AAAAAAAAAAA
Sequence 521
CCGGGCAGGACGCGGGCGGCTCTTAGCGGTGGATCACTCGGCTCGTGCGTCGATGAAGAA
CGCAGCTAGCTGCGAGAATTAATGTGAATTGCAGGACACATTGATCATCGACACTTCGAA
CGCACTTGCGGCCCCGGGTTCCTCCCGGGGCTACCGCCTGTCTGAGCCGTCGCTTCCAAA
AAAAAAAAANAAAAAAAAAAAGGTCCCT
Sequence 522
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CTGTGCAGCCTGCAGAACTGTAAGTCAATTAAACCTCTTTTCTTTATAAATTACCCAGT
C
TCAGGTAGTTCTTCACAGCAATGTGAGAACAGACTAACAACAATCAACTCATGGCTTTAA
CACAAAAAAAATAGGTAAGTTCAAAATTAACATATTACCACATCCAACTTCTTTATTCTT
GAGAAAACAAAAAAGTCCAAAATCAAAGGAAAGCACCCGTTTTAAACCCTCATATCTTTC
TCAGGGCTCACTGCAGTCTGGCCATATCTCAAGCAGGTC
Sequence 523
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AGGGATGCAACGGGGCAAAAACTGAACTGTTCAGGCTTCAGATTGTAACTGACGATCTGA
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AGGGACGGACAAAGAGCTGAGTGATTTACTGGATTTCAGTGCGATGTTTTCACCTCCTGT
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AGAAGACAGAAGTAGCTCAGGGTCCTGGGGGAATGGAGGACATCCAAGCCCGTCCAGGA
Sequence 524
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CCATCTTGAAAATCCCCATGAATGAACTGACAACAATCCTGAAGGCCTGGGATTTTTTGT
CTGAAAATCAACTGCAGACTGTAAATTTCCGACAGAGAAAGGAATCTGTAGTTCAGCACT
TGATCCATCTGTGTGAGGAAAAGCGTGCAAGTATCAGTGATGCTGCCCTGTTAGACATCA
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Table 1

TTCAAGTGATTCTCCAACCTCAGCCTCCCGAGTAGCTGGGACTATAGCAGTGCACCACCC
ATATATGCAATTTC
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Sequence 525
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GGGNGAGAANNCNGGCCACCCNGACCCGGAGAGGAAGGAGACNGTTTTTNAAGNNGCCNC
GGGCCACACNCNAAAAANCGACCCGCAANNNGCACCGACAAACANCGGNGNGCNAAAACA
NAACNNGAACANCCCGAGGAAACCGCCCNATTTTTTTTTTGGGGGGGNCCAANGAGGGGC
CCGNCGCCACAAAAAAAAAACCAAGGCCCCNGGGGGGGGGGGGGGAGCCCAANANNGGGG
NGGGGGCNN
Sequence 526
AACTTAATGTCTTCCTTTTTTTTTTTCACTGGCTTTTTCATANATCGAGACATGTAAGCA
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TATTTATAGACAGCTCTAACATGATAACCCTCACTATGTGGAGAACATTGACAGAGTAAC
ATTTTTTNGGGGNAAGAAGAATCCTACAGGGTCATGNTCCCTTCTCCTGTGGAGTGGGGG
GGNAGAAGGGGTATGGCCCCAGGGNNGGCCATATTACTGACCCTCTACAGAGAGGGCAAA
GGAACTGCCAGTATGGNATTGCAGGATAAAGGCAG
Sequence 527
AGGTACTCACAGTCACGCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGG
ATCCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAG
AACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTT
TTTCCACTATTCACACTCTGTGGCGTAACCTTCTTGAATATAACCCCAAATGTCACCCA
A
TCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGAGACAGTCTGATCAG
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TTT
Sequence 528
AAGGANAATTTTTTGGGGGGNCAAAAAAACCCCANCCCCCCCACAACCANGCCNAACTNA
ATCTTNGGNAAAAGAGGGAAANAGGCCCCAAAAAGGACAAAAGGGNNCANNCANAAAAAC
AAANNNCCAAAAANCCGGCCAANAANANNNCAAAANNNNCCCCCAATTTTNTTTTTTTGG
GGGGGGGAAANGGGAAGNNACCCCAANGNACGCAAAAACNACCCAAACAGGGGGGGG
Sequence 529
CCGCGGTGGCGGCCGAGGTACATTGTATACTGCAGTGTCGTCTACATGGCATTGGACAGG
ACATAATGTAAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGGAATGGCAAC
CGTGACCAATTTTTGGCTCAAGTTAAAATACCAAAAAC
Sequence 530
CGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTGGAAACCCATTTGGATTAATTAGA
GGTCTGTCTGAAGGAGTTGAAGCTTTATTCTATGAACCCTTCCAGGGTGCTGTTCAAGGC
CCTGAAGAATTTGCAGAGGGGTTAGTGATTGGAGTGAGAAGCCTCTTTGGACACACAGTA
GGTGGTGCAGCAGGAGTTGTATCTCGAATCACCGGTTCTGTTGGGAAAGGTTTGGCAGCA
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GGGCGGCCCGNTCTAGAACTAGTGGATCCCCCCG
Sequence 531
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AACAAANCACNGGAGAACAAAAACGAAAAACAGCAGGNCCCNCNNNNAAANCCAANNCAN
ACAAAAANGNCAAAGNAGAACCAAAAGCCANGNGNCCCGCCAANAAAGCCNCCCCAAAAG
CAACAAAGAGGNCNGCCCAAACCNCCNAAAAAAACAAACCCCCAAGANGAAAAAAAACCA
AAACCCCNAANGNAAANGAAACAANCAACCGGGGGCCCCCCAA
Sequence 532
TTTTTTATTCAATTTGCGATNGACAGNNNTAGNTTNAAATGTTNGTAACACTCTTAGAN

Table 1

N
NNCTGGTTTGTTCATTTGACATNGGGGCTGCACCAATTTTTATTACAAAAATCAAAAAA
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TAAAAATTCTTACAATATTTGCAGAGTATAACCACTAGTTGCCTAGACAAAAGCTAATT
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CTACAAAATCAAAAACTTAATGCAGTTTTATTAAGAGAGTCAAAATTCTCTCAGTTAAC
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AAAGAAAATACATGTCAACAGTCAGGTAAATATTTTGACCTGACAGGTTCTACAAATAGG
GGATTTTCACTACATATAAAGGAATCTGTTACATGGGGGTAAAACTTCCAGAGACCAAGT
AGGAAGNGGTGGAATAAAAAACCAATAAATNCAAACGCCACCCCAGGCTGG
Sequence 533
CCAGCTGCTNGCCTGCAAAGANGAGCCTCCTNNGGGGGGGGGNAAAACCCCNCCCNANCC
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CTTGCCGGGAAGGGNTNNCACGAAGAACTGCATTNNGACCTGGNAGCGGAAACCAGGATC
CTGCCAATNTNTNNACCACGGGGCACCCACAGGGACACAAACAAGCNCACCCAACAAAGC
CAACCGCCCCNNCCCGNGGACCNGCCCG
Sequence 534
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CCAAGGTTTCCAAAAGTCTCATTCTTACTCGAGCCTTCAGNGAAATTCAGGGACTAACAG
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CAAGCCTAATCGAAACCGNNACCCNCGANGGGG
Sequence 535
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GGAACNGAGAGAAAGAANCNGGGGCTGGCNNAAGAAAANANAGACANNCNCACAAAAGCC
NAGTNCATNTTTNNTTNCCGNNGGGACCGNNCACCCGCAGAAANANNNCACAANAGGCCG
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CGCCAGGCNGGNNCAGCCAGGAAGGCCAAAANCAAGAGGGAGAAGGAGAAAGGNGNAAAA
AAGAAAAAGGGGAGGNGG
Sequence 536
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CCNTNCCTCCATCTGCGCAACAAACGCNAGAGAANCAATCCTTGGGGCAGATACTGGGGC
TGCCCTCAAGGAGCTNNNATAGAGGNCAGGGGACCTTTGNCGCTNTTTNNCTAGGGGANC
Sequence 537
GGNCCCCCCGGGCTGCAGGAANNCGANATNTNCTTTAGGGNGACCAAAACCCCC
Sequence 538
GGCACCCCGCGGNGGCCCTNGGGGGGACAACNCCGCGCCCGCCAGNAACAGGCCACAGCC
CAGAGCTCNNTCGGGGGCNNAAAAACCCGGACAAGCNGCANGCGGGGGGACAGGNCTGCG
GGNCNTGGAAACACTGGACNGGATGGCACANGAACCAGAACTCCGCTCCGNTTGGCTGCC
CAAGGANCCCACCAACNCATNCTAANCAGCGANCACNGAGGAAACGCNTTTTANNCCGAG

Table 1

GNACNANNNCANAGAACAGGCCNACCGCAAGGGCANACCAAGAAAGGGGGGCGNAAGGAN
AGNNAGGGGGNAACAANGNACCANAGGNCNNCAAANGNCNGACANNCANCNNNACCCNAC
CNCNAAANGCCCNNCCNTNNCACAANANCNNNCCNGANNGCNGNGNAANAGAAAAACAAA
CAAAGACANGGAANNACCGGGCANANNAGCAGAACCAAACCGGAAAANGCANGGAGGGNN
CAAAAACACCACCNACAGGAAGGAANAACCCAGAGGAAAAAGGCCGAAAGAAAGAAACCG
AAANANAAGACCNGGGCCGAAAAAGCNNACCCAGGAGGAACCCACNNNCACGAAANCAGA
ANNNCCCCCNNCCAACCANNAAACAGGGGGAAAAAAAAAAAAANCNG
Sequence 539
GCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTCTTTTTTATAGTTTT
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TTTGGTTCTTAGAAAATCTGAGACACGTGAGGCCAGACAAAGCAAGGCCGGGGCTGATGG
CCTGGCTGCCTGGTGGTTGATGGTTTTGCTCCCCCTACCTTTTTTTTTGAGTTTATTCT
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GTAATATTTTTAAGAAGGAAAAAAAAAAAAAAAAAA
Sequence 540
ATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTATTTGCTAAAAAAATGCT
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A
TTTTGGTGGCTGCTGACTGATCAGCGTGGTGGTTGCTGAAGGTTGGAGTGGTTGTGGCAA
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TGGGAGGCTGAGGTGGGAGAATCTTTTGAGGCCAGGAGTTTAAGACCGGCCTGGGCAACA
TGGTGAGACCGTGTGTCTGCAGAAAAATGAAAAGAAATTGGCTGAGTGTGGGGGTGCATG
CCTATACTACCATCTACTAGGGAGGGTAGGATGGAAGGGTTGCTTGAGCCCAGGAATTCA
AGGNTGGGCCACTGCACTCCACCCTGGATGGCAGAGTGAGATCCTGCCCTCAAATTTTAA
ATNA
Sequence 541
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TTTTCCTGATTTCCACTTTCAGTTTCCATTCGTTCGCTATCTTCTGGTAGCCACAGCTC
A
GCTCCAATCTGCGAAATACGGCACTCTCTTTATTGACTACTGCTTCTCTCGGCCCCCGCG
CGGCCCCGGGAGTACCTGCCCGGGCGGCCGCT
Sequence 542
GCCGCCCGGGCNGGNACAAAATGTTAAAGACGTTGTTTGTATNTGTAAGGCTGGTGTATT
CAGAGAGCATNATCTCTTATTCCTCACTTTCCACCCCCGTATTTTGTAATGACCATGAT
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AATGTTTNTACTTTTTGTNTAATGGGGTGGGGTGGAGTGGGGGCTATCTGAGAGTCANCC
TGAGGTCTTTAGAGGACCANCTATTGTATCACCTTGGATACTTGAAGTTT
Sequence 543
CAAANACTTTGGCCANANTAAAATNGNTGGAACTANAGGTTTCTTTTTAAAAAAAGGAAG
GGTTAAAGAAGCCAAACGGTNGCTTTTNGGGGGAANGCCANGAAAGAAAANAAGGGGGGA
GNAAAAAAGGCCATGNCCATTCNTNTGCCCCTTGGNAATGGAAGCCCCANGGGGGGGNAC
ACCAAGCNAAANNAAGAAAAGGCCCCACCTTNATTCTTCAATTTTTAAAATTCCTTTTA
A
CCAGAACATTCTTCTTTTGGCAACAAGNGGTCTTCCCCTTNGGGATTGGTCGGAAANAAA
TCACCCATTGGAAGANTGAGAGAGTNCACTGGGAAAAGCGGCCCACCTTATTCAGTCCCC
TCCCCTTTCTTGGCGTNTGGCAACCAAAAGNTTNTTCCTGGCGGGGCGTTGGGGACCCCG
TNTTTCAAACCAAGTAAGGAAGGGGCCTTTTAATTTTTGGGGACCTTTATTAATGGCTT
N

Table 1

AGAAAAANGCAATNGGTAAGNGGCCTTTCNTTGNGGGNGAATNAAGGGGCCCCACGGAAA
AGCTTTTTCCCCTTGGAATTGTACCCCGGCCGGNACCTTTTTCCNAANGCCCCCCTTNNC
CCTTTANAAGGACCCCCCAAAGGTTGGNTNGGGCCCCCCC
Sequence 544
TCCGCGGTGGCGGCCGAGGTACCAATACTTACTTACAAATTTAATACTGCTTCAAGGTAT
TTAATCTAAAATTTTACCAACTTTGATTTGTCTGGTTAGGATATTTTGTTTTAGTGGATA
TGCTTTAATTCGGATCAATTACTGCAGTAAATCTCATCCCTAAGCATGAAATGTTGTCA
A
CAAATACCCAGTTCCATTTAGTTATCAATTAGCCCAAATAAGAGATACAAAGTATAACAG
TGACCAACCTTGTACCTGCCCGGGCGGCCGCTCGACCACTGACATAGACTGAAAGCAAGA
AGAGTGCTGTGTTTGTTGCTATATCCCCTCCAACACCTAAGGCAATGCATTTCACATC
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GCTGAGAGCAGATAACCTCAATACCTGGGAACTAGAAAAT
Sequence 545
AGTGAGGGGTTAATTGCCGCCGCCTTGGGCGTAATTCATGGTCATAAGCNTGTTTCCTGT
GTGAAATTTGTTATCCGCTTCACAAATTCCACACAACATTACNGAAGCCCGGGAAGCCAT
AAAAAGTTGTNAAAAAGCCCTGGGGGGGNGCCCCTAAATGGAGGTGGAGGCTTAAACCTT
CAACCATTTT
Sequence 546
GCCGGGCAGGTACCTGATGCAGGGAATTGAAGCCAGACCCAAAACGGGCAACCCAATAGG
ATGGCCATCTGCCCCATTAATGCCAGCTTGTCCAAGTGTAATTATTAACAGTGCCCCCTT
TCACTCTCCAAAGAGTNCCTTGTNCAAACAGNTTAATTGTGGAAGTCGCCTTCAAGATGA
CTGGGCGGGTAAAGGAAAGTGGGAGTGAGGGAAGCAGGGTAGGTGGAGGGTGTGAAAGGG
AGAGGGCCTCATCTCAGGGTGGCTTGGACCTGCACCAGCATCGGCCTGCATGAAATGTGC
TCCTACTCTTGCCCAGGCTGAGTATCAAAGAGAAGCAAGAAATCTAGATAAAAATNCAAA
TCCAGAAACA
Sequence 547
GCGGCCGAGGTACAGGTAAGCCCTGGCTGCCTCCACCCACTCCCAGGGAGACCAAAAGCC
TTCATACATCTCAAGTTGGGGGACAAAAAAGGGGGAAGGGGGGGCACGAAGGCTCATCAT
TCAAAATAAAACAAAATNACAAAAAGTTATTTAAAGGGCGAAANGATTTTAAAAAAAAAA
ATTTTTTGGCAATTTACCAATAAATTTTTTACCACCGAAAAAGCCAAANTGGCCTTANT
A
CACCCCTTCNCCCCNTGNTGGTGGGGACCTTTTGGGGGAAGGAAGGGNACCTTGGGGGNC
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TAAGTGGAATNGGGGCTAAAGGGGGGAACCTTTTCCCCTTGTTAAAACCAAAACCGCCAA
TTTCNTCCAATTAATTTTTTGGGAAAATTGGAACCTTAATTTAAAAAAAAAAAAAACCAA
ACCCAAAATTGGGTTGGCNAAATTCCAAAAAAGGTTCCCNTCNGGGCCCCCACCCAATTT
TGGTGGAAAAACCTTTTTTGGGGGGGGGGAATNGCCTTTCCGGCCTTCCCCAAAACNCNG
NAACTTGGCCTGGTTCCAACCCTTTTCNACCCCGGTTTNNCCAAGGTTTTTTTTTAAAA
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TCCCCCTGGGAGGTTCCAAAAGGCCCCAAAAAAAAAAAAAAAAAAAA
Sequence 548
GGCGCCGGGCAGGTCCCTTTGTAATATCCTTTATAATAAACCAGTAAATGCTGTTTCCCT
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CATTGGAAGTGGGGGACAGTTGTGCGGGGCTCAGCCTTCAACCTGTGGGATCTGACGCTA
TCTCTGGGTAGATGAAGTAGAATTGAACTGGGGGACACCCAGCTTGGTGTCCACTGCAGA
ATGAATTGCTTGCTTGATGTCTAGGGAGGCCGCAGAATTATAGCAGGGAGGTGAAAAGCA
CTTCTTATATAGCAGTGGCAAGAGAAAATGAGAAGGAGCAAAAGCTGAAACTCCTGATAA
ACCAATCAAGATCTCATGAGGCTCATTAACTATAACAAGAATAGCATGGGAAAGACTGG

Table 1

Sequence 549
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CTTCGTACATGTCAATGGGAGAATGGGTGGTACCACTACACCGGAACTATCCCTAAGTCC
ATCCGCCTGGGGCGAAAGGAAGGAAAAAAAGA
Sequence 550
NTATCTTGTTGCCTCATGNGGGCTACACCNACGCTAGNNAGCCCAATGAGACGTTACGAG
CGCGCAAGTNAGAAACNAGATTTCATAGAGCGCTTGTTGGGAGAGGGACATTCGCAAACC
GCGCGTTTAAGTTACTCGTAGATATTGAGTANNTAAGGNCGTTGGGGAAACGCAACCAAA
TACTCCTAGAGCCTTTGCCGNAACAAGNTACTACANTTGTTCNGGGGGAACGAAGGTGCC
CCGGNTCAACCCNTTGGCCCCCAAANAGCCCCAAGNCTTCCNTTGTTNGGGTATGGCAAA
NNNCTTAACNGAACCACATTGGGCCAANGGNNCGCNANTGGNCCCCNTGGTTTTTATCNN
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AAAGGGGGGGGTTGGGGANAACTCCGGCCCCNACCGCCCCTTTGGNCCCTTGGGTAAAAC
TCCAAATNGGGGGGANGGCAACNAAAGGCCCCCTTCNTTGTNGNGNCANTNTTTGGGGNA
AAGAAGNACCCCAAGGNAAGTGNNCCCACCGGGGGGTTNANAAANAAAACCCCCCAAAGC
CACCCAAGNGGAACTTACCCCTTANAAACTTTTTGGNATTANGTTNTAACNAAANNNACC
CGNCCAAAATTTAAANAAAANANAAGGGCGGATTTAATTTTTTAAAATTCCNTTGNCCCA
TTNGGGGGTGGAAACATNTAAAACAAATNTTAAAA
Sequence 551
AGTGGACTNTGTGACCTTGAAAAAGTCATTTAACATCTCTGAACCCTACTTTCTAAGTC
T
CTACAAGTAATATATAGTGGGTGAGGTGTTCTTTCTTTGTTCTGNTACTNGGATGTGA
AA
CTCTCCNTTTGGAGATGAAACCATGGCGTAAGTAATATAAAGACTTTTCCCTGTAGTT
AT
CTTACAGACTGGAGAGAGTGCTAGTGAATGCTTTTGTCTTCAATGCCCATCTCTTGGAAA
TATTGAAGGTGGAGTAGCAACCGGGCATTATATTATCTCTTGGAAAAGGACCTCAGCAAT
GGAGAATATCCCCATCATCACAACTGTCATCACTCTGCCGCACGTGATTGTGGAGAATAT
CCCTCTCCNTGTGAATGCCAGAATGAGATTCATTTACAA
Sequence 552
GGCCGGCCGCCCGGGCAGGTACTACAATGATTCTGAAGCACAGTGTATTCAGACAGATAC
AGTGAACCAAGTGCAATATGTAAGGATGAAAGAAGAAGAGATGACAAAGAAATCCAAGTA
AATGCCTTGTCTTTGCAAATGTTTTTATNTTAAAATCATTAAGGGAAGGGAACTACTTT
G
CCTTTAAATGNTTATCAAAAGAGTTTTCTAACCAAGGNGTAATACCCTTANTTCTTAAC
A
TTTNTTTTTCTTTATGTGNTAGTTGTTTTCATGCTACCTTGTGTAGGGGAAAACCTTTAT
TTACAAGACNCATATTTANAAAAGGGCTANATTTTTAAAATACTCAANATTAATATTAAA
AAGGTTGGCTCCTNGAATTANNAGCCAAGNAAAATTANTATTTTACCAGTTTTTCAATT
T
CCCAACNANGAAAATAGGCCATTTCCCATAAACCCCAACCTCCCNANAAATGNAACCCCA
AAGGGGCCAATTATTTATTACGTTATTTTTTGGGGAAGGGGGAAANTCCAANNGGGGGT
T
Sequence 553
CGGGTGGCGGCCGAGGTACCCATCTCTGCCCATCACCGCTGGAATTTTGATGACCTATTG
GAAAAGATCTGGGACTATCTGAAACTAGTGAGAATTTACACCAAACCCAAAGGCCAGTTA

Table 1

CCAGATTACACATCCCCAGTGGTGCTTCCTTACTTCGAGCGGGCCGCCCCGGGCAGGGTA
CTTCACACCAAACACTAGCTCAAGCACTGACGTTATTCTACAGGACTATGAACCTTCATA
TCCACATTTACAGTCCGGACAGATAAAGGAAAACAACCCAAATCCAGGAGGCAATATAAA
AGGAAGAGAACAAAACACACATTCATACACTCACACTTAAAAATAGGGGAAGACCAACAG
GGGAACTTTTCGTTCTCTTCCTGGGATGTCTACTTAAAAATCCCATGTGGGTACCT
Sequence 554
NCGGGTGGCGGCCGAGGTACTCTTGAGATTGCTTTAAATTTTGTATTGAAACAACAATAC
ATTTTGCACTGTAGTAATGGGAGCACTAACTCTTACAACAGTTAGTGAATCGTTTTAAA
G
AATCAGTTCAGTGTAGACATTTTGAAAAGATTGTTTCCTGTGCTCTACGATAGCTTAGT
G
CAATGTGCACTTCTGTTTTACTTGCCATTTTCCTGCTCTGTTTTCTCTGTGACATGAAG
C
AACAGAAACTGAGATCAAAGTTAAGATTATATCCTGTTTGTAGTATCAGATATTTTTCT
G
TGTACATTTACATTCAAGTTTGATAACACTGGTGGTTTCATTTCAATACAAATTATGCTA
GAGAACTGACATTTTCANACATGGTCATATATATGCTATTTGAATTCCTTTATCTTGATA
CCAGATCTTGGATTGTGAATCTCTTGATGATAGATGTGCAGCTAATTTTGTCCCGAAA
CT

Sequence 555
GGGTGGCGGCCGCCCGGGCAGGTACAAGACCATGACACCGCCCAAAACACTTCCTGCAGA
TGTTGTCGTTGGAAAACTGTCGTCTTACAGAAGCCAGTTGCAAGGACCTTGCTGCTGTCT
TGGTTGTCAGCAAGAAGCTGACACACCTGTGCTTGGCCAAGAACCCCCATTGGGGGATAC
AGGGGTGAAGTTTCTGTGTGAGGGCTTGAGTTACCCTGATTGTAAACTGCAGACCTTGGT
GTTACAGCAATGCAGCATAACCAAGCTTGGCTGTAGATATCTCTCAGAGGCGCTCCAAGA
AGCCTGCAGCCTCACAAACCTGGACTTGAGTATCAACCAGATAGCTCGTGGGATTGGTGG
GATTCTCTGTCAGGGCATTAGAGAATCCAAACTGTAACCTAAAACACCTACGGTTGAAGA
CCTATGAAACTAATTTTGGAAATCAAGAAACTTTTTGANNGNAAGTGAAAGGAAAA
Sequence 556
GAGAGCCCGGGTGGCGGCCGAGGTACGCGGGGGGGGAGTGGCACTCGCAGCTGCAGCAAA
TCTCAAAATAAAGAGGCAACGGCCTTTCTCTTCCTCTCCATCTCTCTATAGCACACCTT
T
TATTTCTTTTCTTCTTTTTTTAAGCCTCACGAAAGATTTTACTTGTAGATCAACTTTCAA
AATGTAGGAAGTCAGAATGGGTGACATCATCAGAAAAATATGTGGAGCTGATCACAAGAA
GTGAAGAACCCAGAGCACNGAAAGCGGTTGTGACTCCTGGGCCCAGGGAGTTGACAGCGT
CTGGGCTTCAGAGGAGCCAGCCGCCTCCGAGTTGTCTTGGAAGTGAGGCTCTGCTGTAGT
CCTGTTCTTCTGGCTCTAAGATCTGAATGTTGTGACCACTAATTTGCTNTTTCCTGGA
GG
GTAACCCCAGTTTGGTCCACAAGGGCTT
G
Sequence 557
GAGCCCGCGGTGGCGGCCGAGGTACTGGATGTCAGGTCTGCGAAACTTCTTAGATTTTGA
CCTCAGTCCATAAACCACACTATCACCTCGGCCATCATATGTGTCTACTGTGGGGACAAC
TGGAGTGAAAACTTCGGTTGCTGGCAGGTCCGTGGAAAATCAGTGACCAGTTCATCAGA
TTCATCAGAATGGTGAGACTCATCAGACTGGTGAGAATCATCAGTGTCATCTACATTCGA
GCGGCCGCCCGGGCAGGTACCGCGGGGGGAGCGGGCCCTACCGTGTGCGCAGAAAGAGGA
GGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACTCAACTGGTTC
GTTGCTTTCCAGGGCCTGCTGATTTTTGGAAATGTGATTATT
Sequence 558
CCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGTTTTTGAGACGGAG

Table 1

T
CTCCCTCTGTTGCCCAGTCTGGAGTGCACGTGGCATGATCTTGGCTCACTGCAACCTCCA
TCTCCTGGGCTCAAGCGATTCTCCTGACTCAGCCTCCCAAGTAGCCTGGGATTACAGGNT
GCCTGCCACCATGTCCCGGCTAATTTTTGTATTTTTAGTNAAANACGGGGTTTCACCA
TA
TTGGTCAGGCTGCTCTCGAAATCCTGACCTCGTAATCCGCCCGCCTCGGCCTCCCAAAGT
GCTGGGATTACAGGCCCGAGCCACCGNACCTGGCCTGTATTCCCGCGTACCTGCCCGGGC
NGGCCNCTNTTAGAACTAGGNGGATCCCCCGGGCTGCAAAGAATTTCGATATTAAAGCTT
AATNCNANTNCCGTCGACCTCTAGGGGGGGCCCCGG
Sequence 559
CGGGTGGCGGCGCCGGGCAGGTACGCGGGGGGTGCCTGGCTCCGTTTCCTGCTTTTGGTT
CTTACAGTAGTCGGCGTAGGCCTTAGGTGGGTTCGTGCGCCTTCTACCTCGCTGTTTCGG
TTTTCCTGGCTCCTCGGCCCTTTTCTCCCCTGTTGCAGCTGGGAGCGGACGAAGCCGCGA
AGCTGGGATTTTTTACTGTCTCCTGAAGAATTTAACACAAACATGGATATCAGACCAAAT
CATACAATTTATATCAACAATATGAATGACAAAATTAAAAAGGAAGAATTGAAGAGATCC
CTATATGCCCTGTTTTCTCAGTTTGGTCATGTGGTGGACATTGTGGCTTTA
AA
Sequence 560
GCTCCCCGCGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGATCGGCA
A
GCGACGCTCATACANGGCNTAGCCCCGGGAGGAACCCGGGGCCGCAAGTGCGTTCGAAGT
GTCNATGATCAATGTGTCCTGCAAT
Sequence 561
CATGTGGGAAGCGCTGTGAAGAGTTGTTGCCTTNCAAGATATACTCCAAATTCCCAGTTC
CAGCCCGTGTCATTAAAACTCCGCTGGCGTGAAAGATGACATCCTTAGCCCAGCAGCTGC
AACGACTCCGCCCTCCCTNAAAAGGGGGATNCCAGCCTTTTAATNTANAGATGAANTTTG
CCTTCCTTTGNTATTTT
Sequence 562
NNNAGCCGGGTATTCANCCTCTACTTCAAAGGCGGGTAATNACCGGTTTATCCACAGAAA
TCANGGGGGAATTAACCGNCAGGAAAAAAGANACCATTGTTGTATGCCAAAATAGGGCNC
ATGCTAAAAATTGCNCATGTGGAAACCCCGTTTAAAAAAAAAG
Sequence 563
CGATAAGCTTGATATCCGAATTCCTTGCAGCCCCGGGGGGGGATTCCCACTTAAGTTTTC
TTAAGAAGCCGGGCCCCGCCCCCGGGGGCCAAGGGTTACCCCCCGGGGGGGGGCCCGGGN
AAAAGTTTGGGAAAAAAAAAAAAAAAGGGTTTTTTTTTTTAAGGTNGGGGCNTTTTGGNA
AGGGGTNTTTTTCCCCCCCCCAAAAGGGAAANACNCGGGGNNNCCCCNGNCCANAACCCG
GGGGGGG
Sequence 564
AGGTACCAAGTAGGATAATTACTACTGCCAACACACACATGCACGCATGCACACACACAC
ACAGATGTATGCACGCACACACACTCTCACTCCTAGACTGCTAAAAGCAAAAAAAAAAAA
AAAAAAAAAAAAAAGTCCCTGCC
Sequence 565
NGACCTCGGCACTNAGCANCGNCACTACTTAGGGGGNGTTAAAACCCCCCCCCCCCCCN
GNAGAAACCNCNGCGCCATGAGNTNTCAAGNGGAGGAAGAAGCGACCCGCGCANGCTGAA
GCGCAAAAGAAGAAAGANGAGGCAGAGGGCCAAGNAAACCGNNAGCNNGNNGCACCGNGG
AGGCNTTNTNGNNTTTGNNGGGNGGAANGCNNGACGCCCNNGGAAGNANGAACNAAGAAG
CG
Sequence 566
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGGGACTGGAGGACCTGTCTGG
TTATTATACAGACGCATAACTGGAGGTGGGATCCACACAGCTCAGAACAGCTGGATCTTG

Table 1

CTCAGTCTCTGCCAGGGGAAGATTCCTTGGAGGAGGCCCTGCAGCGACATGGAGGGAGCT
GCTTTGCTGAGAGTCTCTGTCCTCTGCATCTGGATGAGTGCACTTTTCCTTTGTGTGG
GA
GTGAGGGCAGAGGAAGCTGGAGCGAGGGTGCAACAAAACGTTCCAAGTGGGACAGATACT
GGAGATCCTCAAAGTAAGCCCCTCGGTGACTGGGCTGCTGGCACCATGGACCCAGAGAGC
AGTATCTTTATTGAGGATGCCATTAAGTATTTCAAGGAAAAAGTGAGCACACAGAATCTG
CTACTCCTGCTGAC
T
Sequence 567
GTTTTGGGGGAACACCGCGGNGGCGNTTTNGGGGTANACCGGGCCACNCACCANCNNCAA
GGNCGAGGNNNNTNNNTTNGGGGGGTTTAAAACCCCNCCCCCCNCGGGCNNNGNAGGCCG
NCANNANTTTTTTAGNNNGGGGGGGGGGNNGCCCNCCGAAAANCCCGGACCTGNCCGGGC
GGGCGTTNNAGAACNAGNGGANNCNNNGGGCNGGAGGAANNNGNNANNAAGTTTTTTTTT
TTTTNGGGGGGNNNGGGGGGGGGCCCCNTAAAAAAAAAAAAGGNCCCCNAGNGGGG
Sequence 568
GCGGNGGCGGTTTTCGGNCGAGCCCTCTCTTGNCCATCTTCTCCCGCTGCTGAAATTTCT
NTTGCGGGCGCTGNAANCCCAGGACCCCNCCCCCCGCGTACGCTGGATAGCCTCNTGGCC
AGAAAGAGAGAGTAGCCGCCGAGCACAGCTAAGGCCACGGAGCGAGACATCTCGGCCCGA
ATGCTGGCAGCTTCAGGAATCCCCGCGNACCTGCCCNNTGCGGTCTGTTCGN
Sequence 569
ACAAAAACCCAAACCCCAGACAGCAGNAATGNCAGAAGANCCANGGAGAACAGCAGAANC
TNACACCGCNGCNCTCTGAAGGCTGAGAACACAAGNCAAANACATNNAACTNAAAAACAA
CCGCTGAGAGAACACGGGGAAAAATNTNCANTTTAGAGANGNCCACAAAAAAGGACACGC
AAAGGGGAAGGGCAAGGCGGNGAGACAACGACGNNANNCNNGGGAAGACNGGGGAGGGGG
NGGAGAAGAGCCNNGGNNGCCAGAANNCCGGNCGGAGGNCACGAGGCGGNGACCCACAAG
GGACCNGCCCGGGCGGNCGGNCNAGAACNAGGGGAACCCC
Sequence 570
GCGGGNGGGCCGGGTTTTTTTNGGGGGGGGCAAACCCGCCNGGGANGGAAGGAAGGAAAAA
ANGGGGAAGGCCAAGGGNCCGATTTTTTTTNGGGGGGGGGGNNNAAAAACCCCCGGGGNG
GGGGGGAAACGGGGGGNNNNAAAAAAANGGGGGGGGGNAAATTTGTTAAAGGGGCNNAAA
AAANGGGGGGNAAANCCNCAAGGGGGNGGGGGGNNCNNNGGGGGGGGGGGGGAAAAAACC
NNAAAAANNNNGGGGGGGGGGGNANAANNNNNNGGGNNNCCCCCNGGGGGAAAAAAAAAC
CCCCCCCCCCCCNGGGGNGGNAANTTTTTTTGGGGGGGGGGGGGGGNNNNAAAAAAAAAAA
CCGGGGGGGGGGGGGGGGGGGAAAAANCCCCCNAAAAAAAAAAAAAAAAACNACNCCCCC
CCCCCCNNGGNGGGGGGGGGGGGGN
Sequence 571
CGGTGGCGTTTAGGGACCAAACGATAGCNGTTCTGTTTAAGTAGGGACCTCTCATGGTNT
NCAGGCTNTGACAACCGAGAATCAAACTGGAGAACATTCCGAAGCCGTTCTTATAAGNGT
CTCCATCTCTACCTGGGCTGAAATGGAATGTGCAAATGTAGCCCAGCCTGGTCCTTGGGT
GTTGCCAGTTGATTGATGACTGGGAGCCAAAGTGGCATTTNCTTNGACCTAAACGGGCGA
TGATGAAATAAATCGAGCGGCCGCCCGGGCAGGNACATCTGTGAATGTGAATGCCAAAGC
GAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGAAATGGGACATTTGAGTGTGGCGCG
TGCAGGTGCAATGAAGGGCG
T
Sequence 572
TGNAANNCCCCCGCCACGGAAAAGGNGGCCCCNGAGCCAGAGCTCCAGCAGCCCNGGGAG
GGCGGGGCCCGAGGCANGGANAAGNGGGAAGGAAAACGAAGAACAGGAGCAGAANNGAAG
AAANACAAAGNGAAANGGGGCCAGNCAGCATGTCAGAGACNGACCACAAAGCCCCCACNN
CCACNGAAAAAAAAGGNGGGAAAACACCGGAANNAAAGGAAGACCCAAGCAACNNGGNNN
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Table 1

Sequence 573
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AGGACANAAAGGAAAACANAAAAGANGCAAGGGGACACGACACANANGAAAGGNGAAGGG
CAACGNCGACCAAACGGGGGNAGAAGACAAAAAACCAAAA
Sequence 574
NGGGNGGGGTTNTTTGGGGGGGGNAAACCCACAAANAATACNGGGAAGGGNGGNGGNNGG
GGNNGGAATTNTTTTNGGGGGGGNGGTAAAAANCCCAAANCCCNAAAAGGGGGGGGGGGG
GNAAAGGGGNAAAAAAATTTTTTNGAAAGGGGGGGGGGGGGGGGGGGAANNCCCCGGGGAA
AANNAANGGGGGGNGNGGGGGGGGGGNNNNNNAANNANNNNANGGGGGGGGGGGGGGGNN
NNAAANGGGGGGGGNNNNNNNNNNNAAANTTTTTTAAANTTTTTTTTTTGGGGGGGGGGG
GGGGGGAAAAAANCCCCNNNGGGGGGNGGGGGGNNNNNGGGGGGNNNNCNNNCNNNNNNG
GGGGGGGGGGGG
Sequence 575
GGAAAANCACACGCCAGGAACCNNGCAGCNNACAGNGACAGAAATTNGGGGGGNCGANAA
ACCCCACNCACCCCGANNNCNGGANCNCNAGGGAANGAGTTTNAGCNCCACCGGGNGGCC
CTCCCCCCAGAAACNNANGNCCACAAGNCACTGGGCACAGANAAGAGNGNNCGGNCNCAA
AACNCACAGGGCNCAGGGTTNGCGTGNTTTTGGGGGGGGGGANGGNNACCCCCCCCGAA
AAGAGGGCNGGNNANCCGGGNNCNNCNGGAGAAAGANGGGGANNCACAGNCCANGACACN
ACANGGNAACANAACNGAGNNNNCAANNNGAGCAGNAANNCGGGGGNC
Sequence 576
GCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTAGGAGCCTCTCTCCCTAC
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TCTTGCCATCC
Sequence 577
CAGGTACAGAGACCTCCTTACTTACCCCCCTTCTCCTTCGGCTGGAGCTCGGCGAGCGAG
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AGTAACGCGGGAATGAAGAATCTTAGGCGGGTGCACCCAGTTTCCACCATGATTAAGGGT
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GCAGATACACTTTGGGGGATCCAAAAGGAGCTGCAATTTTAAAGTCTTCTGATGTCATAT
CATTTCACTGTCTAGGCTACAAC
Sequence 578
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TAGCAGAAGGATCTTCTCTCTTGTTCCTGATGATTTCAAGGTCCTCACAGTCCTGATA
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CTGGTTCTTCCCGAAACTCCCAAATATCTATGGAGAGCTGTTCTAGCTTTTGCACAGGGA
ACCAGTGGACAGAGGTATCATTAAACATGTCCATGTATTGNGAAGTCTGAGGAAACTCAA
GCTCCTCCAGTCCTTTTAAAATCTTTGCAATGTAGGGATAATTTTTCTGCAGAATCCTT
G
CCAACAACCTCTCCTCAAGTCCTTTGAAACTGTTCCCAATGATGACCATCTTAGAAAGGG
CATCTACTGACCAGTTACTCCATAAAAGATTGTTGTACCTCGGCCGCTCTAGA
Sequence 579
ATTGGAGCTCCACCCGCGGTGGCGGCCGAGGTACTTTGGACAGTGAGGGTTCGATCCCAA
TTTTAGGGGTAGGGTTGGGGGTGGGAGTGGGAGTGTGGGTTGCCAGGAGGAAGAATGAGT
CTACTTTNGANACAATTAAGTCATGGNCCTCTCTTTTTTTNTTTTTTTTTTTTTTTGGCT
ACNTAGACNTCTTTCTCATGTATTGTTACTAGAACAACTTNTATAGGGTTTTATGGTTN
G
GGGAAAACATTNNTAAAAAATGGACTNATCTCTATTATACAGANNTATAATATAAAAATG
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CT

Table 1

TTCCTATTTAAGCTTATAGGATGAAAATATATAATTAAAG
Sequence 580
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCATCCAAATGCTTCCCTGGTCTTGATGAT
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TG
GAATTAAACCCAATTTGGAAACAACATTGACCCAGTCAAAAGCTTCTAATGGTTTCTTT
T
TCTTCCTCCAGTTTTAGTTTGCTTTTATTAAAAAAAGAAAATAGTGCATGGCCATAGCT
C
CTTCAGTTCTCTTATTGCAGACTAACCATCAGGATGGTATCAAAGCACAAATACTTTGGA
GGGGAATGCGTTGAACTGGGGCAAGTACCTGCCC
G
Sequence 581
CGTTGCGCTCACTGCCCGCCTTTCCAAGTCGNGGNAAACCTGGTCCGTGCCAGGNTGCAT
TAAATGAAATCGGCCCAACCGCCGCCGGGGNAGNAGGGCCGGTTTTGCCGTTATTGGGGG
CGCCTCTTTTCGCTTTTCTCGCTTCACTTGACTTCGCTGGCGCNTCGGGTTNCGGTTT
CG
GGCTTNGCNGGTCGNAGGCCGGGTANTTCAAGTCNTNAACTTCAAAAA
Sequence 582
NTNGAGCTCCCCGCGGTGGCGGCCGAGGTACCAAATTGTTAAATACTCGNAGGCCTTTAG
GAACCTGTGACTGANTNCATAAATANCAGANCCTATATTGTGATGNTGGTNAAAGGACAN
GTGCTCANCTTCCAATTACA
Sequence 583
ACCCTCCTGGAACCGNAATAAGTTNNTGGGGGGGGTNAAACCCNGGNCCACNGAATNNNC
GGACCACANGANCNAAACTNAAGGNCTAGCTCANAGAAAGCAAGNGNCAAGCNGGGCANT
AGCTGCTGCTTCCCCTGGNGGAACATNGCCTGCTNCCTCATAANCCATNNCCAGACAAGC
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NGGGGGGGCTNCCAGGGGAGANGAAANGGGAAGNCGGGCNGCAGCAACNCNGGNCAAAAA
AAACACCAANNNCNGGGGCNCAANGGCACNAANCAGAACGGCNCGCCCNNNGGGANCCAC
AGCNAAGAACCGGCC
Sequence 584
TTGGTTATACAACATTTGTTTAATAAATGCANTTTNCAAAGCTACACANGACTTAGATA
T
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CAAGAAAGCATTTTCACCTCCTGCGCTTTCCTTCCTGTGTGCTTGTGGTTGGTTCTTT
CT
TCTCAGGCTTTNTNATTCTGATGCTGAGATAGTTCTGTTCACTTAGCAACTTGGGACA
GT
GACACAGGGTTTGTTCTGTACAAGCAGGTTATCCAAGAGGCATCCATACCCTGGGTTTTC
CTCCAACCATAAGGAAAATTGATGCAGCTGTTTCTGACAAGGAAAAGAAGAAAACATACT
TCTTTGCAGCGGACAAATACTGGA
Sequence 585
AGGTACCTGGGCCACCAAACACAGCTGGACTCAATATATGGGGAAGGTAAGTGTCCTCAG
TTTTTGGAGAGAGATTACCCTCTTCCAAAAGAGTGCTTGATTCTGGTAGTCCAAGCTGTC
TCCGTCTGGTGGCACCCCAATTTCCCCTGCCTAGACCCACCTCCTTTCCTCAGCCCCCTT
CGCCTGCCGCTGAAAAGTGAGAGCGGGCTCTTGCGTCCCCCGCGTACCTGCCCG
Sequence 586
GGGGGGNNAAACCCNGAAGANGCGGNNNACGCCNNNCAGAGCCACANNATTTTTGGNCGA
AANAGGGGNCCAGNNCCGAGGAAGGNGGAGGAGGNCNGNAGGNACCNNGGGCGGNNNAGA
ACNAGGGGANCCCCCGGGCNGGAGGAATTTTNNATTTTTTTTAGGGGGGNGGGGGNNCCC
CCGGGGGGGACCGGGACCCAGNNNCCNGNNNNGGGGGGG

Table 1

Sequence 587
ATTGGAGCTCCCCGCGGTGGCGGTCGGGTCAGCTTTAAAGCATCATAATGACTAATTATA
GGTGAATAATTTTACAGACAGTCTATATTCTAGGAGGCAGCTGTAGGCGTTTTAATTGGA
AATAAGCATTCTGAGATAATGATAATAGCAGTGTAGAAAAATGAAGCTAAAAAAATTCAA
AGTGTTGAGAATCCTCCTGTCCTTCTGGGATTTTTATTTTAATCATCTCCTCCACAGAG
A
ACAAGCAGNACTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGTTATTTTATGCACAAAGAGCC
ATCGTGGTTTTTTATTAGGTAGATGCCCTGGATAATCCTTTCAAGGAAGATCACTTAGT
C
CAACTTAATGAAACCAATATCCTTCGCATAC
Sequence 588
GAACACCGAAGAGCCAGANTNTTTAAGGNCAGAGAAANCCCCAGANNGCCGAGGNACGGG
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GACTANGAACAAGCAGAGGCAGAAGCCAGGCACCNGGNCNANGAANCAGACCAAAACAAG
GATGNNAAGCNGNCNAAGGAGGAGAACCGCCGACAAGNANGACANAAAAGACGGCAGCCA
GGNNACAGAANNNGGGGAGGCCNNAGNACCCCGGCCGNNCCAGAACCAGAGGAACCCCCG
GGCNGGAGGAANNCGANANCAAGCNNAANGAAACCGGCGACCCCGAGGG
Sequence 589
GCAGAACAGACTTGCAGCCGACCAATTTTTGGGGGGATNAAAACCNAAANCCCGGANTNC
ACCTTTCCACTTTTTGAGGACANTGGCCAGGGGCNCTGGGCTACCCGATGACAAAGCAAA
NCAGCACAGCATCCCGAANCAGGGGAAGAGAGGGGGCGGACANTGGCANAGGAAGGAGAA
CCCGAAGTGTNCCACAGGCNCAACNCTANNCCCNGGGGGGCGAANNCAAAACCGGCCGGG
NAANNCGNAAACACTGGAGGAACGNAAANCNCGGGGAAGCAGNCCCNGGCGAAG
Sequence 590
GCGGNGGTTTTTGGGGGGCAACACGCGGGACNGCANGCCACNGNCNAGAGCNNGTTTTTT
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NAAACAAAAGGCCCANGCCCGGACCACNGCCCCGGACCNGGGACAANCNGGACNANNNCN
GGGNNNAANNGNGGCCGAGNGGAACAACCATATAANAAATTNCCNCGGGNGGGGGGAGC
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GCGGCCGNNCNAGAACNAGGGGANCCCCCGGGCGGCAGGAANNCGANANCAAGCCNANCG
ANACCGNCGACCNCGAGGGGG
Sequence 591
CGCCCGGCAGGTACTCAGGTTTTATCTCTGCACTCCAAGTAGGATGAAANGATAAGAGCA
AAGGCTCATGTTTGCCAAGTCTGTCCTTTTGTAACAAAAAACCCAGCAGCTTTATCAAGC
AGAATTCCACCTGTATTTCTTAACTTGCCAGAGCTGAGTCTCATGGCCACCCTTAGCAGG
AGTTGGGGAGGTATTTTTAACAAGGCACATTATCATCTCCCCCACCCAAAGTGGAGCTAT
TGCTAATGAAAAAGATACAATGAGATGTTTATGAAATTATCTGTAGCTATTAATGTCAG
G
TTTTTGAAATTTACTGACCTGGAAGAATACTCATAATGCAATGTCAAGTGAGAAGCAGGA
CAAAGA
A
Sequence 592
TTGAGCTCCCGCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTGCCCACG
C
AATTAAAAAAATTTTTTTTTTGTAAAGACTGGATTTTGCCATGTTGTCCAGGCTGGTCT
G
GGATTCCTGGCCTCAAGCAATTCTTCCTCCTCGGCCTCCCTAAGTGCTGGGATTACAGGC
ATGAGCCACCATACCTGGCCACTTCTTCATTCTTGTTGGCTTTGCGTNCCCGATTTAA
AA
TTGGNGAGAAGTTCCTTCGGCTGGGCTGAGGACCCGNGGTCATGGGTGGATCTCATGGAG
AGAGGGCNAGGACAG

Table 1

Sequence 593
GTGNATTGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACATAACTCCCGCAGGATCT
CAGGGCCTGCCGCCCCATTATGATGATGTCGAGGTTTTCATCCTGCAGCTGGAGGGAGAG
AAACACTGGCGCCTCTACCACCCCACTGTGCCCCTGGCACGAGAGTACC
T
Sequence 594
CGAGGTACAGGTGCGATTCTGGATGACAAAAGAAGATGCTTACTTCACAGAAATTCGAAA
TTTCATTGGGAACAGCAACCATGGCAGCCAATCTCCCAGGAATGTGGAGGAGAGAATGAA
TGGCAGTCATTTTAAAGATGAAAAGGCTTTGTCGAGCGGCCGCCCGGGCAGGTACTTTNT
TTTTTTTTTTTTTTTTTTTTAAGGAGCTTTTATTGTTTTAGTAATCTTAACATAACTTAA
AATAAGAGAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCAC
ATTTCTTGGGTCTGTTTCTCTATCTCTAAGGGCAGTCTCAAAACCCCAGC
Sequence 595
TCACGGGTGGCGGCCGCCCGGGCAGGACATGGCCACCAAGTAAGAATGGTTGGTGACAAC
GACAGAAGGCTAAAACAGGAAGGTAATCTTGTGCACCTGACAAATAGAAAGAATAAAGGA
TCAAAATTGAAGGCANGCTATAANAGTATCAAAGAAATTTCTTAAAAACCAAANAGTGAT
TTTGGAAGCACAAAAACTTACNGTTAACTGCTTNCCCAAATGTTCAATGATTGTGGCCCA
AAGAACANTTTGNGGCATTNCTAAANTTTAGAAAAAATTGCNNATNTGCNAAAAAATTTT
TANAATNGGGANACACNACCTACCATTTTTTTTTTCTAAATCCNAAATTTCTCCCCCCC
C
TCCTTCCCAGAAANAGAGAAATTTTGNTNAAACCTTCAATNT
Sequence 596
TGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATTTAAGAAAAGAACAAGGTTAAC
TAACTAAAAGCAGGAACTCACTTATTTTTTGCTCCCTAGCCAATTAAAAATAAGTTCAT
T
AAAAGCACTTGAAATTATATATTTAACCTGAAAAAAAAGTTGCTAAAATTCCAATATAAA
TGTAAATATCTTTAACTTGCTTAACCCAGCTATCCCCAAAACAGTGTAAGTGGGGCAAAA
TGTTCAAAAGAAAAATCATCCAGTGCACGTAAGATGGGGCACCCAAGAAGGCTAAGCCTT
CCTTGNGCCGCGTACCCTCGGGCCGCTCTAGAACTAGTG
Sequence 597
CCGCGGTGGCGGCCGCCCGGGCAGGACTTTNTTTTTTTTTTTTTTTTTTTTTGAGTTAC
TC
TGATGTTTATTTTAATGCATCTTAGTCCACACAGTTGGTATAAAATCAGAAAATGCAAA
G
CAAAAACAAAAGGTCTGGAGTCTTAGCATCAGAAGGGCACCATATATACATCTACAGTTG
GNGGCCAATACAAGTCATTGCCAGACAGTCCTTGGAGGCACAGAACAGCCCAGACCCAGC
CAAGCTCTAGGAACTTCACGGGTCCCAAGGGGTNTAGACCNCTTGTTCTNGATGCTCCGA
ACCCGTAAAAAAAAATGTGGGGAAGTTGATGAAGGCTTTTATGATTTACTCATTATCCCC
GCGTACCTNTGGC
Sequence 598
TCACGCGTCCGGGGAGGTAGTAGAAAGGCGCTGGGTGTTCTAAAATAAGGCTCTCCTGGC
CCACGGCTGACTGTCTTCCTTGTGTCTCTACAGTGGACCGTGACTCTGGACCCAGACACG
GNCTACCCCAGCCTGATCCTCTCTGATAATCTGCGGCAAGTGCGGTACAGTTACCTCCAA
CAGGACCTGCCTGACAACCCCGAGAGGTTCAATCTGTTTCCCTGTGTCTTGGGCTCTCCA
TGCTTCATCGCCGGGAGACATTATTGGGAGGTAGAGGTGGAGATAAAGCCAAGTGGACC
ATAGGTGTCTGTGAAGACTCAGTGTGCAGAAAAGGTGGAGTAACCTCAGCCCCCCAGAAT
GGATTCTGGGCAGTGTCTTTTGTGGTATGGGAAAGAATATTTGGGCTTTTTACCTTCC
CA
ATGACTGGCCTACCCCCCCGNGGNCCCCCGGTTCCACCGGGGTGGGGGAT
Sequence 599

Table 1

ATAGAGGTTCTGACTCCTCAGGAGCAAAAAACATAACCTGAAGAGGGAGGAAGTGGATTT
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Sequence 600
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Sequence 601
AGCNCTNAGCTCGACGCGAAAAAAAATAAATAAAAATTAAAAAAATCTGTGCAATAATTT
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G
ATAGTACTTTTGTATTTTGATATGGACAGTTTATTCATTTGCATACAGTTATTGACTTTT
TCCCAGCTGATTAAAAGATAGTCAAGAAATTCTGCAATATAGCTGCCAAAATAGACAGCT
ACATTTTTATGATATTGTCATCTTTTCTGNTTTTTTTTTCTTTTTTTTTCTTTAGCTATTT
TACTTAAGCATAATAGCCACAATAGGACATATAAAAGATTATAAATACAGA
Sequence 602
CAAGATCGGNGCAGCGACGCTGCGGGCTACCCCCATGCCACCCATGACCTGTAGGGACCA
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CTGAACCAGGTGGCAAGACAACAGTCTCACTTTTGCCATGANTGCACGGNGGGACNCGGA
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CCAT
Sequence 603
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TNGACCAAAAAGTCTTTGGCTTTTTTTTCTTGGGTAATTGNTTTCCTAAANGNTGGTTA
T
NTTGGTGGANCTTTTTTTAACCTGGTTTAATAANTTTAAAATNTGGCCCCAAATTAATT
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Sequence 604
CCCGCGTCCGAGACAATACAAAGTTACATTTTTGGACCATATTAAAACTGCAAGAAGACA

Table 1

GGGGTCTTACTGAAGATCTTTTAGAAAACTTAAATCCTGTCACAGGATATTTAGACATG
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GGCAGNATCTTGTTGTANTGTATATAAACGCTAACACCAGGAGTTTTTTAAAAACCANAA
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C
NAAGAAANTTAAGGCCAAGTTNGCCCCCCTTTTTCTTTTTTTTTGNTAACCATTACCTT
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GNATTTTGGGGAACC
Sequence 605
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GTCTCTCTCCACAACGGAGCCATGATACAATGTGATGGTCAAATTCAGATCCCGAGGTTT
CAGAAAATCCCCCAGGAAAGGAGCTAACGAATCCCCTCTCCATCGTAATTTATCCTCATT
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Sequence 606
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CCACCGGTGCAGGTCTNTCCGNTCATCAAGCT
Sequence 607
CGGCCGATGAGAAGAAGAAGGGGCCCAAAGTCACCGTCAAGGTGTATTTTGACCTACGAA
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CAGTGGATAATTTTGTGGCCTTAGCTACAGGAGNAGAAAGGATTTGGCTACAAAAACAGN
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Sequence 609
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CATTGGCGACCTGGACTCTGAACTCAGGTTTATTCTAAACCCAGTGAGAGGTGAGGGGGA
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Table 1

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Sequence 610
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TTTTTAATATGTTTTGATAACTTTAATAACTTCAGGGTGATGTCTGTATAATTTTTAAAG
TGCAGCTCTCTCTAACAAATGTGCCCTACAACTCCTGATTAAACCGGCGTCTTGAAGGTT
CAAAAAAAAAAAAAAAAAAAAAAAANGTACCTGCCCG
Sequence 611
GTGGCGGTCGAGGTACTTANGAGAAATTGGCATGCTTTGCTAATNTTTATGCAGAGGTAA
CCATGTTGANNACATATGTANTGTTGAGAGGNATGTCTAATTTTATGGTCNTAGGAAAAA
TTAAAAGAAAACTGCTGCTTTCCTGAAGTCTGAAATANAAATGTTTACAACTTGACNAGG
ATCCATTTGGTGGCTAGNCTCGCCTTCCAGGGNGGNAAAGAGAATATGCCAGTTCTGTNG
TATGGACTNTTCACANAAGCTAAGGNAGGGGNAGTTCCTTTCTTGGTGGNGACAAGTTCC
TGCNCACTTAATTTTTCCCNTCCTGNCTTCNAAACCTGGGAAA
A
Sequence 612
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CCAGTTTTCCAAGAAATTTTGTAAAGTTGAACATGGCCATCTACTCTTGCCTTAAAACT
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TTCTCACCACACCCACCTTCCCACATGCATGATATCCAAGGTCGACAGACCTGGATTAGA
ATCCACTCTCAAGCTTCTCATGCAGTGCGTATTGTATTTTCTGCATAAGAAAGGGCTGCC
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G
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GAAACTTTTTTTNCATTT
Sequence 613
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Sequence 615
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Table 1

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Sequence 616
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AAGCTGCATTTAGGTACCTGCCCGGGCCGGNCG
Sequence 617
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NTTTTTAANAAAAAAA
Sequence 618
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Sequence 619
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AAGATAGGCTGCAGGAAATGTAACCTATGAAATTTTCTCAAATTAGCTTTCAAACACACA
CAAAAAATTGCATTTGTTTGAGGAGCAGAATGTAACTTATATTAAAGAATAAACTACTA
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Sequence 620
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T

Table 1

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GATGGAAGGGCTTCCAGG
Sequence 621
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Sequence 622
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NTATTTTACCTTTATTTTTTTTTTTTAAATAAAAAAGGGGTTT
Sequence 623
CCGCGGTGGCGGCCGCCCGGGCAGGTACAGCCATTGCTCTTTGAGTTTGGTCTGGCTAGC
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Sequence 624
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Sequence 625
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CACTGGAGTCTCCTCNATCATAGAGCTCATCCCGCGTACCTCGGC
Sequence 626
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CAGTATGTCAGTACCTCGGC
Sequence 627
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TGTTTGTGACCTGTTTTAAATGAACCAAACCAAATCATACTTTTTCTTTGAATTTAGCAA
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Table 1

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Sequence 628
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Sequence 629
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GTGGGATCTGCAATTGCAGCTACTGTCGGAAGC
Sequence 630
CGCGGTGGCGGCCCGCCCGGGCAGGTACATAGTGTCGCGAACTCAAATCGGCATTTAGAT
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Sequence 631
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Sequence 632
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CAGGCGCCTGTTTCAGCCAGAGCCACCTACAAGCCCCCTCCCCGCGTACCACCACACTGT
CCCAAATTACCTCTTCATTACCCAAATCAAAGAATCTTTCTGTTTTCCCAATCCTCAAA
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GGAATGAAGAAAAACCAAAGAGCAAACTCAAAAGATGATTTTTACCATAAACCTCAAATG
TGGCTTAACAAGTACCTGCCCGGGCGG

Table 1

Sequence 633
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Sequence 634
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CAAGGTCTCTGTCTGTAGTTACTGGGATTATCCAGATACACTATCAATGATACAAATTC
A
TAGGAGTATTAATGCATTTCTTTAAACACAACTTGATTAAGAAGCAAATATGTTAAGCA
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CACAATTTTCTGGCTGTAGTCCCTGGGGCATTTCATTTGCTGGCCTCCA
Sequence 635
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ATTAATTTCAAAATAAGTATCTTACAAGTGTTTCATGAAACATTGGTTTT
Sequence 636
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Sequence 637
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Table 1

CAGCTACGTGAATGGGGATGAAAATCTAAAAGATGATTCTCTTCCTTCAAATCCAATAGA
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CTTT
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Sequence 639
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ATCAGCTGCTAGACGGGTACCT
Sequence 640
AGACGATTGAGCTNCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGGGCTGTCTCACCGG
TGAGACCTGGAAGCGGGCGAGTCTCGTGCTGTGTCGGACCTGCAGTCCCTGGCCTTCCGC
CACCATGGAGTACCT
Sequence 641
CCCCGCGGTGGCGGCCGCCCGGGCAGGACGCGGGTCTTCAGAAACCAGGCTGCTTTCAGG
AACATTGCTGTGGATTCCCAGCTTTCAGACAACACATGACTAAGACAGAATGAGACCACT
CTAGTTGCCTCATGGGAAACTCGGGAAAAGACTGCAAAAACAACATTGTTTCTCCCTTTG
GAATTCTGGAGTTATAAGGCAGAGGTCCCCCATCTTCCCGAACTGGCCTATTCCGCTAGA
AGCAAGATGGCTGAACTCAATACTCATGTGAATGTCAAGGAAAAGATCTATGCAGTTAGA
TCAGTTGTTCCCAACAAAAGCAATAATGAAATAGTCCTGGTGCTCCAACAGTTTTGATT
T
TAATGTGGATAAAGCCGTGCAAGCCTTTGTGGATGGCAGTGCAATTCAAGTTCTAAAAGA
A
Sequence 642
TCCCGCGGTGGCGGCCGAGGTACTTGGAGAATATTTCCACAATAGCCGATGACTTGTTCT
TGTTGACAAGAGAAAGTTCTTTGGCTGTTACCCTCAATGATAGTGAGGTCCATTGCCGTC
TATTAAATGGAGATGATTCCATCTTGTCTACAGACACTGAAATACCTGGCTAAAAGCCGC
CTTTCCTCTGCGCTGCTACCAGCCCTGTCACAGGTCCCGGCGCTCTACCTCCCCGCGTAC
CTGCCC
G
Sequence 643
CCCGCGGTGGCGGCCGAGGNACNAGAAGCTCACTGGCTGTGCTAAACCAAATGAATGGAA
AGCGCCAAAAGTGATTTTATACCAAGGGNCCATNCATACAAATAAACAAAATCCTATCCT
CTTCTTTCTATATNNTNTTTCTTACATTTCTTATACAAATAACAGAATGCTTCATTTTAT
TCACTTCAATAGGACAAAGTCCTTAAAGAAAGACTGAAAAGAGCTGATAATCAAAATCCC
AAATTTTATGCTTATTTTTGGGTTAGNCGCTATCAATTTTCTGACATATTAACATAGGCA
GGAAAACATTCTCAGTAAATTGAGCATTTGAGTCTACAAATGTCTTGAAGCACTCTGGCA
AGTTACATGTATCCCATGTTGCTTTTGGNTTCCCATCTCTTCTTTGCTTCAAACCCCCA
T
GCAAGNTTTTTNTTTTTTCGGGCAGNCTGTGAATTTTCAACCTCCTTTTT
Sequence 644
GAGCTCCCGCGGTGGCGGCCGAGGTACACCCTCTGGCCTCTCCCAAGCAAGCAGTGAGGT
GTGCATTGTTAGAGGTGCACCGGGAAGGGAGCTTGGTTTCGGACCCCAGGACATCCTGTC
CGCAAGCAGCTGCTACTTCTTGGGCTTCTCTAGAATATTGAGGAATTTCCCCCGTGTCAT
CTCTCTGGACTCATCCAGCCCCAGCTGATAGGCTAGGTTCTGTAGGCCTCGAACCTTCTC

Table 1

CATCAAATTAGCCGTGGTGAGACTCCCCAGTTCTTTCAACATGTCGATGTCATCACGTTC
TATCTCAGCCATCCATTTGGGTGGAGAACTAGTAATAGGACTTTTGAAGGAAGCTGCAAA
TTCAGCAACACCTGGTAATTGTTCTGGCCAAAGATCTGGTGAGGCACGGTCAAGTTTTTC
AAAACTTAGCAAAGATGCTTCCAGATCTGTCCCCGTCTGTGGGAGACGCCATCTTTCAAC
CCATGTCACGTCCCCGCGTACCTGCCCGGGCGGCCGCTCGAGCCAGGAACCGTAAAAAG
Sequence 645
CCGCGGTGGCCGGCCGCCCGGGCAGGTACTTCAGGGAGGCCTATATATTGGCACCCAAGG
AATGCCAGGACTGCCACCTGCTGCTCCAGCGTTAGCCTCACTCGTGTGCTTACTCACTTT
GACTGCCTTTTTGTCTATTTCTGGGAGGTTGGTAGAATGAAAGGGATGCTCCAAGGCAAG
CAGATGGCCTGTCCACCTCCTATATATTGACAGTGCCAATGAGTGTAGAGTCTTGCTACA
AGAAACAAAGTCATGAGAAATGCCAGGCTTCCTGTTACACCCAAAGACTGCTGGCCCTCC
TACTCTATCCTTTAGACCAGAAACTTTTTCTTCTAAGCACTTGCCTACCGGGAAGGTT
GA
GGAGTCTTGTTTTACCGTACC
T
Sequence 646
TCNCGCGGTGGCGGCCGAGGTACCGGCCAAGCCTGGTCCCCTTCTTGTTGGGCACTGTGT
ATGGGCGGAGAAAATCCANCTTGTTCTTGCTGATGACGCAAAGGTCAATGTTGCTTCCGG
AGCCCAGGTTCACTGAAGATTGCCANNTGCCGATGGCTTCGCTCACCANGATTCTNGGCT
TNCTNCTCCTCCATTGTCTGGCCTAAACTTTATCTTCAAATACAGACCATTGCTTGCTC
A
ANNGAGACCAAGAAACCCATNNGGTGACCACTAAGGGCAACTTATCAGNTTTGATTNCAT
GAAGGGATAGGATGTCTTGTATTAGGGTNGGAGAGTCCCAGGTAAATCTATGCTACTNCC
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AAGGCATTCTGNCTTTTNAGCNATCCGATTTGGCCTGTNCACAAACTCTGGGGGAAAGAC
TGGTCCAGTTGNNAGAAGGGGAGTTGGGAGCNTCCAGGTTTGGAAAAGNAAA
Sequence 647
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TACACAATATGTCAAAATATTAAAGCTTTTTTTTAAATTGGGAACNCTCAGGATATTGG
G
ATAATTAATTAGGCAATGATNCAAAGATGTTTTGTTTTAAAATTCANAACCCNCCAAAG
G
TNNAAACCNTNGNAANAATTTTTTGGGTTTCCCCCCCCCCNNTTTTTTTTTNTNNNCC
C
CNTNAAAAAAAAGGGGGGCCNNCCCCCCNTTGGGAAAANNNTTTTTTTTTTTTNNNNGCC
CCCCCCNNTNTTTTTTTNCNGGGGGGGTTTTTAANAAANGGGGGNAAAAAAAANNGNGN
GTCCCCCCCCTCNNNNAAAAAAAAAAAAANANGGGGGGGGGG
Sequence 648
TGGCGGCCGCCCGGGCAGGACTTTNTTTNTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTT
NATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCNGGGGAANNCCCCNTTNTNNGGNNTTT
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NNNNGNGNNNNAANNNGGNTNNGNGGGNGGGGNAAAAAAGGGGGGGCCNANGGGGNCCCC
NCCCCNTTTNNCTGGGGGGNNAAAAAANGGGNCCCCCCCCCCCGNNAAATTNGGGGNNNT
NAAAAAANANGGGGNCCCCCCCNGGGGGGGGGGNNAATNTAANANAAAANTTTTNNTNCC
CCCCCCCCCCCCNGGGGGGG
Sequence 649
TTGACTCCCGCGGTGGCGGCCGAGGTACACGATAGGAAGAATGTATATTCTGTGGTTGTT
GGGTGGAGTGAATGTCTATGAGGCCCCTGACTTCTTTCATTCAGGAACACAGATTCAGAG

Table 1

CTTCTGCTGTGCAGTAGGGGGCATCAATAGTTCATTTTCTTTTTATTGTCTGCTACCAT
T
CCATTGTATGGATTCAACCTAGTCTGTTTATTCATTCTCCCAGGCTTTCCACCAGGCC
AT
CTCTTTCACTTCGGGGGCACCTTTCCCAGGGAGATGAAGAGACACAGGTTGGCCTCTGCT
GGGACTCCACATGTCTCCCCGCGTACCTGCCCG
Sequence 650
TTGACTCCCGCGGTGGCGGCCGAGGTACTGAGTGGGGAAGAAGGTAAGAAACACGTTGAT
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CAAGGATGTCCCTCTGACTGCAGAAGAGGTGGAATTTGTGGTGGAAAAAGCATTGAGCAT
GTTCTCCAAGATGAATCTTCAAGAAATACCACCTTTGGTCTATCAGCTTCTGGTTCTCT
C
CTCCAAGGGAAGCAGAAAGAGTGTTTTGGAAGGAATCATAGCCTTCTTCAGTGCACTAGA
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AGGTGAACTTCGTCATGTGGAAGGCACCATTATTCTACACATTGTGTTTGCCATCAAA
TT
GGACTATGAACTAGGCAGAGAACTCGTGAAACACTTAAAGGTAGGACAGCAAGGAGATTC
CAATAATAACTTAAGTCCCTT
Sequence 651
GACTCCCGCGGTGGCGGCCGAGGTACTGCGTTATGCAGAGGTGTCCAGCCCCCTTCCTCT
TCCTGGAAATTAACATTGGCTCCACCTTCCAGCAATTGCTGGACCAGGTCAACATCTTCG
TTTTGAACAGCTTTAATCAGCAAGTGATTGTCTTCCACTGCAGCCCTTCTACCGCTGGAG
GACGTGGGTCCCTCCTGGGGGTTGTTATGATCCCTGCTCTCCATGACGGTAAATGCCACC
TGCTACCACTTTTAGCCTTTTCCTTGAGAAAATGCAAATTTATCTCCTAGCACTTAATC
A
AAGAAGCTTTGAGTGTAAATTGGGATTCTCTGGCAACAGAGCAGCAGTATGAAGAAGGAA
CAATGTTCTCAGTCTTCTGACATTCCACCTGCTCAACTCAAGACGTCTCAATTATTCCT
T
TGGCAGCCGCAAAGCCTGGAAGACTGCTTGCAGCCCGAGCAGTTTCCTCCTGCTGCCCCC
GCGTACCAGTGAGGAAGGA
Sequence 652
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TTCAGAGTTAGCTGGAAGCCACAGCCCTGCCTCTTGATGCAGCCTGGATCCAGCCGGTGT
GAAGAGGAGACCCCTTCCCTCTTGTGGGGTTTGGATCCTGTGTTTCTAGCCTTTGCAAAA
CTCTACATCAGGGATATCCTGGACATGAAGGAGTCCCGCCAGGTGCCAGGTGTATTTTTG
TACCT
Sequence 653
TCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTGTGAACTGAGGAATTATAGATAAACCTT
AGGTCAAATCATTTCGCAATTGCATTGGTGGTATTGAAAAATGATGAGATTTCTCTGACA
GAGAGCTTTGTCCTAGTTTTTGTTCTTCATAGGTCAAAACTGGCAATATTCTCTTGTCT
G
CAAGATAAAGTGTTTGTGCTTCTATCACCATATGCATGAACATGTAAGAATCAGATACAA
TTTCTGCTTCATCAGTTTCACATGTTCATGTTGTCACTGAAAAAATGCATCTACTGTTT
A
TAGCTCCCAAGGAGACCCCAAATCCTTTTTTTCTTTTGAGATGGAGTCTTGCTCTTGTT
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CCCAGGCTGGAGAGCAGTAGCGCGATCTCAGCTCACTGCAACCCCCACCTCCTGGGTTCA
AGGTGATTCTCCTGCCTCAGCCTCCCCAGTAGCTG
Sequence 654
GACTCCCCGCGGTGGCGGCCGAGGTACCTGTTACCCTTTCAAAAGTAAGTTCTCCATCCC

Table 1

ATAAAGCCATTTAAATTCATTAGAAAAATGTCCTTACCTCTTAAAATGTGAATTCATCTG
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AAAATGGTATGTCATTTTTTAAAATTTGTATTTCTTTCATTACAAATAAGATTGTTATGTC
AGTATTGTTATTGGCTTTTCGTATTCCTCTTAACGTGAACCGTCTGTTCATTGTTTTTAC
CTGTTTTCGTTTTAGCAAGTAAGTACCTGCCCGGGCCGGCCGCTCTAGAACTAGTGGAT
CCCCCGGGCTGCAGGAAATTTCGATATCAAAGCTTAATCGATACCCGTCGACCTCGAGGG
GGGGGCCCGGTA
Sequence 655
TNCCGCGGTGGCGGCCGAGGTACGCGGGGGAAGTCGGCCATGGACTGGAAAGAAGTTCTT
CGTCGGCGCCTAGCGACGCCCAACACCTGTCCAAACAAAAAAAAAGTGAACAAGAATTA
AAAGATGAAGAAATGGATTTATTTACAAAATATTACTCCGAATGGAAAGGAGGTAGAAAA
AACACAAATGAATTCTATAAGACCATTCCCCGGTTTTATTATAGGCTGCCTGCTGAAGAT
GAAGTCTTACTACAGAAATTAAGAGAGGAATCAAGAGCTGTCTTTCTACAAAGAAAAAGC
AGAGAACTGTTAGATAATGAAGAATTACAGAACTTATGGTTTTTGCTGGACAAACACCAG
ACACCACCTATGATTGGAGANGGAAGCCGATGATCAATTACCAAAA
Sequence 656
CGGTGGCGGCCGCCCGCCTGGTACGCCCAAGGCATTTAATGCCCACAGTAACAGGGCTGT
TTGACAGTGGCAGAAGAGGACGGGACTAAAGTTACTTTGTGCTGAGAGGGGGAAAGAAGC
ACAAAGTTTGGTCTGTTGCATAATTGAATTTTTAACACTCTTATCCACAACAAACACTTT
TTCGTGTCCTGCTGTGTAAAAGACATCAGATATATTACAGATTTTCAAACAGGTGAGCAT
NCTTTTACGAGCTGGGCAGGTGGGGAGTGGCGTGGTTTTG
Sequence 657
ATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTCCAATGAAGAATTTCTTCATTCTGA
TCTCCTAGAAGACAGCAAATACCGAAAAATCTACTCCTTTACTCTTAAGCCTCGAA
Sequence 658
CACGGGTGGCGGCCGAGTACCTTGTGGGCATTAGGTCANTNTTGTTATACACTTTCACAA
AAGATTTTATCTTTGATCTCTTGGCGATCTTCTTCTTGCCCATGGCAGCTGTCACTTTG
C
GGGGGTAGCGGTCAATTCCAGCCACCANAGCATGGCTTGTAGGGGCNATCTGAGGTGCCA
TCATCAATGTTCTTAACGATNACAGCTTTGCGTCCGGAGTAGCGTCCAGCCAGGACAAGC
ACCACNCTTCCCAGGTTTCATGAACTTGCCCATTTCGGCAGCAACCACCCCGGGGCNCTA
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GTGGGANTCCCCCCGGGGCTGGCAAGGNAATTTCCGAATATTCAAAGCTTTATTNCGATA
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Sequence 659
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AAGAAGCACAAAGTTTGGTCTGTTGCGTAATTGAATTTTTAACACTCTTATCCACAACA
A
ACACTTTTTCGTGTCCTGCTGTGTCAAAGACATCAGATATATTACAGATTTTCAAACAG
G
TGAGCATCCTTTTACGAGCTGGGCAGGTGGGGAGTGGCGTGGTTTTGATGGAGTGAGGAG
ATTTGGTTGAATGAACGCTAAGATGGCCAGACNCACCTCTTNGATCTCAACTCTGCAGCC
TGGG
Sequence 660
CCGCGGTGGCGGCCGCCGGGCAGGTACTATGACCTGAAGAGGGCAGAGGCCATCACTGTT
GGTCCGGTCTCCACCTGGGGAAACTGAGGTTGCACAGTGTCTCTGTGGTGACGAGCAGGG
CTTCATCCAGTGCCTCTGTCCCCACCGAGGGGACTATGGGAGACATGGAGGGTGTGTGAG
CAACAGGTGAGACTGGAGCCAGCTGAAAACTGGGAGACCGACCCAGCCAACAAACAATGT

Table 1

CGGTCTCTGTCTTGGCACCTGCAGGAAACAAGCTCCTACTTCCAGAAAAAGTGCTCCTGG
GACTCCAGGATACCAGGCATCTGGGTAAGCTACAATGCTTAACCACTTAACACAATCAGG
AAGCAACAGCCATGCATTCGGGGAAAGGAACTTCAGTGTTGTGTGGCTTAGTCTCCAGAC
CTAACTTTTCTTTGGTACCTCGGGCCGNTCTA
Sequence 661
TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGAGACGACTTTTTTCTCACCATGAA
TGTCACCCCAGAGGTCAAGAGTCGTGGGATGAAGTTTGCTGAGGAGCAGCTGCTAAAGCA
TGGATGGACTCAAGGCAAAGGCCT
Sequence 662
GAGCTCCCCGCGGTGGCGGCCGCCCGGGCNGGTACTTTTTTTTTTTTTTTTTTTTTTTT
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TTT
TTTTTGGNCNANANAAACNAGTTTTTTNAATTNATTNAGGGGGAANGNGGGGNGNCTTTG
GANAANCCNCNNNGAGGGCTNTNGGGGNGTNTCCNGNGGCNNGGGGGNNAGGGGTNGGGG
NCTNGGGGNGGGTTTNAGGGGCCCNNGNCCCNNGGCCNCTNTAAAACNAGGGGANCCCCC
GGGCNGGNGGAATTCGATNTCAAGCTTNTNGANCCCNCCCCCCCCGGGG
Sequence 663
TCCCCGCGGTGGCGGCCGAGGTACTTGTGGAAGGTAGTGACCAGCACAGCCNGCGCCTGC
TCCAGAGAACTGCACATCATGGATCTGTGGCAGACCAGGTGGCAGAGACAGACCCAGGAA
GGAGAGCAAGGCCCCCGCGTACCTGCCCG
Sequence 664
TNCGGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCGGTATCTGTATCGGGCCNTACTGG
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ANCCNCTNTTTTTTNATCNCGNCAGCANCTTAAAATGCCTGGGAAGATGGTCGTGATCCT
TGGAGCCTCAAATNTACTTTGGATAATGTTTGCAGCTTCTCAAGCTTTTAAAATCGAGA
C
CACCCCAGAATCTAGATATCTTGCTCAGATTGGTGACTCCGTCTCATTGACTTGCAGCAC
CACAGGCTGGGGAGTCCCCATTTTTCTCTTTGGAGAACCCAGATAGGATAGTCCACTTGN
ATGGGGAAAGGTGACCNAATGGAGGGGGACCACATNTTACGCTTGACAATGNATCCTTGG
TTAGGTTTTTGGGGACCGAACCACTCTTAACCTGGTGCCCAAGCAACCTTGGNGGAATCT
ANGGNAAATTG
Sequence 665
TCCCCGCGGTGGCGGCCGAGGCTAACAAGGAAAGCCCCTGGAGCTCCTGTAATAAGAATG
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TGATCATCATAGGCTTATGTCTTGCTGCAGTAACTTATGTTGATGAAGATGAAAATGAAA
TACTTGAATTATCATCAAACAAAACATTCTTCATCATGCTGAAGATTCCAGAGGAGTGTG
TTGCTGAAGAGGAATTGCCTCACCTGCTCACCGAAAGGCTCACAGATGTGTACCT
Sequence 666
GGGTGGCGGCCGCCCGGGCAGGTTTAATCTCAGGTCTCCCTCATACACTTCTCAGCCTCA
GCACCTAACCCTCACACAACACTCCAGTATTGATGCAGTCAATCTTGTATAACATTTTT
T
GAATGTCCAATGTGCAAAGCACGATGTTGGAAATTATACAGAGGTGAATAAGACAAAAAC
TCTTGCTCTCAAAGATGTCAGTCTTTTTCTTTGCAAGGATAACACATGTAGAGTAAAAT
G
CATAAAGGGGACTAATTTTAAATGTACCT
Sequence 667
GGCCGAGGTACTGGAGAGTCGGCTTTGACCATGGCCTCAGCTCAGCTCCAGGTTTGGAGC
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AGGCCTGGGGCTGAAGCCAGCGCTGACGGAT

Table 1

Sequence 668
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G
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GCAGATTCCCAGAAACTTTATGTATTTGGGAAAAGTAAAATATACAACAGACATATCCCT
GCCCTGATTAAGAGGGTAGATAAAAACAAAACATAAAACAATTTTACTTGAGATAGTAAT
AAGTTATTTGAAA
Sequence 669
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AGCAACTGACGACAGATGCTGCCCGCATTGGTGCAGATGCAGCCCAGGTTGGACTGAGTC
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AGTAGGGATACATAGTTGGTTGCGCCTAAGTTGCTTCTGGCAGAACCCAAGGAATAAATT
TCTCCATATCGTTTNCTAGTTACCCTAATCTCTGCACAAATTTTGTGTGTTACAGAAGC
A
GATCCAGAGCTTGAATA
Sequence 670
TNCGGGTGGCGGCGCCCGGGCAGGTACATTCTTTTTTTTTTTTTTTAAACTTTTAGGGT
CT
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GNCAGACCATGGCGGATGTAAAATTAGCTGCTTTGGTGTGGGCTGCAAAAATAACAGCTA
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GCAGTAGAGAAGAATGGTGGCTACAACCAACTCTGTGATATCTGGGCAGTAGGAATAACA
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ATCAACATTCATAATTTTTGTCAAAATAGCACTTATCNAAAAAAAAAAAAAAA
Sequence 671
GCTCCCGCGGTGGCGGCCGAGGTACGCGGGGTCTTCTCATGCTCCGTGATGCATGAGGCT
CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGA
Sequence 672
AGCTCCCGCGGTGGCGGCCGAGGTACTCTTCTGCACTGTTCTTTCTTTCTAATAAAACTT
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C
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CAAGGGAAATCATTTAAGAAGTGTCTGGTATTTTTCAAATTTCTGTCAGTTGTTACATT
T
GTGATAAGTAAATGTTTAGGAATAAAGGATGGAGACATGCTTATTTTATTTAACTCCCC
C
CNAAAAAAA
Sequence 673
GGATTGAGGTCCCCGCGGTGGCGGCCGTGCCTCTTAATCATGGCCTCAGTTCCGAAAACC
AACAAAATACGAACCGCGGTCCTATTCCATTATTCCTAGCTGCGGTATCCAGGCGGCTCG
GGCCTGCTTTGAACACTCTAATTTTTTCAAAGTAAACGCTTCGGGCCCCGCGGGACACTC
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T

Table 1

Sequence 674
AGCTCCCGCGGTGGCGGCCGAGGTACTGAAGCCCACCAGTGTCCGGATGGAAGTCTGCAT
CTGAGGTTGCTCAGTGTCCCGGTCATTCATTTACACATTTTAACTTGCATTAAAGAGCT
G
TTCTTTTCTGTGGCCTAGACTCTTTTCACTGATCTCAAAATAAACTGGTTTTTTTCAAAA
AAAAAAAACAAAAACAAAAAAAAACACAAAAGCTGCATGTCTAAAATTACATGGAGTTAG
TGTCTATTCTTTTTCCCCTTTTGCAGCAACTTACACAGCATTTTTAACACCTTTTTTTTC
TAGTTTTTTTGTTCGGTTTTGTTTTCCATCAGGAATTTGAGTTCTCTCTAACCCAGCTTA
CTGTGGGACATAGGAAAACTCAGTAGAAATACCTTTGGTGATCTTGTTGAGTTTAAGTCT
GATCTTGGATCTTAAACTCA
Sequence 675
NATTGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGCTGTAGTGGCTTCGTCTTCGGT
TTTTCTCTTCCTTCGCTAACGCCTCCCGGCTCTCGTCAGCCTCCCGC
Sequence 676
NCCGCGGTGGCGGCCGCGAGAGCACATGATGACCACGCCATCGTCCAGTATGAGTGGGCA
CTGCTGCAGGGGGACCCGTCAGTGGACATGAAGGTAACGCATGTTGTCACTGCTGGCAGC
TAGGTCTGCTGGGGCACACCGAGCTGTGAGGGAGGGAGGCCAGCATGCGGTGCTCCTGCC
CG
Sequence 677
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A
CTGTAGCAGGTAAACACTACTCTAACGTGGAGAAATGAGCTTCATGCTGAGGTAGTGGTT
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TTTCCCCTTTTCCCGGGTTTTNAAAAANNGGNGGGNGGNTTTAACCNGGNCCCCCCGGGN
CCCCCCCANNTTTTTTGNAATTTCCCGGGNCGGGCCGTTTTTNAANNAANANGGGGGTCC
CCCCCCCCNCNCGGGNNNAAATTNTNTTNAAANACATTTTTTTCCCCCCCCCCNCCCCCC
TCCNGGGGGGGGGGGNNGGCCCCCCCCCCTN
Sequence 678
GCTCCCCGCGGTGGCGGCCGAGGTACTTGTGGCATGACGTCGATGATCGAGTTCANGGCT
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GNTGACANGAGACATCCNCGCGTACCTGNCCG
Sequence 679
NCCGCGGTGGCGGCCGCCCGGGCAGGTACTGGTGTTGTGATCGGAACGTGTCGATCCCCT
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CCAATGTGTTTAGCGTGCCTGCCCACCTGCGCCTGAGCACAACTATCCTGCAATCTGACC
TGCCCCTCCTGCACAGGAAACCACCTTCCCCTCCCAATTGATGGTTCAAACACTGCCACC
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ATTTGTAGAAAAGGNGCTGAACTGCCAAGGAAGGCATTTCTTGTGCCGTGTCTGGAACCG
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Sequence 680
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AAGTCAAAAAAGTTCTTATTTAGGGTTTCTTTGAGATGTGGGGCCACTTCCATTCCCA
CC
CGGCACAGGTAGGCACGGGCATACACCGACACTAGTGGGTCTCCGATCCCTCTGATCATG
CATGTCAACCGGGGCAGGCACTCTGAAATTCCCGTTTTGGAGAGGAATTTGTTACATTTC

Table 1

AGGATGGATGCCTCCACGTAAAATCTTGGAATGAGTTCCCTGATGGAGGCAATCTTGAAA
AACCAATTTAGGCATGTTTCCTTGGCCGTGTCATTTGCATTCTCTGGAGAAAAGTGAT
CT
GGTAAGACGCTGCGGCTATCCACACACATGGAAAAGATGC
Sequence 681
GCGGCCGAGGTACCCTAATGTAGTAGTAAATTTAAGGCCTGTCGAGGAAATTTTAACACT
TCCAACAGGTGACTATATCAGGAAGGAGAAAACCAAGTGCTTCCTGCTTCACCTTCTGCT
GCTTTTGGGACTTTTTATGAAGCCTAGGTAGNCTNAGGACANGACCCTGAACCCATTTTT
TCACTGGGAGAGGAAAACCACCAGGCTTCTCAGCTATTGGCTTGGCAACTCTTGGAGTTC
CTATGGCTTCCATCAGGGGCTCCAGGCCCTGATAAGTGGCCTCAGGCCAGGNAGGGAGGA
TTCGGNGTAGCCGGGATTGGGGAGCAGCTAGGTNCAGGGAAGGNTGGGAAAATAGGGGAC
CCANTCCCCCAAAACCACCGTTTGGCCGCNATGGATGGAATTTGGAGGGGAACTGGGACC
GNTAAGTTTCTGGCATTGCCTGGCCGGNTTGGGATGCCTTCTTCGGGACTGGCTCCCAGG
GCCGAATNTTTTTCAGGGTCTTGCAAGCCCGGCT
Sequence 682
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GCTCGGCTTGCGCCCGCCGGGTTTCCGGAGATATGTTGTATTCGGCTGGGTCGAGGGTCT
CAGGCAGAGTGCGCAGGCTCGACGGCTTATACTTTGGGAACGACATCTTGGCGAACCAGG
GCACAATTGCGCCTGCGCGATTCTGAGGCCCTTTGTCTCCCCGCGTACCTGCCCG
Sequence 683
GCGGTGGCGGCCGCCCGGGCCGGTACGCGGGATGGCACATGCAGCGCAAGTAGGGTCTAC
AAGGACGCTACTTCCCCTATCATAGAAGAGCTTATCACCTTTCATGATCACNGCCCTCAT
AATCATTTTCCTTATCTGCTTCCTAGTCCTGTATGCCCTTTTCCTAACACTCACAACAA
A
ACTAACTAATACTAACATCTCAGACGCTCAGGAAATAGAAACCCGTNTGGACTATCCTGG
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NGGGGGAANGGACCCNTCNTTTANAAAAAAAAAAATNGGGCCCNAANGGTTTTNGCCCCC
NGNGGGCCCTNGGGCNTTTTTAAAAAANNGGGGGANCCCCCGGGGNGGGGGGGANTNTTT
TTAAAGNTTTTTTCCCCCCCCCCCCCCCGGGGGGGGGGGGGNCCCCCCCCNTTTTTT
Sequence 684
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ATCGAAGCCTTGTTGAGCTTCACAAAGGTTCCATTGAAGATTTGACNGAAGGCGAAGAAG
CTGCAACACCTTTCGAACCTTTGGGCTCACTCCATTGATACCTCTGATTCTGATGACAAA
CGCCAATTTGGGTTCTGCAGGTACGAGGACATTTTGCCCCGCGGCTTGTTGGGGTCTCCT
TTACCCATGTTGACAGATCCGCGTCCACCCGAGGGTATTGGAGGGTATTCTTGCCTGGTG
CGAGCTTTTCCTCAGAGTCCCGCAGAGCGGCCGCTCTAGAACTAG
Sequence 685
CGGTGGCGGCGAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGGTTTCC
G
NTCTTGTTGCCCAGGCTGGAGTGCAATAGAGCGATCCCAGNTCACTACAACCTNCGCCTN
CCAGGTTCAAGCAATTNTNCTGCCTCAGCTTCCTGAGTAGCTGGGATTACAGGCATAAGC
AACCATGCCCAGCTAATTTTGTATTTTAGNANGAGATGGGGGTTTTTCNATTNTNGGNAA
GGNGGGTTTTGAACCNCCCCCCNNNGGGGGNCNCCCCCCCTGGGCTCAAAAAAANGGGGN
GGTTAANTANGNGGGGGGGNGGNCNNATATTCCNCCCCTTGTATAAAAAAAAAANANCNC
CCCCCNCCCGGNGGTGTGGATATANATATTTNTACATTNTATNTTTTNTCCNCCCCCC
NC
GGG
Sequence 686
CCGCGGTGGCGGCCGCCCGGGCAGGACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTT
T

Table 1

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAACNGAAAT
TCTT
CANNCTTTATNAAAAAAGGNCNTAANGGGCCTNTTATTAAAAAANGNNTAAAANCCCCAN
AAATTCNGGGCCCCNGGGCNGGGCAGGGNTGANANCCCTTAAAGGG
Sequence 687
GCCGAGGTCGCGGGGGCTTACGATGGCNACAAGTATGGCGGCTGCTAGTGGTACGATTTG
AAACGTGCTGAAGAGTATCGAAGAGCGGAAAGAACAGACCCGGAATGCCAGGGCCGAGGT
GTTGCGCCAGGCTAAAGCCAATTTTGAAAAAGAAGAAAGGCGTAAAGAACTTAAGCGACT
TCGGGGTGAGGATACATGGATGCTACCTGATGTGAAT
Sequence 688
CTCCCCGCGGTGGCGGCCGAGGTACACTCGCCAGCGGTTTTGCCACAAGAGTATACCGGA
ACAAAGGAGACANGGCTCATTTATAATCTGACGCGGCCACCCTCCTGCTGCGTTCGGTTT
CCATTGGCTGGGACGGGACCTCACCTTCTGTATTTGTCCCGACTGGCTAGCACTTAGAAC
TTTTTAAAAGAGGCAAA
Sequence 689
CTCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAACTGGGCACTGGATAGGTAGTTCCTTT
GGTGGTCAAGGTGGCTCTACCTGTCCTTGAGCTCTCGTGTCACTCGCTTGGTGATCCGTC
CACACATCAGGCCAATCAGGAACAATATACAGATGCTCCCACTGATCACAGAGAGAATGT
AGTTCTTAGATGGAGACGTCATTACTTGCATGGCAAGATCAGAGAAGCCATCTGCTGGGG
CCACCTAGAATGACACAAGGCAATGTGATTCTCTGAGAGAGCACTGGGCTGGTGGCAGTG
CTAGGTCTAACTTATCCCTCTCAGTTCCTAGTTTAATTTATGTCTTTTCTTTTGGAGAG
G
GAGGGGCAGGAGATAAGAAAAATCAACACAGAGCTACAACTCTTTTTCCTGGATCATAAA
ACTATACCCCACGTCTACTGCACCAAAATTAGGAA
Sequence 690
CCCGCGGTGGCGGCCGCGTTTGTTTCTTGCCGTCCTGAGCGATGGAGCCCGGGGGTGCCT
GGTTATTGTCCGCTTTCTCTCTCAGATGCTTGGCTTGTTTTTCAAGAGAACCTTTTTCG
A
TATTCATTGCTCCATCGATTGGATCCAGTCCTTGTTCAGAAAATTGTTTCAAGGCACTT
A
AGGCTGCCTGAAAGCCTTGAATCCTTGCTAAATATTCCAGTTGNTTTGAAGGTTGTACCT
Sequence 691
GCGGTGGCGGCCGAGGTACTACAGGAAGAAACTAGAGGAAACGGGAATTTCATCCATGTC
CTGTGTATCTGCTGGCAACAGGTCAGAACCGGCCAGTATGTTATTCCCTGCAGGCTGCCT
AGGGTGCTCTCCTCAAACAGATCACCTGAGCCTCCTGCATCTATGAAAGTTATGACACAG
CAACCAGTTACTCAGAGTCTGATGAGAAAAACAGATTTTAGGTTTGGGAAATGGGATTAC
TGTAATTTACACATCCAAATGCAAACTGGAGCTCTGATTTGAATTCTACCCTGGGGGAAG
AACTTTGATGCTAACCCAACAAGGTACCCTGCCCGGGCGGCCGCTCTAGAACTAGGNGG
GATCCCCCCGGGCTGCAAGGAATTTCGATATCAAGCCTTATCGATACCCGTCCACCTCGA
GGGGGGGGGCCCCGGGTACCCCAACTTTT
Sequence 692
GAGTGACTCCCCGCGGTGGCGGCCGAGGTACACCAAATGTGACATCCTTTCCCAATATAG
ATTACTTCATACCACATTGTCAAGGAAAGGACTAGAAGAATTTTTTGATGACCCAAAAAA
CTGGGGGCAAGAAAAAGTAAAATCTGGAGCAGCATGGACCTGTCAGCAACTAAGGAACAA
AAGTAATGAAGATTTACACAAACTTTGGTATGTCTTACTGAAAGAAAGAAACATGCTTCT
AACCCTAGAGCAGGAGGCCAAGCGGCAGAGATTGCCAATGCCAAGTCCAGAGCGGTTAGA
TAAGGTAGTAGATTCCATGGATGCATTAGATAAAGTTGTCCAGGAAAGAGAAGATGCCCT
TAAGGCTTCTTCAGACTGGTCAAGGAAAGAGCTAGACCTGGTGCTTGGAGAAGAGACATT
NTTTNGGAAGAATCATTTTGGCCCAAGGTTCAAGCNNTGGGGTTATTCCTTTGGCCCCCT
TAAATTAAAAAGGATNCCCATT

Table 1

Sequence 693
TCCCGCGGTGGCGGCCGCCCGGGCNGGTACCTCAGGGACATTTAAGAGTTGGACGGTGCA
AATATATTCCAAAAGGGTGCAACATGACACAGTGTATCCCCCTGCTTCTGTTTTTGTAT
A
TTTTTGCTACT
Sequence 694
GGTCTCTGTTGGGGCTCCCCTTTCCTGAACTTTGGCCAAAGACAACAGGATATTCTTGGG
GGTTTTGTTGTTGTTTTGTTGGCATNNTTTCTGTGCCTGTTGGTGATTCCAGCACAGN
CC
AGNGANCCGNGTACCTGCCC
G
Sequence 695
GTGACTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGTATAATGGAGGCTGACCAGAGC
AGTTTAGGAGATTGTAAAGGGAGGTTTTGTGAAGTTCTAAAAGGTTCTAGTTTGAAGGTC
GGCCTTGTAGATTAAAACGAAGGTTACCTAAATAGAATCTAAGTGGCATTTAAAACAGTA
AAGTTGTAGAGAATAGTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCT
Sequence 696
NCCGCGGTGGCGGGCGGCCGAGGTACAGCAGGGTGCCTCATGCAAGAGAGGACTGAGTGG
ATTTTCCTTAGGGATATTTATGAACCTTAAAGCAGGAGCTTAAAGGGAATTTGGGCCATA
TTAACCACTTAGGTCATGATAAATGATTACATTTTTGGACATTTTGGTGTCTTAATGTC
A
GCAAGGGTTGCACGATAAGTTTTGACATGCATGCATGGGAGACATGTAGAAATTCTAGTT
ACTTACAAGTTTTTGGGGAAGAAGCCTGGACCCAGATGCCAGCTTTAAATAACAGGGGAG
TCTAATTACTTCTAAATTCCTCACATAAGGAGTTTTTGCCTCTGGATGGCCTGCTTGAT
G
GNCCTAGGGNGATCTTTGCCCCTTTTATACTAANAAGCCCTTGCCCTGGAAAGGGNTNTT
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NNNGAATTANAACCCCTTTTTTTTNGGNGGGAAAAATTTNCCCCCCCCCCCCGGGGGGGC
CCCCTNTTTTTTGNGGGGGGNANAAANCCCCCCCCTCGGGGGGGGAAAAAAAAAA
Sequence 697
CGCGGTGGCGGCCGCCCGGNCAGGACGCGGNGANGACAGCGNCAGGCGCTTGATTTCCCT
GAGTCCCGGTGCCTCANCTGCCCAGNGCCCACGTTCGTAAGAAGGCAACAAGNTCTTCTC
CTCTACAGAAGGATTTTGCAAACANTTCGGCAAGNTCCAAATGATTCTGATCGCAAATAC
CTGGAAGATTGGGCAAGAGAAGAATTCAGAAGAAACAAANGTGCCACCGAAGAGGATACA
ATCCGGATGATGATTACTCAAGGCAATATGCAGCTCAAGGAGTTAGAAAAAACACTTGCT
TTAGCAAAATCTTAACTATAGCATTATTCTGAAGGGA
Sequence 698
ANCCTCACCGCGGTGGCGGCCGAGGTACGCAGNCCNCCTGTAGGGATCNGTNTTGTTCNT
GACNAGCCCTACGGTAATGCAGCCCGGAGCTTGTTTTCCGTAGCTGGGGACAATCTTCTG
TCCTTGCTGTTCATGTCGTGGAAGAGAGGGGCAGAGTCTTGCTCTGTCACCCAGGATGGA
GTGCAGCGGCGTGATCTCAGCTCATTGCAACCTCCACCTCCTGGGTGCAAGCGATTCTCC
TGCCTCAGCTTCCCAAGTAGCTGGGATTACAGGCGTGCACCACTACATCCAGAGACTGGG
ACTACAGGCATGGATTTTCAGGTTTATAACATGGCAGAGTGAATTCTGGCAACACACTGA
GTGATGCTTGNCAATGGCCACTATCAGGAATTTAAAACAAGATTT
Sequence 699
CGGNGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTGTTAGTGTTTTCTGATGTCTTTT
CTAACAAATCTTTGCCTGCCCAAAAGTCTCAAAAACATTCTCACGTTTCTAGATTTTTAG
CTTTAGCTTTTGTGTTTGGGACTATGATCCATATTTAGTGAATTTATTTTTGGGGGGGCA
GAGTCCATGTTGCCCAAACTGGTCTGGAACCACCACACCCAGCTAATTTTTGTGAATTGC
GGGTACCAGCACACCGGCGCCGTCCTGGACTGCGCCTTCTACGATCCAACGCATGCCTGG
AGTGGAGGACTAGATCATCAATTGAAAATGCATGATTTGAACACTGATCAAGAAAATCTT
GTTGGGACCCATGATGCCCCTATCAGATGTGTTGAATACTGTCCAGAAGTGAATATGATG

Table 1

GTCACTGG
Sequence 700
CGGCCGACTTGATGAGCGGAGAGACCTGCACCGGTGGCACCATCTTGTCCCTGACCTCCG
CACCGGAAGCCCCCGCGTACCT
Sequence 701
ACCGCGGTGGCGGCCGAGGTACGCGGGGGAGAGAGGAAAAGAACACAGATCTCGCATGGT
TCAGATTTTTCTTTTTAGGTCCAGGAGTAAGATATATCATACGAAAATGAAAATTATAAT
NCTTCTTGGATTCCTGGGAGCCACATTGTCAGCCCCACTTATCCCACAGCGTCTCATGTC
TGCAGCAATAGCAATGAGTTACTTCTTAATCTTAATAATGGTCAACTTTTGCCACTACAA
CTTCAGGGCCCACTTAATTCATGGATTCCACCTTTCTCTGGAATTTTACAACAGCAGCAG
CAGGCTCAAATTCCAGGACTCTCCCAGTTCTCTTTATCAGCTCTAGACCAGTTTGCTGGA
CTGCTCCCAAATCAAGATACCCTTAACAGGAGAGGCCAGTTTTGCCCAAGGAGCCCAGGC
AGGCCAAGGTTGATCCCTTACAGCTTCAAACACCGGCTTNAAACACAACCAGGCCCCAGT
CACGGGGATGCCCTATGTATTCTCCTTCAAAATGCCTTAAGAGCAAGGGCCAGATGGTTT
CAATACCTATNCAGGTTTACATGGGC
CCGCGGTGGCGGCCGCCCGGGCAGGTACTGCAAGCAACAGTTACTGCGACGTGAGATCAT
CAAGAACACGTAGAGAAACCCAGCTGTAATCATGCATGGAGATACACCTACATTGCATGA
ATATATGTTAGATTTGCAACCAGAGACAACTGATCTCTACTGTTATGAGCAATTAAATGA
CAGCTCANAGGAGGAGGATGAAATAGATGGTCCAGCTGGACAAGCAGAACCGGACAGAGC
CCATTACAATATTGTAACCTTTTGTTGCAAGTGTGACTCTACGCTTCGGTTGTGCGTACC
T
Sequence 702
GCGGTGGCGGCCGAGGACTTTTTTTTTTTTTTTTTTTTTTATGAATTATTTATTTTCTTT
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CACAGACGGGGTGGTTCTAGACGGCCGCTCTAGAACTNGTGGGATC
Sequence 703
GGTGGCGGCCGCCCGGGCAGGTACAAGACCTTGACACGCCCAAAACACTTCCTGCAGATG
TTGNCGTTGGAAAACTGTCGTCTTACAGAAGCCAGTTGCAAGGACCTTGCTGCTGTCTTG
GTTGTCAGCAAGAAGCTGACACACCTGTGCTTGGCCAAAGAACCCATTTGGGGATACANG
GGGTGAAGTTTCTGTGTGAGGGCTTGAGTTACCCTGATTGTAAACTGCAGACCTTGGTGT
TACAGCAATGCAGCATAACCAAGCTTGGCTGTAGATATCTCTCAGAGGCGCTCCAAGAAG
CCTGCAGCCTCACAAACCTGGACTTGAGTATCAACCAGATAGCTCGTGGGATTGGTGGGA
TTCTCTGTCAGGCATTAAGAAGAATCCAAACTGTAACCTAAAACACCTACGGTNTGAAGA
CCTATGAAACTAATTTGGGAAATCAAGAAGCTGTTGGAGGGAAAGTGA
Sequence 704
CGCGGTGGCGGTCTGCCCAGATCCATGATGTGCAGTTCTCTGGAGCAGGCGCTGGCTGTG
CTGGTCACTACCTTCCACAAGTACACGGGTCTATTTGGCNGTGACCTTGCTCTGGAGACN
ANGATATCCCTTCAGCCTGAGGGAATTGATGTTGATGAACCCGGAGGCATCAGTTGGCTC
ATAATCACCCTGCACGTTCATGCTCACCAGCTCCTNATTGTNNAGAGACAGNCNGGGACT
CCCGGCCGAGGATGTACCT
Sequence 705
CCGCGGTGGCGGCCGAGGTCCGACGCAGCAGGCTCCGAAGATCATACAGACGCCATTACC
ACTCTTGGCTCCCAGAAACCTCTGCGCCCCGCGTACCTGCCCG
Sequence 706
CCCTTAGCGTGGTCGCGGCCGAGGTACGAGTAAATTTTCATTACCTTTAATTAGGCAATG
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NAAAAGTAAACGCTTCAAAAGATACTACTGAGAAAGTCACAGAATAGGAGAAAAATCTGA
TGAGACTTTATGTCTAGAGTAATGAATTCTTGTTAACGAATAACCAACCCCCTTTTAAAA
ATGGGCAAAAGATTTGAATAAACATTTCACTACAGACAATAAACAAATGGCCTTAAGCAC
AAGAGATGCTCAACATCAGTAATTATTAGGGAAATGCCAATCAAAACTACAACGAGATAC
CCTATATCCACTAGTATGGCTATAATAAAAAAGAGTAACAAACCGTTGAGGAGGATATGG
AGAAACTCGAGCCCTGGTCAGGTGTGGTGGATCACACCTGTAATTTCAACACTTTGGGA
Sequence 707
CCCTTAGCGTGGTCGCGGCCGAGGTACCCATATCCAAGGCTTATTGCAACTTTTAGTCTT
GCCCCTGCTACTTACACAGTCCAGAATCACTTGGGTGAGCATTCCAGTAGGACGGTGGCA
TTTTAGGATTCAGAATATTAACCTATAAACCTGTCATTTGATTCTTGATTATTAATGTCT

Table 1

GGATCGCCTGTGGTAGGGGTGTAATCCCAGGAAGGCATTAAATATATTTGAATTAATGTA
TATTTTGAGAATAAAAGGCTATTTCTAGAAAATATTACACACTTGTCTTATGTTAAATAA
AAATTTGCTATTTATTGAATATCCCTTACCCACCCTTCTTCCCAATGAAGATCTTATGCA
TACCTTCACTGGAAGGTTTAAGATGTGACAATCTTAATAGATCTTTGTGAGACCAGCCAT
TTCTCTGTTTATATTTTGNAACCGCCANAGCAAGGGCCATGCCACCTTTCTCATTGGACC
T
Sequence 708
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATCCTTTTGCATGCTCAAGAGCCCATTCTTT
TCATCATTCGGAAGCAACAGCGGCAGTCCCCTGCCCAAGTTATCCCACTAGCTGATTGCT
ATATCATTGCTGGAGTGATCTATCAGGCACCAGACTTGGGATCAGTTATAAACTCTAGAG
TGGTAAGTGTCTTCACATTCTTTAAGCACTAAAGAAAACTTTTAATTAGCTACCTTGCTT
CCAGTAATCAAACTAGAGCTCCTCTGCCTTGTGTAAGTTGCTATAAAGTATTGACTATTA
GAATGTCTTGAACTTTGGTTACTGNGAGCCAAAGTCGGTGCTCAAAGTATATTTCATAGT
CTCAATTATATAGTAATTTANGTTCTGAAAAATAGGTTCTGGCTTTGCATATGTAATATT
TTGTGAGTATTTACTTTGGAAAGTTTGGTCGACCTAATGGATAAATTTAGAAGTTTATTT
TCCTT
Sequence 709
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGCATGGTCCATACCACTGTTTACTTTTCTAG
AAAGTTGTTAGACTAATTTTTCAACAAAAATTCTTTATTGTCTTGGTAACAAAAGAAGCA
TACTAAAAATTCTCAATAAGGCACAGTGTCTNTAGAAGCTTGAGCATTCAACATAAACTT
CTAATTAACACGAACTTGTGCTCTTATTTCAGCCATTGCTGTGTGGGCTTGGAGCCAGGA
GAAGATGCAGAGGAATTTTACAATGAATTACTTCCATCAGCTGCAGAAAATTTTCTAGTT
TTGGGGAGACAATTACAAACATNGTTTTA
Sequence 710
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGCTAATCCCAGTTATGAGGGCTCTGCC
CATGACCTCATCACTTCCCAGAGGCCTTACCATCTAATACCAATACATTGGGTTTAGAAT
TTCAGCATGAGAATTTGGGGGAGACAGTCAGACTGTAGCGATGATTCTGGAGTATTCATC
ATTTAAGAGACACTTAAAAATGATCAGAAAGGAGAGGATGAAGGCTAGAACTAAGACTTT
AGCGTTGAACATGGAAAGGAAGTGATGACTGCAGATATCTCCAGTACCTCGGCCGCGACC
ACGCTAAGGGCGAATTCCAGCA
Sequence 711
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGAT
AGCCATATACCAAATAAATGTTCTGTGACTAGGGGTTATGGCACAATGGGTATTGAGACA
CTAAAAACTCTGCTTCAGGCTTCCATCCTCTTAATTTTANAATATCTCTGATTTCCTAAT
TTTCTGATTGACATCTTTTGGTAGATTATCGGGTTTTTACTTTATGTTATTGACTGATCC
TTTAGAATGATTTTCTTTTTGTTCTGGGAAAAAAAATGCATTCTAAATCANATTCACTAA
TACTTTGATTCACTTCCAAGGAT
Sequence 712
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ATTAAATGGAAGACACCTGCTAGGTGATACTTTTTATAAAACATATGAGTAAGTCATATA
TCTTTGTTAAATTTCTGTATGTTCTTTTTTGTATAAAGATGGAGAGAAAGGATGGAGTGA
TACTAAGGACCCTAATAACATCTCTGTTCAAATTAATTACTAAGTGATAGAAGTATTCAT
ATGCCATTAAAGATTTGCCAATTCTATTT
Sequence 713
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACTGACACAAGGACTCCAGGCCACACATATCT
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GGCCACAAAATGAATTGTCTTCTTGTGGGCTGTGTTTCAGAACGGCCGGTTTGTGGGCGA
TGCTGACCTTGAAAGACAGAAATTTTCAGATTTGAAACTCAACGGACCCCAGGTAATTCT
TTGGCTCAAGACCTGGGTTGCTTCATTCATATTTTCTTATTTCCCCAGCCTATAAGAGCA
TATTTGTGTCTTGTAAGGTGCCTGG
Sequence 714
CCGGGCAGGTACATATGCACTATTTAGAATATGACATTAATCAACCACTAGAATTAAAAT
CAGGTTATAAATCCTCAAAATCACCAGAAGTATAAATTTAAATGAAAAACCCAGACCACA
GAACAAAAACAGAAATACCAAAAAATAATCACAAAATATTAAAAACAGTATATAAACACA
GTGACAGAATTAGGACTAAACATATCTGTAAAACAATAAATGTAAGGGTAATCTCACCAA

Table 1

TTATGAAAAAGACCTTCAGATCATATTTTAAAACAAATTTAAAAACTCAACTGTATGTTT
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AAAGAAATAGCAAACAAATACAGGCATAAAAAAAAACAAAGATCCCAATAGTACCTCGGC
CGCGACCACGCTAAGGG
Sequence 715
CCCTTAGCGTGGTCGCGGCCGAGGTACGTGTGCTGGATATGCAGGCTTGTTACATAGAAT
TGGTGTAAAATTTGAAAACCATGAAAAAATAAAACAATAAAGGATCTAGATGCTAATAAT
GTGGTTAGTTAACATGTTGACCATTTCAAAGCAAAATAAGTCTTTGATGTTTTATACTAT
TCATAGCAAGATATAAGTATTTAATCTGCAAAGACGTGGATTTGAAAATTCAGCTGCCAA
ATGTAAAGAACAGATTCCTAGATTATTATTAATAATATCTCTATAAATATTATATTTATC
AATAATGGGTACCTGCCCGAGCGGCCGCTCGAAAGGGCN
Sequence 716
CCCTTTCGAGCGGCCGCCCGGGCAGGACAGTGGTGTGATCTTGGCTCATTGCAACCTCCA
CCTCCTGGATTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCAC
CTGCCACCATGCCCCGTGAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGG
CCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCTGCCTACCTCGGCCTCCTAAAGTGT
TGGGATTATGGGCGTGAGCCACCATGCCCACCTCCTGGGTCATTCTTCTGGATATTACCA
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TAGTTCTACCTATGACATGAGGGTGATCTTTATAATTTTTTTTTGTTTTCACTGAAGAAA
TAAAACATTGCTTAANGGGAGAGTTTGGGGGAAGTGCATANGGGATCTGCAGTTGGGACT
GGATTTTTCGGGT
Sequence 717
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TGGTGGCCAGCCTCCAAGATGGTCCTCAATGATCTTTGCATCTTCATATTTCCACCCTGT
GTAGTCCCCTCTCTCAGGGGATTAGGGTTGGTCTGTATGATCACCACATGGCTGCAGTAA
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TCTCTGTCTCTCTGATCTTACACTCTAGTGGAAGCTGCCATATTGTGAACCTCATGGAAG
GCCCACAGGGTGAAAAACTGAAGCATCTAATCAACAGTTAGCAAGAAACTGAGCCTGNCA
ACAACCATGTGAGTGACCCCGGNAAGATTTTCCAGTCCCAGTCAAACACTTGANATAACC
GGCAACCCTTAAGCTGACAGCTTAACTGCNANCTGATAAAAGACACCCTTGGGNCAAAAC
CATTNGGAACCATTCATACCCCA
Sequence 718
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AGGCGGAGGTTGCAGTGTGACGAGATTGCACCATTGCACTCCAGTCTGGGCGACAAGAGG
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TTATGCATTTTCCAACTATGTATGCATCACAAGCTATTCTTTTTCTGAGTTATAGCTACA
GTTTTCCTACTGTTGTCTNCATGCCATTTTCATTTCACATGGTACCTTG
Sequence 719
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TTTGCCCTTAATGGATTACAAATGCTAACCNACATAAAGACCCTGGGAAAGGGTTCANAA
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TCTATGTAAGTGATGACNTGNCCGGNGTTCCAGGNGTTTNTTAACTNAAACTTGAANAAA
GGCCCTAACTTAAAATGGGTTTTTGAAANCCTTTTCCAAATTNGGGTNTTTGGTTTGGAC
CCCNTTNAAANCTTTTTTANCAATTNTTTNTTTTAAACCCCTTGGGGGGGGGGGGCCCCC
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Sequence 720
CCCTTAGCGTGGTCGCGGCCGAGGTACTTGAAGAACATGGTAAAAATATGTTCACAATAA

Table 1

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ATTATATAGAATAAAAGCTGAATTGAACTTTCTTCACAGCACACTGAAAAATATCTTCTA
TAGCATTAATCAGATCACAGAATGCATATTTAAACCAAAATTTGACTAAATTATTTTTTA
ATTATTTAATTTTTTTCTGANACCGGAGTCTGGCTCTTGTCNCCCAAGCTGGANTGCAAT
GGCNGGAACTNACTTATTGGAAACCTCCGCCTCCTGGGTCAAGCCAATTCTTCCCNCTTG
GNCCTCTAAAGTGCCTGGGATGGCAGGCCTGTGCCANCCTTCCTGGCCCCANAGNNCCGG
GTTTTGGATGGTTGGGTNGGTTNGGGGGGTTTTTTTTCCCTAAAAACCTTNAAATTTCC
CCTTTTGGTTTTTTTCCAAAAAAAAAAAAAAATAACCCCTTTTTTTTTTACCCCCCCCTT
TTTT
Sequence 721
GCAGTGTGATGGATTCTCANAATTCCCCTTGACGGCCGCCGGGCTGGTACGCGGGGTTAA
CTATGTTTTCTTTAACAGAAAGTTCTGTTTTTGTGATCCTTTTAAAAATAAAGCTTCACG
GAAGGTATGAGAATAGTATTTTTCAACTTTAAATTTCTCATTACCAGAAGACCATGTGGT
AATTCTCTGTATACAGTTAGAACAGCACGGAAACTTGAAGGCCTAAAAAATTAGCTGACC
TTGTTAAAAATGTTGGCGTGAGCAGTATATTATTACCTATCTTTTTTTATTGTGTGTGTG
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TTGAGAGGCCAACCAAGGTAAGTCTTCATGTCAGTNGTTTGGTTGAAGGAAACGAGCCTA
TGAGGGTCAGTTTTTCCCCAAAANGGAA
Sequence 722
NGCCCTTAGCGTNNTCGCGGCCGAGGTACATGAACCTATTAATAAACCATTCATGCTTCC
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TTACTTTACAGAAATACTGTCAAGTCCAATAGAGAGCACAGACTTGGGAGGCGGATTGGG
TGGGTTTGAATCTCTGCTCTGCCACTTTTATTAATCATGTGAGTTGAGTATGTGACTTAA
TCTCTTTTAGCTCAATTTCCCCATCTGTAAAATAGGAATAATAAAAATACTGACTTCAGA
GAGGTTTGTGAGGATCAATTAGACAGTCATGTTAAGTCTGTAAATTGTTTCTGTAATGGG
CAAGATAGCAAATATTTTAGATTTTGTGGACCATGCAGTCTTTATCATAACTGCTTAACT
GCCATTATAGTGAGAAAGCAGCCACAGACAATATGTAAATGAAAAAGTGTGTCTCTGTTC
CAATAAAACTTTATTTTCAAAAACCAGCTGGCTTGNCACATCTGGCCTATGGGCCCATAA
GTTGGCCCATCTCTAATGTAAAGAAAGGACTTTANCCCAAAGCCACAACTTGCATAGTAA
TGCCTTAAAAAAATGGTAACATCTTTACTGGTATTAATAATTACTACTGCATCTATTACC
AGNAGCCAATTGGAGTAATGAATCCATGAATGGTATAATGGTAAAATACTAACCCTTT
Sequence 723
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACTTACTTTGTTGCTCT
TTTTCTAAGTTTTAAAGATGGATGCCAATCTCAGGCTTCTTTTCGTGTGTGTATGTGCGT
ATGTCCATAAATTCTCTTCTAATTACAGTGTAAGCCACATCCCACAAGTTTTGATAGTCA
CAGAACTGTATCGTCACACTATTTTTTAATTTCAGTAAGTTCTTCACTGATCCCTGTGTA
ATTTAGAAATGTTTCATAATTTCCCTACATTGGAGGGGAAGATAGTTTTGNTTTTATTAT
TAATTTCTAGCTGTANTTGAGCTCTTGTCAGAAAATATGGTTTATTTTAAGTC
Sequence 724
CCCTTTTNAGCGGCCGTTNNGGCAGGTACTCCTCAGCTTGTGCTGCCCTTCTCGAATGAC
TCGCGTTTCCTGCTTTCATCACTACACCTCCCACCGCTCTCCATCACCTGCTCTGCTCTT
ATAAGGATCCAGAGAAATGGAATAATCTTATTGCTGATCTATGTAAACAAGTTGAAGAAT
CGTCTGAAAGAAAATACAGTGTGTCTAAACTGGAAAAGTCCTGTAATAGTTTGTTCATGA
GCATTTGCACAGTGGAGTTACTGTTCATCATGGGGGTAC
Sequence 725
CCCTTAGCGTGGTCGCGGCCGAGGTACTAACTATTCCTAAATATTAAACACTGGTCAACT
AAAATGCACAAATTCATGAATTGGATTTGCACTCAAACAAAAAAAAATACCATAGGCAGT
ATCATTTCTACCTTTGTAAGAGGCAGGAATATTCATTAGACTCTATGCTTGACTTTTCAT
ATGTATTTTAACACTGTAGTAGGCTATCGGGTCTAGTTTAAGCTTCATTTCTAAACTACT
CAACAGCTCAGAACTGACAAAGATCACAAGAAATCAACTATTAACCTCTTGCCTGAAGAC
ACAAATGAAATATTCCCTATTTTACAAAGCAAATTAGATTCCAAGATTTTCCAAAGCCAT

Table 1

ACTCCTGCAGTTCACTGGGTTTCAAACTTAAAAATCAT
Sequence 726
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACTCACTTAAATAAATAATTGGTAAGATGATT
TTATCTGACAATTAAAAAAAGGTATATGTGAAAAACCTTAAAAAAAATCTATTTCATTAC
ATGTTGAAATGTTCTGTGCTTAATCCAATACATCATTTAAATTCTTTTCACATTTGGACA
ACAGAAAAACTGAAATCTATGGATTCCAAGCTGCAAAGTATTTTATCTAAATTGCAAATC
AAAAAAC
Sequence 727
GATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACATTCTATTGTTATC
TCTATTTTTTGGATGAAAAAACAGCAGCACAAAGAAGTTCAGTAACTGGCCTAAGGCCAC
ACAGCTTGTCTTCCTGAAGACTGGACCCAAACCCAGGCAGTCATAGAACATGCTGGTCGC
TATTGGGCCGCTTGCTCTATGGGGGACGGTGCTCCAGGAACACAGCAATGCGGTTTAGGA
TTCCAGGACCTGGGGCAGCTGCTGCTTCTTTCTTAGTTCTCGACAGACCACTGAGTGCAG
TTTTTCTAAATCTTTTCCCCACTTTGATATGTGGTCCATAAAACTGCTTCCACACGTATA
ACCCACTGTGAAGTTTAAAATGATTTCATGTTTGGGCAAATTCCTACTGAATGTTAAGCT
AGATAGGAAACAAGTTCTGACTAACACAAAATGAAGGGCTGAATGAAGAAGTCNTACTTT
TATAAAGGAATTTTNCCCTTCCTCACCAAATC
Sequence 728
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTAGAG
ACGGGACCTCACTGTGTTGCCCAGACTGGTCACAAACTTTTGGGCTCAAGCAATACTCCT
GCCTTGGCCTCCCAAACTGCTGGGATTACAGGGATAAGCCACTGTATAGAGTATGAAAAG
TATTTAAAAGAATCTTCCAAAGGAGGACAGCAGAAATGAAAATAAAGTAAGTTCAAACTA
GAATCCTTGACACAACTGGTTTTATTCCCAATGCCTCTTAAAAAGAATCGTTCCATGGGT
GGCAGGAGGGGTGTTTTCATGGTGTGATGCACCGTGACTTGTTATTNAAGATGTAAGTCC
AGTGGTCCATCTATCACGTTTTATACCTTTCGAAAAAAAAAAAAA
Sequence 729
TCTNGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTT
CGANCGGCCGCCCGGGCAGGTACTTATCAGGATGAAATCAGAATCACAGTTGGCCTTTTG
CCATAAGGGAAGGGTATTTGGAGAAGAGTCAACCACCACTCATGCCTCTCCCCTGCCCAG
CAGCACCTTGGATTTTCCTGGCTTTATGCCTCCTGTTTCCCCTGGCTGAGTAACTGCAGG
CATTAGGTTCCTCTACACACGATATATTACAGGGAAATGGCAGCGATGGTCTGGAAGGGC
AACACTGGCCTTCTTTCCTCCTGAGCACTAAAATCCTAAACATGCAACTTAAAAAAAAAT
TCTAAATGTGAACACCACCTTTCAGT
Sequence 730
GATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACTCACTTAAATAAAT
AATTGGTAAGATGATTTTATCTGACAATTAAAAAAAGGTATATGTGAAAAACCTTAAAAA
AAATCTATTTCATTACATGTTGAAATGTTCTGTGCTTAATCCAATACATCATTTAAATTC
TTTTCACATTTGGACAACAGAAAAACTGAAATCTATGGATTCCAAGCTGCAAAGTATTTT
ATCTAAATTGCAAATCAAAAAACATCTATAACATCTTGTTGGGGATACAAAGTTCTCCTG
GCTG
Sequence 731
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTTTCTGAAGAATACATCTTCGTTCAATGTGG
TCGTATTCTTAATTTTTTTCTATAATATTGCTTGTAATCTTTAGAGTTATGGTTTCATTTT
TTGACTATTAAATTTGAAATTGTTGACATCAGCAGTTGACTCTTCTGTGTAGATCATAAT
TTTTTAATTAAGAAGACACTCTCAAGTGTTGAACTATAATTGTAGAGTAAATTCTAAGTG
GAGGATATCGTAAATTCTTTTTTTGTCTTGGTATTGACATGTAAATGTTAACATATGTGAA
TAATTCAGTCCCCGATTGTCACAGGTTCTATGTCTTTACCTCCTTTCAAAATACTTTCTT
TAACAAATACTTTGACAAATTTATTAACCATTTATAAGACAAGACTTACCAAGGTGGTGT
TCGTTTATGAATCTTTAAATGTTTTCCAATACTTAAGATACATCAAAATTATAGGACTTC
TCAATTCCATCCTATTGTTACCAGAATATNAAA
Sequence 732
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTCTTTCTTTTTTTTTTTTTTTTTTGAGATG
GAGTCTCGCTGTGTTGCCCAGGCCGGAGTGCAGTGGCACAATCTCGGTCACTGCAAACTC
GGCCTCCTGGGTTCATGCCATTCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGTGCC
CGCCACCAAGCCCAGCTAATTTTTTTCTTTTTTTTTGTATTTTTAGTANATACGGGGTTTC
ACCATGTTAGCCAGGATGGTCTTGATCTCCTGACCTCGTGATCTGCCTGCCTCGGCCTNC

Table 1

CAAAGTGCTGGGATTACAGGCGTGAGCCACCACACCCAGCCTATTCCTTTACTTTCTTAA
ACTTTCTTTCACTTTACTCTATGGACTCACCCTGAATTCTTTCCTGCTCAAGATCCAAGA
ACCCTCTTTTGAGGTCTTGGATCGGGACCCCTTTNCTGTNACACNAACTGTATCCCCCTT
GGCAGACATATGAATTTGCACCCCCGCTTGGGTCTTCAATNTCCAGGGGATGAAACAAGG
GAGGNAAACCGAGGGGAAAA
Sequence 733
CCCTTAGCGTGGTCGCGGCCGAGGTACAAAACTATGTGAGAACGTATACTACTTCTCGGC
CACAACTACTATTTTTAGATATTCATAAAATAACCTCTGATTGTGTTTTCACATTGCCCA
TTCAGTTCTGTCCCAATCTTATAATTCTGATTAAATGTTCTGGCCTCAAACTAATTTTTA
AAAGGCCACTAACTCCAAATCTAGGAACAAAACACTCTGTAAAGACTCTGTAACTTGTAT
AAAATTAACTTGAAAAATTCACTCACTCCAATAAAACTATGATTTATGTAGCTCATAAGA
GGGTGAATTTTGAATATTTACTCTATGAAAAAAGCCTAAGCAATTCAATAAAAACTTGAT
AACTGCACGTTTAAGTTTGCAGCATCTTGTACCT
Sequence 734
NGCCCTTTCGNTTTNNCGCCCGGTCAGGTACTTTCTCTGAATTTCATTAGCTACATTAAA
AAAAGAAAAGATCAAATGCAATAGATAGCACTGTAATAGATTTTGCTACATTAAAAAAAA
TCCATTTGAATACACAGTGAACTAAAACACCAGAGTGGCTAAAAAGTCCCTTCATGCATA
TTTACTTAGCAGAGAGCTCTTGAGAAAGACCCAACCAATAAACCCCAACCAAAGCAAATC
CAGCTACTTCTCTAGCTGAGAGGGTGGAATGACTCCAAAATATTGTTTCAAGCTCAAAAA
GCCTAAAACAACTCCACATAAAAAAACAAAAATCTATCTAATTGGACATTTACCTTTTTG
GAAATAAAAGGCCCAGTGGGAAAAAAAAAAAAAAAAAAAA
Sequence 735
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ACAGGCTGGGAATTTCCCAAATCTTACAAGTTCTCGTCCCCTTTCCCTTAACAACTCTTT
CGGAGTATCTCCGTCCTTTCACACTTTATTGTAAGCGAGGAGAGCAGCCAGGCTGCACCT
TTAACATTTCATTCACAGGATCTCAGCTCAGCCAAGTCCTCAGCCATTTTGTAATGAGGA
TCACTTTCTTCCGGTTCCCCGTGACCTGTCCCTCGCCTCCTCTAAGCCTCAGCAGAAAGG
CCTTCAACATCCACTTTTCCACAACATTCTGTCTATGATACCTGCATTCTCTGAGATGCT
AGAAGCTTTCTCTCCAAGCTCTTCCCTTTCCTNTCTGAGCCTTCACCCGAGTC
Sequence 736
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTGTCTGCTTCAATAAAATTTGTCTTTGATT
TCACTGGTGGAAGGGTGCTTGATCCAGCTTTTGCTTCTCCATGAGGAGGACTCTGTTTTT
CAGTTTCCGCTTTTATTTCCTCTGAGGGGAAAAAAAAGAAGCATACATTANAAAACTGGA
CAGCAGAAAGACTGAGTAATTTCTTAAGTTCTATAAACTCATTTGGAACTTCTACAAAAA
GTTGGAAAGAATGCAAATTTAATAAAAATTAGATGCTAAAATTGTTTCATCTAAATTTTT
TAATTTACACAAATAACATAAAACTATATGAATAGGTACCTCGGCCCGCGACCACGCTAA
GGG
Sequence 737
NATTTTTTTTTTTTTTTTTTTTTTNGTTTTGAAAACCCTTTATTCGGTTTCTCAGTAACAGT
GATGCATTATAGAAATTCTTGTCTGCTAAACTTCATAGCAAACCGATCCCAGTCCTCACC
TNATTGTGTGGTAGCCCAGCAGCAGAGAAGATAGGAATTTTCTGCCCCCTAGCAATACTG
TTCATCCCATCAGATGGCCGAAATGCCAGTCTGAATCATTTCCTCTGGGTAGATTCNACA
TTGAGGGTTGATTGGCTGACCTAATGTNTTTTCCAAAAAGGAAAATTTCAACAAGTTGCC
CGCATTATTCATGAATGANAATTAGATNTCATATCAAATTAAAAGAAANGAAAAAGCACC
AGANGACCAGAACTACATAAAGCATCTCTTTACTACAAAAAA
Sequence 738
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CACCTGCCGTGCCACTACACATGGACATAATCAACTGCTAAATTATGATTTGTTTTCTTC
CAGTTACTTTTCCAATTATTTTTACATATACAAATATTTTCTTGGTAGAAGAACAAAAGT
GGCACTATTCATTGTGTAGTTTTTTTGTAACTTATATTTTACCCTAAGCATTTTCTCGTT
GTCTTAAATTATTAATNGAAAATTATTCATGGCTAAATAATGCCTAGGCTGCCATGAGTC
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ATGATTTCTTTGGAATAAAATTTCTAAAGTTCGCTGGATCGAAAGAATCAGGGATTTTTA
AGTGTTCTTTCAATTTGGCAAAGTATTTTTTCAGAAACAAGCCCATTTTAAGTTCTGAAT
AAACAAATTCTTTTTTATGGNGCATTTAAAATCTACCTCCTTGTAGCCATATGCNNGGGA
AAAATGGAATTATTTGGNCAACCATGCTTTCAGATACTTGGAAGAATTGGTCCTAATTNC

Table 1

TTCTTTATGACCTATTCTGNGTTCCTGGGACTNTACATTAATCTTTNCCCATGGATATTT
ACCATTGGAAAGGG
Sequence 739
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CTAGCAATGGTCACCCCTACATACTTCCGCACACATCTTTCAAGAACAGGACACCATTAC
CACACCCAAGAAAACCAGCATTTAATGAATTTATTCAGGAGTNTCATCCAACATACTCAA
ATTTCCACAGCTGTTCCGAAAGTATCCTTCAATTCTGGATCCATTGATGGNTCACAGGTT
GTATTTGGCTGTTACATCTTTTTAGTTGTTATCCTTCAGAGTAAAACTGGCCTGCCCCTC
TTTCTTTCTTTACAATATTGACTCCTTTGAGGAACCGGGGCTGGATGTGGAGCATTCTCC
ATTCATCTGATTGTTTCCATGTGACCAGATTCGGGGTCACAAAATTTNTGGCAAGAACCC
TTCACAGATGACCATGTNTTGGTTATTAGGTAACAATAGATTCTCAAAGTAGAGAACTGG
GAAATTGACCTTTGTCCATTCACAAATAGAATTTTTTTTTGAAAATCTAGAATTCCTCAN
GAATNAATTGATTTCTTTTCTNTTTTCTTTTTT
Sequence 740
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACATTGTCTGCATTTTGAGATTTTCCTATTAT
CTTTCTGGTGTTGATTTCTGTTTAATTATACTGTGATCTACAAGCAGCACTGTATTATTT
CCATTCTTTTAAATTTGTTAAGGTGTGTTTTATGCTCAGAATGTGGAGTGGACTATTTTG
GTGAGTGTTCCATATGGACTTAGAAGAATGTGTTTTCTGCTGTTGTTAAATGAAGTAGTC
TATGTATGTCAATTATTGTTTGATGATTGATGGTGTTGAAATCAGTTATGTCCTCACTGA
TTTTCTGCCTGCTGGATATGTCCATTTCCAATAAAGGTGTGTTAATCTCTATCTATAATA
GTGGATTTATCTATTTCTCCCTGCAGTTCTATCAGGTTTTGCCTCATGTAAGTTTTGGAT
GTTCTGTTAAATGCATACACCATTAAGGACTGTTAGGTATTCTTGGGGAATTGACCCCTT
TGGTTTCTATGTAATGCTCTTCTTTATCATTGGATAACTTTCCCTTGCTATAAANGCCTG
GTCTGNCTGGGAAAAAAANACACAGGTNGNTACNTCTTCCCTT
Sequence 741
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GCTAAGATGAAAACAAAAATCTCAGGAAATTTATGTTTATAAAAATGATACTTGCAAAAA
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GCTCAAAGAACTGCCCATCAACCACTTGGTTTCATCTTTGGACACCACACTGGTTATCTT
NCTTTGGCCTCTGCCATAACGGGTCCAGGCTACGTGCACCAAAGGGAAAAGAATTGGGGT
NCTTCTTCCCTNCCCTGGTTTGGTTAGGA
Sequence 742
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTTTCCCTTGCCTCAACTTCTCATCCTGGGT
GATGAGACTGTTACTTTCCTTCTTGTATAAAGAGGGCAACTTTCATGTAGAAATTTTACC
TCCTACTTTTAAGAAAAAGGAAAATCAGAGTGCTTTAAAGGAAAATCAGAGTGCTTTTCT
TGCATCTGCTATTTTTCAAGTGTCTTTAACTCAAAAAAATCAATATGCCAAAGTGGCATG
TTTGGGGGTATCTGGTTCTGAATTCCTTCAGGAAAGATAGAAAGCAAAAGCAAAATAATA
GGTTTAAAACTAAAAATATCCAGGTGCGGTGGCTCACGCCTATAATCCCAG
Sequence 743
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CAGCCCACACCCGGCTCCTAAAGACAAGAGAGCAGAGAAAGCAGAATGGTGTTTAGAGAC
CATCGCAGTGACCTGATCCTGAAAGCACCTGTAGGAAATTGGCCTCCGCCAAGTGAATGT
GACAATGCAGTCAGCCACAGTGACGGAGTGCAAGATCGGATCACCACACAGATCCAAGAG
ACCGCTCACCACACCTGAGAAACAAGAACCCAAGACAGCCTCATGGAGGTGGAACCGTGC
TACGCAGTTATGGCTTCACTACTGAATGCGATCTTGCAAAAG
Sequence 744
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AGATATTCATTTATCTTCCTCGTATTAGACTGCTTGTAAGAGACTCAGTGTTTAGACATT
CATTTCTCTTCCTTGTATAAGACTCCTTGTATAAGACTCGGTGTTCATTTATCTTTTTAA
ATTAAACCACAACAAATATATGAGTTTTTAACCATTGCAATGTGCAATAAATAAATATAT
CTGAAGTAGCATTAGCCTTCTAGTTTTAAATAATAA
Sequence 745
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTTTTTTTTTTTTTTTTTTTCGTCAAAGTCA

Table 1

CTATTTGGGCCCTAACATAATCCTGCTCAGAGCGACGGAAAAAAGGCAAGCCTTTTCAAA
CATAACTCTCTCTACAAGCCAGCTATTATGGCAAGGGAAAAAAGAAAGCATCTAGATAAA
TATCTATCAAAATTAACTTTAAGAGAAATACTCTCTTTCCTTAAAAGCCCTTATTTTTTA
AGACACTAGAAAATAAGTTACTATAAAAAGTGGTGGTCTGGGGGCTAAAAACAAAACAAA
AAAAATCCTCTTTTCTACATTTTTTAGTTTTCT
Sequence 746
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTAGTTAAAATGCT
TTACCTCAATGGTTGAGATATTTTGAATGGATTTTTCAAGGGGGGGAAATGCTTATTATA
ATAATAAACCAAAATACTTAACAGAAAATTGTCAGCTATTCTGACAAAAATAAACATTTT
GAGAGACTTTATTTCTTTTGTCCGTTTCTGTGGTATCACTCATTGTCGTTAAGTAAGTAA
AGCTTTTTATATTTAGGTAAGAACTGATTTTATTTTTTAAATTATATTTTATATTTATTA
GCACAGAAGAATAATGAGAGCCACATTTTAGTTCAACT
Sequence 747
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCTTTTGTTTAGGTATTTCCCTCCTGCTGTG
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TACCAGTCAGCATCCCAATTAAATATTTGATGTAACTGTGATCTTTGAGCCAGGCTTATA
TATTCATTTTCAAGCAGAGGAGTTCCCCATTTTAAATAGAGGCATTGTCTGATGTGTTTA
TGGTTAACTGCATCTGGCTTGGGTCTTTCTGTTTTCCTTTCTTTGCTGAATTAGAAGGGG
TTACTCTGAAGAGTCCAGGTCTTACAGTGTGGTT
Sequence 748
CCCTTGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
NCATNCAANAAANATAATTTTACNCTTATTNTTTGAAANANAAATTNTANGGAATTTTCT
TCTTCTAATTNAATNCCANAATACNTTCTNTNANCCCTATGCCCTNATACTANTANCTTG
ATGGTTAGCGGGTAAGTAGGTAGTAGTANAANANCANAANGGGAAATTNGGGGAGCAAAA
ANGGGANAAAAANAAAAAA
Sequence 749
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACTCACTACATTACAAAATAGTCTCTAACA
TAAAATTGCCTTAATAACTATACTATTATAGAATCTGATAAACCTTACATTATTAAATTG
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TATTTTAAGGGCCTGTAAACATTCCATTCTATTAAAGCACAGNAGAATAAGTAATGGATA
TTCAACTGCATACAGAATATATAATCAAAAAAACAATTTATTATTGTATTTGTAGAAAAT
CATTACCAGAGTAAGCAAAAA
Sequence 750
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTGATTGTGGCATATTCAACTATGATTTTAG
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CTATTCTACAATGAAATTCAATCTCTTACTTAGCTATTTTGAAATTGTGTCCCAATACCA
CATTAACAGAGCCAAAATGAAATTTAAAATTATGGTTATACTATTATTCACACTAGGTAG
GGTCAGGTTTTTTTGNCTGAATTAAATGGCTCCTTTACNCTAGCTACTTANGAACCACTT
NCCATACCCTNAAGCTAGAGTAATA
Sequence 751
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CATTAACAGAGCCAAAATGAAATTTAAAATTATGGTTATACTATTATTCACACTAGGTAG
GGTCAGGTTTTTTTGTCTGAATTAAATGGCTCCTTTACGCTAGCTACTTAGGAACCACTT
CCCATACCCTCAAGCTAGAGTAATAGATACCTGACC
Sequence 752
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTGGGAGCCAT
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TCTTTTTATGCAATGTTATCANGTAAAAAAATGGCTAAAGTATATTAGCATTTACCCGAG
TGGTATTCTTTTATAGAACTCAGCTACTAAAACCAGGGAGAGTACTTGGTGTATTTCTGA
AACACTCTGCGAAGTTGTGGATAGCTTCTGGTGGTAAGGATGGTATTGAACACGTTTACG
TCTGTCCCCTTTCTCCTTTCTCCTGCTTCATACAAG
Sequence 753
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTATTAT
ATAAAATAATAATGCATCTTACAGGGGAAGTCATAAATCCAATGAAATAAAGTATTTACC

Table 1

TGACATATTTTTCCCATCTTCTTATTTCAACCATTTGACTGGTTGTCCAGCCCCAAATTG
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CATCCCTTTAAAATCATTTAAAAACATGATTTTTAAATTTATCTCCATTACCTTATTTTG
NGTTTACTTTTTTACTTTTATTTATTTCCT
Sequence 754
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTGGTGGGGAGCTGTAT
TTATTTCCCAGGGCTGTCAAAACAAATATCCATAAATTGGGTGGATTAGAACAACAAAAA
TTTATTNTCTCTANAGAANAACGTTTTCTTGCCACTCCCTGGCTGCTGGTCATTGCTGGC
AGTCCTTGTCCTTCCCTGACTAGTANCTACATCATTCTCATTTCTGCCTCTGTCTTCATA
TGGCTGTCATTTCACTGNGTGCTTGTCTCTGGGTCTTCAAGTGGCCTTTTTATAAGGACA
CTGGTCATTGGATGTAGGGCCTACCCCAATC
Sequence 755
CCCTTAGCGTGGTCGCGGCCGAGGTACATGTTGGAAGGGTTTTTAAAATGTTTTGAAACT
GTGCACAGGCCAAACCCAACTTTCAGGACATGGGTTTTCAACTTCTGGATGGTATGATGG
GGTGATAGTAGGGTATAAAAGTATCCTGAGAAGTTGAAAGCAGTGTGTGAATGGGGTGTT
CTTTTCTCCCCACAATCCTTTCCCATCTGCTGACAGTAGACTTAGCACCTCACAGATGCT
TGGGCCTGGAAATGAAGCCATGAAAATGAAGCCCTCAGCCTTCTTGGAGATCAGAGCCAT
GGTCCTCACCCACAGCACATGGG
Sequence 756
CCCTTAGCGTGGTCGCGGCCGAGGTACACAAAATATTAAATAGGATATTTATTTCTAAGC
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ATAAAAGGAAAAGTATAAAACATTACTCAAGTATATATAGAAAATGAGTGGGCTGCTGAT
CCCCCTCTATATTATCTATTGCTGTGTGACAGTATTACCACAAATACAGTAGCTGAAACA
ACACATTTGTTTTCTCACAGTTTCTGTGGGTGAGGAGTTCAAGCATAGCTTGGTCCTCTG
CAAGCTTACAATCCAAGGGTTG
Sequence 757
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GTACCTGCCCGGGC
Sequence 758
CCCTTAGCGTGGTCGCGGCCGAGGTACTTGTTTTAAAACAATGTTGGAAATGAGGAAAAT
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GTTACATAGTTCAGTCTTAGGGATGAAGGGATTTATGTCTCTCCTCCCTCAGGTACGCGG
GGACTACACTGGTGTCTGACTTTTTTCCTAGAGATTTCTCCCTGAAAAATACAAGGGCTG
TTGGTGAGAGCAGACTTGAGGTGATAATAGTTGGCCTCTGGTCTACAAAGATTTCATAAC
TCCTTGGAAAGCTTC
Sequence 759
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCCGATTGCCTCTCCCATGCTTCTCTGCTTT
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CCATTGTGAGTTGTTCAGTCTGAGGAGTTAGGTATAAACCCAGAGTGGTATTCTCTTTTC
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TATATGTTTTTTTCTGTTTCTAGATTTAAAAATATTCCAGAAGCCTGGCCTCAAGATAGA
TAATATTTTACTTTT
Sequence 760
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAT
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TGTTAAATNGATTTNAATGCTNTTTTTGNATTNGTNNATANATTTTTTTAAATTTTTAAA
NCGNGNAATTGGGTNNTTTAATNGGGNGTTTTTTTTAAA
Sequence 761

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTACAGATATAAAAAGGCTACTATTCCAAGAACAAAA
TCCTGGAAACAAATGTCTATCAAGAAAGCAAAGATAATCTAAACAGCAGCATATTCATAG
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AAGAGTTTCCCAAACTATCATGCTAAAACAGTAACAGCGAGCTTCCAAATTAATGTTGCC
TTTTTTTTTTTTTTTCCAAACTGAAAGGAGGGTGGGGAAAACAAACGCATCATATGTAAA
GCACTGAGTCCAGCCT
Sequence 762
CCCTTCGGCCGCCCGGGCAGGTACGCGGGTATGGTTTTACGAACAAATTTTTAAGGAAAA
AAATTATCATGGTTCTAATCTTACATGTTAACATTTCCTTGTTATGTAGGGATCAGACTT
GTTATAACATAATTCCACTTTATAATTCAATGAAGAAGAAAGTTTTGTCTGATTCTGAGG
TATGTAATATTTCATTATTATTACCATATTGATATTCTCTATATAAAAAAATTTACATAT
TGTAGTTTTCAGGTAAAAGCTGTTGTGAACATTATTTTTTGTCTAGTGTAGTTAATTTAA
AAAAAAAAAACAACTG
Sequence 763
CCCTTAGCGTGGTCGCGGCCGAGGTACGCCTAAGGGANGNNNGGAACTCATNAAAGAGAC
AAAANGTGCNTTTTTGNTTNNAAGGCATGCTGTGGTGGTTGGGCGCAATAAAATAGTTGG
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CNCACCTGNCCANTTCACAAAGACCTTGNCCCCATTCNTGGGAATGNAAGGGAGNGTTAA
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CCTGGAAAATTGGTTTTAAAAGGGGGGGNAGNTNGGGATCCAAAACCCTGGGGGGCCAAA
ATAAGATACAATCCGTANCTTGTTNGGGAAANTTCAAATTTTAATTGTTCCCCCCAAGNA
TTNGAATTANNAAAAAAAACCCCAAAATTTGGGGGAAGGNAAAAAAANGT
Sequence 764
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CGCGGGATTCATTTGAGTGGGAATCTCAAAGCAGTTGAGTAGGCAAAAAAAANGAACCTN
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NAACNTTTTNGTTTTNNAACCTTTTTTTTTTAANGNCCTTTTTTTTGAAATCCCAAAAAA
AAAAATTCNTTTTAACCTTTTTTTTAAATAAAGGGGGAAGGCCAAGTTTTTTTTTCAAAA
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ACCTTTTTTTNGAA
Sequence 765
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAAGCAATGTTTTTTGAAAGTTTTCTATCTGT
GGNTTGTTGAATCCACAGATGCAGAACTCATGGAAACAGTGCCCACTGTATGTCACAATT
TCAGAAAATCAGTATTTCATACAATCANGCTAATAGCCTAATTTGTTGAGCACAAGAAAA
ATACACTGAACCAATTCTGATTATTGCANGAGAAATGATTGGCAGGATATTGGGAAATAA
GAATGAAGGGCGGANAGAATTTCACATGGATTCAATATACTCTCCGTCAGNGAATTTTTG
TT
Sequence 766
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAAGCAATGTTTTTTGAAAGTTTTCTATCTGT
GGTTTGTTGAATCCACAGATGCAGAACTCATGGAAACAGTGCCCACTGTATGTCACAATT
TCAGAAAATCAGTATTTCATACAATCAGCTAATAGCCTAATTTGTTGAGCACAGAAAAAT
ACACTGAACCAATTCTGATTATTGCAGAGAAATGATTGGGCAGGATATTGGGAAATAGAA
TGAAGGGCGGAAANAATTTCACATGGATTCAGTATACTCTCCGTCAGGAATTTTGTTCCC
TTGATCTTTTTGTGGTTTAATGCCTTAATTTATTGGGGCCCCTCTCATANGTTTGGGGG
Sequence 767
CCCTTAGCGTGGTCGCGGCCGAGGTACAATCAAAGGAGTCTAATGGAACCAAGTAGCAAT
GTTCCCGAAAACAAACAAACAAAAAACCCCAAACATTTTGCTGTTTCTTTCCCCTCTGTA
TTTGCTAACTTTATCATGACTTTATTCTTAAAGCCTATCACTGGTCTGCTTTTATTAATA
GATTAGTGGAAATTTTCACCTGGCCTATTAGCACCTTATAAAGAAATAGATTAAGAGTAG
GAAATATATAGATGAAGATGTACTGTATAGAAGTTGTGTAAAATCAGTATGAAAGTTCAA
TGTTGCTGTTCTTGCTCAGTGGATTTTAAAGAAATTGAGTAGTTCCTATGTGGATTTTTT
TTTTTTCTTTTCTAAACTG
Sequence 768

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACATATACATTATGTAATNNANAAGCGTGCATG
GGGATGAAAAAAAAATTTTTNNTNTATAATCNNGNTACAATATATACAATAAAACACCTA
AAACGCAGAGGCTTGCCTTGTTTNTCCACAAATANGTTAAATACCCAAATTAGTAATTAA
ATGGATTGGTGGTTATGGTAGGAACACCAAGACNAAAAAGCCAGGCCGGGACCGTNATTT
TAATTNNGGGCCAGTACCACCACNATATAAAGGCCACCAACCAAAAAAAGTCCANANANG
CCAANAAANAAGNCAACCGCCCCAAGTTNAAATNGTTTTGTTGGGGAATTGNCCCAGTTA
NTTCCAAAANGGAATTTTTGGTNCCCANTTANTTAAGGAACCAATTTAAATAATTCCCCC
AGGTTTANGGAACNACCTTNGTTNAAATTAAGGTTTTTTTTTTTGGGGTTNACCCCTTTC
GGGGGCNCCGCCNGNAACCCCANNCCGTCCNTTAAAAGGGGNGGCCCGAAAAAT
Sequence 769
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTATTTTTTTACTAAGGTTTTGTTTTGGAGA
CTTGTTTGAAATAAAGTGATCCTCATTCAGGATTTAGAAACAAAAGTTATACTCCACATG
CTAGGGATTAGGAAGGCTAATGTGAACTGATCAAAAGTATGAATTATGGAATGCCTTTAG
AATAATCAACTTTTAGGTAATTTGATACTGCTATAATTTCAAGCTTAGAGAAAAGTTGTA
AGAATGGCATAAGGAACTCCTATATATCC.TTATCTAGATTCACTAAATGTTCATTTTGT
GCCATTTGTGTTATTCTTTGTCTCATCCTAGCCCAGTCAGCCTAACACCACCCAGGGGAT
AAACCAGTAGTCTGATA
Sequence 770
GATATCTGCAGAATTCGCCCTTTCGAGCGGCCCGCCCGGGCAGGTACCTCTCATTTGTCA
CTTTTCAACACTTCCTGGCAGGCAGGCAGCATAACTGGTCCTGCTGGGTGATCCAGACCA
CACTCTGCAACTCTTTCTTCTGAGCCAGGCTCCCCTACTGTCTTTTCATTTATGTCAAGG
CAGGGGAAGACCTCAAAGGGCTCTTGCATCCCAGTCTCACTTCCCAAGAGAGGCACGAGG
CCCTCCAGGATGTGGGGACAGGAACTTTGGGGCAAGCCCGGGGCTGTCCAGAAGATCACC
AGGAGGGCTAAATAGTAGAAAGGAAAAGTCTTATTGGTGATATGTTTGCAAACTGGGAAA
AAGATAGCCTCCAGTGTGGAGCAAAGATGCTCCTTCTTCAAAGAGGGCAAGGGCAGCTTG
GATTTTGTGCCTTACANGGTCNGTATTATATAATAGAGTCATGCATATTCANTAGGTTTG
GGGGAAAAGCTATATATATTTATGAAGGGGAGCCAACTACATGGGCAATGGATAAACATA
CATGTAACACATCCATGTTCACTTTAGGGGCA
Sequence 771
GGATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACAAATAAAGTATTCCA
AGGGNGGNAGAATNGAAAANGANGNCTNNCANCTTGNTNNCNTTTGGGAAATTGGGATAT
CCTTTGGGGAAATGTAGTAATCAGTATATTCTGGGNAAAACATTAGTTAGAAGAATTGAA
NTAAATAAAATTTCCATTGAATTTGGAATATGTTGTCCATTCTCCCTGTAAACTAATGCT
ATCAANGATAAAGTANGAAATACCACATTTCAGNAAACAAGCTTGGAAGTAGNACAAGGT
CCTTCATTAGNGCCNTAGCCTTGGNAAACCCTTAATAANCCTATNTAAATAAAATTGAAA
ANTTTTTAAATTTATNACTCCTGG
Sequence 772
TGCAGAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACCACCAATAATGAGGCCCACATT
GTGTATGCTAAAAAAAAAGTGNTTTTNNTTNTTCCTTGGGCCTACAAGAACATGTTTCTG
TCCGCTAAGGAGAAANTNAAGAAAAACAATGGCCCCCTTNCCTTCCCNATNAANCCCAAA
ANCCTTAAAACNTCACAGGGGANGTTGNAATTTTAAGGAANTCCACCCCTTTNTNGGGGN
NNCANTTTTTTTCCCCCCCCAAANAACCCAACNCCCCATTTACCCTCCTTNGTTAAGAAA
TTTTCCNTTGGAATTNAATNGCCNACCTTCCTTTTAAANAAGGNANAAGCCCTNNACCNA
AGGCTTTCTTTTTCCCCCCCAATTTNCCCCCCTTNATTCNTTGGAAAAAANGGCCCNAAC
GGGGGAAACCCCCCACCCTTTGGGCCNTTTTTTGGNGGGTTCCCAAGGGGGAAAAAAACC
AAGGGGCCNATTTANCCNAAAACCCAATTCCCANGGANATTGGTTTGGNAATTTTAATTA
AAAAAATTNGGGGGCCCCNACCCATAATTTTCTTTAAAAAAAANGGTAAAA
Sequence 773
CCCTTAGCGTGGTCGCGGCCGAGGTACTATCATCCCCCAAGGCCTTTTACAGTCTGAAAT
ATCAAAATTGAAAGCAAAAATAGGATGACCAAAGGACTACTATTTNACTCTCTTTTCAGN
AACNTCNTACAATATGTATGAAAACCTAAAATATCCACTNTATGGGATCATCANNGGGGG
GAANNTAAANTGTTGCCCNTGTTTTNGNAAANGGGGCATTCANGATGTATTTGGGATGTN
CNCANGGNCCTGGGGCANTTTTATNTCAAGGATGNAAGGGGNTNNCATTAACCTGAACCA
AGTGGANTGACANGNGTCTTCNCNTTATAAATACCAANGGGGCCGNGTTNTGGCNAACCC
CANGCCACCCCAATTGGAACCTTATGGGGGGGCCTTNGGCCNTTTTTTANAAAANAACCA
AAAAATTTTTTTCTTAAAGGGGGAACCTTTTACCCGGNCCTTCCTTNTTTTGGGGGG

Table 1

Sequence 774
CCCTTTCGAGCGGCCGNCCGGGCAGGTACATATACATTATGTAATTAAAAAGCGTGCATG
TGTATGTATTAAAAATAATGGTATATAAAACAAAATTACAATTATATACCAAATAAAAAC
CACNCTAAACGCCANNAGGGCATGCTTGTTTATTCCCACCATATTAGNTAATAACCCAAA
TAGATAATTAAANTGGAATTGGGTG
Sequence 775
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTGAGAGGGGTCATC
CTCCAATCATTAACTACTTCTAATCTTCACTGCTACACAGAAGTTTCCAATATTTAGCAA
CAGATGGCTTTGCTTTTACCTTATAGATGAGGCCAAAGCACCAGGTAGGTGGAAGGTTCT
TGTATCGGTTCGAACCCCNACAGCGCGCCAAC
Sequence 776
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTGGNCTGCC
GTGGAGAGGATGGATGGGAGGGGGAAGAACGAGAGCTTTGTTTAGAGGCTGCTGTANTAA
TCCAGGTAAAGGCTTTTAATCATGTCCTGAACAATGATCAGCAATGGCAATGGANATGAC
AGAACANAATTTAANAAGGAATAAAAAAGGCTTGCTGACTACTTGGATGTGGGTGANG
Sequence 777
CCCTTAGCGTGGTCGCGGCCGAGGTACTGCAAGCCAAATGCAATGAACAAACCAAGGTTA
TTGATAATTTTACATCACAGCTCAAGGCTACTGAAGAAAAGCTCTTTGGATCTTGNATGC
ACTTCGGGAAAGCCAAGTTTTCCGTAAGGGTAAAATCGGNAAANTGAAAGNAAAACCTTT
AAGACCAGNCAGCTTTGAAGGTCAGCCTTGAGTAANACAGNAATTTAATACCAATTTTAA
GAAGGAATTTGGAANAAANGAAAATGGCCTTGAAANAGGTTAGGCCAAAGGGGCCTTAGG
GTTAAGTTCNCTTTAACCCCAAGGAAAGGAAGGCCTTNCCCATGGGGGGGGGAAGNAAAG
NANGNCCTTNAAAAAGGCCCTTTTAACCCTTAAAACCCCTTTTTTCAAGGGGGAAAAAAA
AATTNTTTGGAAAGGTTNGNAAAGGGTCCCANGGTTTCCANAAGGTTNGGAAAAAAGTAA
AGGAACCTTTTTTGGGGGATAAAAAAAAGGGAAACCCTTTCCCAAGTANTTTTTTTTGGG
AAAAAAGG
Sequence 778
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGTTATCAGGATAATACTAGCTTCACAGAAGA
AGCTGGGAAGTATTCCCTCCTCTTCTATTTTTTTGGGAGGACTATGTGAAGAACTGGTNT
TAATAAAAACTCCTTATTAAGGAAATTTTTTAACATACCAAAAAATAGTAAGAATAGTAT
CATGAGTTCCTGTGTTGTATTCCCGCCTAACTTCAATAATTATCAATAGTCCACCATTCT
TATTTTACTTATACTTCCCCTCCCCAACACCTTACTCTTTTGGCGGGGGCTGAAATTATT
TTAAAGTAAATCCCAAGACATATCATTCACCTTTAAATACTTCAAATGTATATCTTCTAA
CAGGATAAAGGACTTTTTTTT
Sequence 779
CCCTTAGCGTGGTCGCGGCCGAGGTACTACGAAGCTGCAGATCATTACGCTGATATGAAT
GACTGCTTGAAAGAACAATGACTCTGGCACAGCCACTGCTTTTCACCCAGGAAAGCAGTT
TTTCACAGAATGGCTTTGATTTATACTTTGCACACCATTGAGAGAATAAAAAGAAAATCT
AAAAGTTAGTCTTAGAGCATACAAACATTCTATATACTATTTCATCAACTTTATGTGATA
ATGATATATAATTTATATATACTGAAATTATTTTCAGGATCCACTTACTGTGCTTAAACC
CGAAAGTGAATGATTAAAGAGGCAATGGAATTATCTAATGTATCTTTTATAAATTAAGAA
ATCAA
Sequence 780
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGACAGTGTGATGGATGATGCTGCTGGTTGT
AAATTTCATCGTGTGTGTCTAATTTTTTTTCCTGTATGAATGGGGTAAAAACAAAACANN
AACTTTTTTTTAGGAAGATTGTAATTTTGCNTGTCATGTTTTTNGTAGGNAATGAGGGGN
ACTCGTTTGNAGTCTTCACCTAACNCATCCCTGNGNAGTTTNTGAAGTTTTGGAAAGNCC
ATTGAAANNATTGTGTTGCCCCCCAATGNCCCTTGGACCNGCCTTNACAGTCCGNCNCTT
NNGGATTCTTGCAACCGTTGTC
Sequence 781
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGGCGGATGAG
TCTTTTAATAGAAAAACACACGTGCAACAGTATCAANACACATTTTTTNGCAATCCTGAC
AGCAGCTGAACTTCAGTTCTTCACCTTGGGGGGTGGCCTGTACATATCAAAATCTATCAA
ATTGGACCCTCAACTATGCATTTTTCTGNGTGCAAGTTATATCTCAATTACAAACAAACA
AAAACACAAAACCCTATGGTTAACCCAAAACCTAAACTATNACCAAGAAATATCAATTGG
GGTTATGGCATGACCATCCTCCCCAAGAAAATAAAATGCTTGACAGATTCTGAGCGGGA

Table 1

Sequence 782
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAATAAATGAGTTTGCAGTGAATTGGGCCTT
CAAATTACCTCAAGTGACAGATAGTAAGAAAAGCTTNTTTGAGCAGGTGGAGGTCACTGA
ATCCCCTACTATGCACTTATCAAGATTTTACTTACTTTAATTTACTGGAAATTGATTTTT
TAAAAAATGACTACACTGTAACAAGGGAAGGGATCTGGGTTTTTTTGTTGTTTTATTCTT
GTTTTTTTTAAGTAGTTCAAATTCTGAAACTGTGATTTAAAAATTTTTTACAGTCAAGCA
TTCTGATTTTGAACATAACTCCCTTCCCTTTCTGTGTAACAAAGGTCTCTCTGTTATCTC
TTAAATTT
Sequence 783
CCCTTAGCGTGGTCGCGGCCGAGGTACTCTTCACTGTCTTTGCCATGAAACTTTATAACA
TGGCTCTCCAGGTGTTGAATCTGGTGCCCTGTCACCCTGTGCTCAGGGAACACATGGCGG
CAATCAGCATGTGAGGCGCAGAGGGAGGGCAAGCTCCCCTTGTGATATTTGAGGTATCAG
CTGACTCAAGTCTCTCTCCCTTCTCTCCTTATTCTCATGCTACCTNTCCCAACCATTGTC
TTAACTTCCCTGGCCAGGATGCCTGCCATATTAAATGGAGAGGAGGCAGTTTCTAAATGG
CTTGACTTTGGTTGAAGTCTCAACTCAGGAAGCTCTGAAATTAATCCACCC
Sequence 784
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACTCGATTGTCAACGTCAAGGAGTCGCAGG
TCGCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAAGTTGAAGATTAGTCCGCCGTA
TTTCGGTGTACCCCTGGGAGGTGCCAGTCATTGAATAGATAAGGCTGTGCCTACAGGACT
TCTCTTTAGTCANGGCATGCTTTATTAGTGAGGAGAAAACAATTCCTTAGAAGTCTTAAA
TAT
Sequence 785
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGAGGATATGTGTGCATTACATGCAACCACTA
CACCATTTAATATCTGGGGTGTGAGTATCCGTGGGTTTTTGGNATCCGTGGGGGTCCTGG
AACCAATTTCTCCTGGATACTGAGGGATGACTGGATTACTGTGTGTTTGTGTGCTTGTTT
TTAAGCTTCAAAAGATTATGTGATCTAGGAGTTGTTAGATTTTATTATTGGTCTTAAAAG
ATAAGCTTANATGTTGTTACTTTTTTGGAGTTTTTAGTTTACAGTGATTTCATGAATCGG
GCAGCTTCANACCACAGGAGACATNAAGCAGGTTTNAATTTTCAANGAAAGGCNTTTACA
AGGCAAAAATATTTTGATTTGGTTTAGA
Sequence 786
TGAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTAAAACTAAAACTGAGCAGTTTAAA
ACATTCATTTAAAGGGATATCTAATGTGTTTATTATTAACATAAATAATGTTTTTATGAA
AAATGTAACCTTNGTTTTCCAAAACAAAAATGTTTAGGGCAAGAGTAACATTATTTTACA
TTATTGCATCTCAGTTGAAAAATAAATGGCAACAAAAATTCTTATATCTGCTTCTGCAGT
TAATCTGNTCATTTTGTTTTGGTTGAANTATATTGAAGGAAATCTGTTCCTCCACACAGT
TTGTGTAGTGGGAAAAAGGGGGGAC
Sequence 787
CCCTTTGAGCGGCCGCCCGGGCAGGTACGCGGGATTCCTGGTTAAGCAGGCATTGCTTTG
CCCTGGAGCAGCTATTTTAAGCCATCTCANATTCTGTCTAAAGGGGTTTTTTTGGGAAGA
CGTTTTTCTTTATCGCCCTGAGAAAGGATCTACCCCCAGAGGGAGNAATCTGTAGNACAT
TCTTTGCCTACTTNTTACTTTTATTTAGGCTNTTCTTCCCTNCAATTTCAATTTTCCTGT
ATTACCACCCTTTTTTCCCCTTTTTTTTGGGGGGGGAAGA
Sequence 788
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGCAGGCCTCCTACACCTACCTCTCTCTGGGC
TTNTATTTCGACCGCGATGATGTTGGCATCTGGAAGGCGGGAGCCACTTCCTTCCGTGAA
ACTTGGCCGTAGGGAGTAAGTCGCCGAGGGTCTNCNAGNCGTTCTTTNCTTGAAGGATGC
ANAANACCCATGGCGTTGNGCGGACCGCGCNTCTTCTTTCCATNGGAACATTCAAAGGNN
AGNCNCAAGTTTTGNATAGTANTGTAANTTTGGGNGGGTTAAAAAACCTNCCCAANGNAC
CGGCCCTATTGNAAAAAAGNCCTTGNCTCCAANTGNGGCCCCCCTTGGGGTAAGTNAAAA
AAAAAAGTCCCTTGTAANCCCCAAGGGGCCCCCCCTTTTTTTGGGGGAATTTCC
Sequence 789
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTAATTTCTTTATAATTTGTTCAGCTATTT
AAAAAGATAATCCACAATCTCCTACCGCCATTAGAGCACAGGAAAAAAAAATTCAAAAAT
AAAGGAAAAACATGGCTCATATATCTACAGAAGTCACAAAAATACTATAGGGCACATATA
CCCAGGCCTCAGCGGTGGGAAGAAAACATACAACCACCGGGCAAAATGTTTGAACACTGA
AGACGGGAATTTTTTAGGGCC

Table 1

Sequence 790
CCCTTAGCGTGGTCCGNNGCCCGAGGTACTCAAGTCGCCCTTATGGAGCCCTTGATTCAG
GCTTCAATAGTGTGGACAGTGGTGATAAGAGATGGTCAGGGAATGAAGTAAGTGTTTTTT
ATGTTCCGTGTGTTATAACACCTGATTAAGAGAAAACAGAATGATGAAAATGAAAAGCCG
TCTTAACTGGATTCAAGTTTCTCACTACATAAAATACAGAAAAGTCAAGGTGGAGGCAAG
ATTCCCACCCTCTCCAGCAGAATTGGCATTCTGCGTCCTTACCGGCTTTCTGTCACGTGG
ATTTCCGCCTGTTTCCTCATTGCCTCATGGAAATAGTTTCATATCATAGAAAGGCAAACA
GGAGCTGAGCCAGTTTGAAACTGAACCTACAATCTGAGGTGGGGGTAATCTCGAGCAGA
AGTGCTAGATGGTGAAAAAACAAGTAGGACTTTCGGCTGATGGGTAGAAACAAGGACCTT
NGTAAAGAATATTCATGTGCTCAAAAAGGAATAACTTCCTGGCTAATTCTTGCGTTTTTC
TCGTTTTTAAAATTAATTGGATATTATGTTTTCTGCTCTTAAAAATTACTNNGTNCACAG
AAGTCTACCAAAAAAAAAAAAAAAAAAAA
Sequence 791
GATATCTGCAGAAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTAATTCTTTTCCTCT
TTCCTAGACCGATTCTAGTTTGTTGCCTTCCCTTTCCTCGGAAACCCCAAGTTTGTGGAT
GCTGCAGACACTCTGTGCCCCCCTGCATGCTGGGTGCCTGGCCAGCTGCCAGGGCATAAA
GACAGAGACGATGTGGCCTTTGTCCTTAAGAATGAGGTTTGAAAGCCTCAGTTCTTCCAT
GTTAGGTGATTNCTTGCAGCTCTTGGTATCTGCAGAATTAGTGTGAATGCTTAAAAAATA
TTAACAGCTTTATATCATCAAAGTTTTAACAGTACCTGCCCGGGGCGGNCCGCTCGAAAG
GG
Sequence 792
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAA
GCTGAAGGCCACAGTAGCTAGCTAAAGGCCACACCACTGAACACTAAAACTTAACCTTTA
CTGGCTACTTTGTANATAACATTCACAGCTCACCATGAATGCAGCTGCAGTCAACTAACA
NATATGAAGTTACCACTGTATTACATGGTTATATTAGGGACTGCTTNTACCTACTGGAGG
CTGGGGAGGAATGTAACAGCACAAGCCATAATGAAGTTTATATACAGGCTTAATATAAAA
NAAAACCCTAGAATGAACTCAACACAATTAT
Sequence 793
TTTTTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACCATGCAGGGATAGCTG
AGTCTTCATCCTCCTCAGCCCCTATCTGTTCAGTGCACTGAACACCAGCTGCTCTCTTCC
TCTCTGGCTCCCATGGCAGCCATGGTCTGTTGCAGAGAGAAGAGGATTGCCTGTTCCCTC
TTTAAGGGAACCTCCGTTTTGCTTTCTGGAACCAC
Sequence 794
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACGAACTTAAATTTATGATGAATATCTTTGAT
AATGAGAAATCCTGAGAGATTTTACTTTCAATTTTATTTTAATTTGAAAGAGCATATGAC
ATCTGGAATATTTTTAACATATAGCCATACTGTTTATTTAAATTTGTAATAATAGAAATA
GAGTAATTCTACTGTTGGATTTTAATTTTTAATCATATTAAAGTTTAACTGGATTTTATT
TTAGGACTAAAATATTTAGGACTAAATAAAATTTTATTAATTAATTTAGGACTTTTGGGA
AAAGATATTTCAGAAGTTCAGTGCATATCAAAAAAGCGAACAACAGAGGCTTCATCTTTT
GAAAACTTCATTGGCTAAAAGTGTCTTCTGTAATACTGATAGTGAAGAAACTGTTTTTAC
ATCCCGAGATGTGTTTGATG
Sequence 795
CCCTTCGAGCGGCCGCCCGGGCAGGTACCCTAGGTGATCTTTGGCTTCCTCAAGTTTTTG
CACCACTCAGAATCATTTCATATACCACCTTTGGCAAACATGCCAGACCTGCAGTAGACT
GAAGGAAGCTCTCCCAAGCTCTAAATTGATTAATTTATTAGTTCCTAGAAGAAAGAGATT
ACATGTTTATCTTTTTGTTACAGAAGAAACTTTGAATAGCAGTTGAAAATTTGGCAGGGT
GGACCACCTAACTTGACAGTGTATTATTGTGTCTGTTTTGAAGGAATAAAATGGAATTAT
TTATAAAGTTTTCATTTGTATTAGAGA
Sequence 796
CCCTTAGCGTGGTCGCGGCCGAGGTACACTATCTGACCTAATCCTCAACACAAACTAAGG
CAGGAGACACAGGGCTGCAAGGACATTTGCTGCCATCCAATTTGTGCCAGCCTGTTTTAT
CAATCTGAACCTATATTATTTTTAAGACCTCACGGCATCACTGAAAGATGAGTATTATTA
GTTGGAATTTTAGGGATGAGAAAACTGACCCTCAGGGAGAATAACTGACTTGCCCCGGCT
CCAACAGTAAGTGGCCCTGCTGGGATTTGAACCCAGGTGTGTCTGACCCCGAAGCCTGAT
CTGACCTCTGACAGTCGTGATAAAAATAAT
Sequence 797

Table 1

CCCTTGGCCGCCCGGGCAGGTACCGAAAAATGATTTTGTTATATATATTTACCACAATAA
AAAAGTTTTAAATTTATTATAGGTGACACTGTTTGCTCACTGTAGGTCAGGTATTTTTTG
GTTTTTTTTTCTCTTTATTTTATTTTTGACCAATGGATTCACGTCACCAGGTGATTTTTT
AAACAGCTTTATTGAGATATATATCACGTGCCATAAAATTCACCCATTTAAAGCACACAG
TTAAATGTTTTTTAGTATAGAGTTCTGCACCTCTTATGACAATAAATGTTAGAATATTTT
CATCACTCAAAAAGAAACCAGTATCCATTAGCA
Sequence 798
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATTTTTATGTTTACAGCTGTAACCCCTGAG
TTATCAAGAGATGGAACATTAGATATGATTTATTCCTATTTAAGATAATAGGACATTGCT
TGATTACATTTTCAGAAGATATTTATCCAAAGAAATTTTTTTTTTTAATCTAAAGGAAAG
GTTTTGATTCTTATGAGAAAAGAATGAGATTTCTTTAACTGGAAAATTGATTTATGTCCT
ACAGTCCATTGTGTAGTGATGTTGGATCAATCAGGTATCNCTAGGGTGTCTGNAGAAGTA
TCTATATATTGCTTTTTAAGTTCTTAT
Sequence 799
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCATGTAGCTCTACTTTTCCATATACAGAGTT
GTTTCCTAGCTTTCTGCTAATCTAACTGGATTCCTCTTCCCCATTTCCTCATTTACTAGA
TTATAATGCACATCACATAATAAAAGCTTAAAAATGGGCTTTCACAGTTACTGTTTTCTT
TTTAAATAATTGTGAGAGAGCTTTTGCATCATTTATTATCTAATCATGATTCAAGTGACT
AGGCTGTAGCACCCAAGAACCTTGCCTTAAAACAGTTTATTTTACCCAATAATACTACTT
TGCCTTCTTACTTAAAAATGTCCCGTGCTTAACCCTTTTGCTCTTTATTTTGATTTAAGC
ACTTGACC
Sequence 800
CCCTTAGCGTGGTCGCGGCCGAGGTACTNTCTATTTTTAACAAGGCTCCCTCAAGATATT
AATGTGACAAACTTACATAGCCAGCTGTAAGATAATTCTTTCAAATGCGCAAGTAACCTA
ACAGATTTGTGCATGTCAGCCAGTAATTTCAACATACATTATAAATATGGCCAATTTTCC
CAAATTCTAAATGAATGGAGATAAAATGCTATATAATAAATATGTTAGAGCACCTTTCTT
GAGAAACTTNTAAAAGGAAAAAATAAAAGACATAATTATACTCACACCACCAGTAAAACC
TCTGGTCACCTGTTTTGGGTTGTGGGAATGCCCCCAGCAGCCGAGAGACCTATATT
Sequence 801
GATGGATATCTGCANAATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTGATTATTCTCC
TGCTTAGGGAGAAGCGGAAGAAGGCCCTTGGAACTGTGAGTTTTGCATTCCAACTTGCTA
ATTCAACATAGATCCTAATTCCTTAAATGCTTGTAATTAGAAATTCTCGTGAACTGTATT
GGTTTTTGTCAAGCAATCTGTTTGGGGAACTTGAGCAACTGGGGCACTGCTGGCTAGGGT
GAAGTTTATTTAATTTGGTTTTATGACATTCTTCATCTTGGAAATGGGGTTTTCAAATAT
TGCTTTCCCAAGCATCATTACTTATTTGCTGGTTTTTA
Sequence 802
CCCTTTGAGCGGCGCCCGGGCAGGTACGATAGGCATGCAATTAAAGAAGACCTGCCTCAA
ACATTTTCTGTGTGACCTGAGGCANGTCCTTTTATAGCTATAAACTAGGGACAATATTTG
CTGTCATTTTTTCTACAAATGTCACAAAGAACAAATTTGAGCCTGTCGCTGTGAAAGAAC
TTAGCAAATGAAAGCATCCTAGGGAGTGTTTTAGATATCGATATTTTTATCCAATTAACT
TTTCAAAATGAGTTTATTTGCTCACTGAAACTGAAGTACCTCNGGCGGGACCACNCTAAG
GG
Sequence 803
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGGTTCAGCTGTCTCTTACTTTTAAC
CAGTGAAATTGACCTGCCCGTGAAGAGGCGGGCATGACACAGCAAGACNAGAAGACCCTA
TGGAGCTTTAATTTATTAATGCAAACAGTACGCTTGGGAGTCCTCAGCAGGGGGATCATT
CACAGTGAGGACAGACACAGGTGAACCTATGGGTCGTGGAACAAAAGTTATCCTACACCT
GAAAGAAGACCANACTGAGTNCCTNGGCCGNGACCACGCTAAGGGCGAATTCCATCACAC
TTGGCGGC
Sequence 804
CCCTTAGCGTGGTCGCGGCCCGAGGTACCTTGCACAGTGCCTTTTAAATTCATTTTGCTG
GACAGTTGGCAGGCTCTTTCACTTGAGAGGCTTATATCTTAACGATTTAGAATGGAGAGT
TTGGCTCAAGCTCCCTGTGTGTGGTCTGTGCTTTCTATACTTTTATTCTTGGTATTCCAG
AGTCTGGAGGCTTCTCTTTTTAAAAATTGCTAGGCTCCTGCCAAATGTTATAATTTGGGG
ATGTGAGTTCACTAAGAAATCAACTGACAAGAGGCAGATTAATAGGAGAAATGACATCGA
AATTTATTAGCATGCAGGGGGAAAAAATTGATTACCAAATATCCCAGTAGGGTAGAGATG

Table 1

CTTATATACCCCACCTCTTAAGAGAGAGGGAAAGTGGATGATTTTAGGGGAATAGTAAAT
ACTTTTTATGGGAACTCACTGGGCTTGAAGAATATAACAAAGGCCTGGGACAAAGTCTGT
TGGGCCCACCAGAACAAGACAGTGGTTTATGACAAAAGTCTGTTGAGAATGTATTGAACA
GACTTCAATCTTTCTTCTTGGAATATGATTCAAGTTNAAGGAAAACTAGGGAAGGGACTA
GAGGGAAATNGT
Sequence 805
CCCTTCGAGCGGCCGCCCGGGCAGGTCCGGGCAGGTACTATTACTAGGTTCATTGTTTCC
AGAGGGGTGAAACGGGGCTTTGGAGAGGTTAAATAACTTGCCCAGGGTCACACAGCTATT
AAGTGGTAAAGCTGGGATTTACATGAGCCCAGACAAAGAACCCAAGAAGCTAAGCTATTC
TCTTGTAATACCTCCAACATAGGAGGCAAGAAGTGAGGTATTATACAGGTTGAGGAGATA
AAGGGGAGAGAGGCCTGCAGTGCTAACAGGAGGAGCTGGGATTCATCCTGGCTTGTTCTG
ATAGGTCAGTTAGTCTTAGAGATACCCATGAGGTCACCTACTCAAAATGGGGCTCAGAGT
AGCCTTGTCCCATTCTTGTCCAGTGGGCGCAGCTACAGTCTTCCTGGCCTGGAGTGACTG
GAGGCTGTCCCCACGTCCCACTTCAGTGAGGCATTCATGTGCACCCAACACACTTTCTAG
CTTTATTTGCCTGGAGGGGAAGATTCTCCAGAACCTTGTTAAGATGCACAGTGTGGTCCT
CGGACTGGCAGTGTGGCCTCGGCAGTCCCTGGG
Sequence 806
CCCTTAGCGTGGTCGCGGCCGAGGTACACATATATACACACATATATAGATATATACACC
CACATATATATTTGCTGACATTTTAATGTGAAGTTTTAGTCTGGGATATAAAATGGAATG
TATGACATCCTCAAATGTCTGAATACTGTTCACTCCTATGTTTTACATTTAATTTTCCAA
AGCAAAACATTTCAGTTGAGGATTTTATTAGAAAATAAATAATCATTTAGCCATATCTAG
AAACCAGAATAAACAATGCCATAAAGCCTATAGGAAAATGCAGGTCAGATTCATAAATAT
TCATGTGTTTACTTTCAGTACAGGGAGGAATTTGAAGTAGATAGAAACCGACCTGGATTA
CTCCGGTCTGAACTCAGATCACGTAGGGACTTTAATCGTTGAACAAACGAACCTTTAATA
GCGGCTGCACCATCGGGATGTCCTGATCCAACATCGAGGGTCGTAAACCCTATTGGT
Sequence 807
CCCTTTCGAGCGGCCGCCCGGGCAAATTCCCATGATGTCAGACCACTGGAGTTTCCAGGG
GCAACACCCCATAACCGTCCCGCTGCAGAAGAGCATCANANGTTCAGAAGAATGCAAAGG
ATCTCAGTGGGAACGCGGACAGGAGAGCCCCAAACCAACACATGCTAGGGCTCTCTAGGC
CCTTTCAGGCTAGATCTTGACGAGAGAAGAGTAAAGATCTTTCTGAGGTTGGTGCAACTG
AGGAAACGAAAGTTTCGGCCTCTGCTGTCAGATCTATGAAAGGAAAGAACTGTGAACTTG
TCCCCTTTTGTTTTCTTTGACTTAAAACAAAAGAAAATCACTGGAACAAAGTCTTAAAGT
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CTTATAGCATCCACTGAGATTAGCCCGCATAGGATTCTTCCATGTTAGAGCTAAAAGGA
Sequence 808
CCCTTAGCGTGGTCGCGGCCGAGGTACTATCCCCTACCTATAAGGCATTTATAATGTGCT
GGGCATTGTGACACTTTTCATATATTATCTCATGAAATCCTCACAATAATTCTGAAGGTA
GCTGGTATTTTTATCTCCACTTTACAATTCTGAGGCTTACAGAAGTTAATTCAGTGGCCC
AGGGTCACACAGTTTACAAGTGCCACATTGGTGAATATAAAGTAGCAACTTCTAAGTTTC
ACTCTCCCACTTCCCTAGTTATTTTCCTAAGGCATGAATGTCTGGGAAATAGCATGCATC
AGATTTTCCACCTCTTTAAAACTCTTCAGTTCATATAATTTAAGGGTGTGACTATTCATA
GATACCTTTGAGCTAATCTTCTGGGAGCCAATGTAACCGCAATGCACACTGCAAAACAAT
GCACGCTTNCTCTGTAAATTAAAAATGCCAACCCGAGCTTTGGGAAAAGCCCATCTTTTG
ATATGAACAATTAGGGCAGTTTAAGTTTTAGAAATNAAGAAAGTCCACTGGTCCTGCTTT
T
Sequence 809
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GAATATTGCATACCTATTAGAAAAGTCTTTTAACAATTAAAATTGGAAAATGACTGACAA
ACTTACACTATTTGATTTAAATAAATAAATAAATGGTCACATGATAACAATCTCCTGATT
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CANAGGTAAGTGTTGAGTGTTTAATGGGATTTCATATTAAACATTAAGATCGTATTTGAC
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TTTGAAAAAATCACAAATTTCAGTTAAAATTGAATAATTTTATTATAGGTCTCATAATCT
TTTTCAGCTTACATGGAATCAATGTGTCTTGATTTTTATTCTCGGTAATTTTATAAGGCC
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Table 1

AACCTACCGCTGCAAAATAGATTAATATTCACATGGGAAAAATCCTGGNCAAGGGGAANT
TTCNNCATTAAATTNTTTNCAGGGGAGTCCGGTTGGCCANCCAGAANTAAGGTNCTGGGT
TNGGGGGAATGGCTTAAAAGCCCTTGGGAAAAACAAATTGGCCAAAAANGGGAGTTACCT
TTTAATTGAANAANTTTTTTTTTACCCTNAAAAANGGGATAAAATGNACTTGNCCNAAAA
AAAAAAA
Sequence 810
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AATATTCCACTGTGTAGATCTATCACATTTCGTTTAGCAGTTTATCAGCTGGTGGACAAT
TTGGCTGTTTCCATTTTTTGGCTGTTATGAATAATGCTGCTATGAGTCATAGAAACCATT
CCTCTTACTCAAGAAACAGGTTCTCCAGAAACTAAGCTAAACTTGTTTGAAATGTAAATT
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TTTTAACAAGTCCTCCAGTGGATTCTGATGCAATGCTAACATTTGTGAACACTGTCAAAA
TCAAAATGGAGTCACTTGTGTTTAAAAATCCTGACAAATAAAGCCAGGGACAGCTATGAA
GAGAGGGTTCTCATGCATCAATGCCTGATTAACAAAAACTATCCCAAATGACTCTGCAAA
AACCC
Sequence 811
CCCTTAGCGTGGTCGCGGCCGAGGTACAATCATTAAAACTATGTTGTAATACTGTTTGTC
TTTGTATCCATTCTGGCGTGTCTCCATACACTTCACTAATATTTGATATACCTGTTTTAT
ACCAATATAATGCTGCTGCTGTACGTAGAAGCTGTAGTCACCATATCCTCTATTTGTTCA
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AAAACAAAACCTCTGAATAACCCCATTGTTCCTCTCTAGTTATTCCTGGCTCAAATGTTG
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GGCCGTTACTAGGTGGATCCGAGCTCGGAACCAA
Sequence 812
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AAAAATTTAATAAACCCTGTGTGATCCCATTGTAACAGAAAGGCTGATGTTTTCTGTTGT
GAAATACAAATGCAAGGAAAAAATCATTTCTTTGTTTCAAAGGATGCATTTCTTCCATAA
AGAATAATTTGTATTTATTTTTAAGGGTTTATTTTAACTTATACATCANCCTATNTAAAA
TACATTTCAAAATGATCTGTGCTCTTTAAATTACCAAAAGCAA
Sequence 813
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GCAGGGACCTTGTCAGTCTTATTCACAATATCCCCAGCCTCTAGAACAAGGCTGGCACAT
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Sequence 814
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AANATACTTTNTGGAATTGAAATGATACATTATATATACCTATNANGATAATNGNNTATA
NCGNNNCTAAACTACAAATTAGTCATAAAAANGACTTNTGTNCTATATCAATTAAAAACT
GGTATTAAAATTGANTATNATAAGACAATA
Sequence 815
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CGGGGAGCACAGCTTGCTTTAAACATGAGATCCAGCTCAGTGATCATGCGGGGGAAAAGG
CCCGGCATTGCTGGAACTCCTAATATTTAAAAAGATGATGGAAACTTGAAATTTTTATATT
TAATCTTCTCATTTTTAAGTGTTGGCAATGTATTGAAGACTTTGAAGCCTCTCTGCTGGT
CAAACAAGATGTATCTGTAGGCTGGATTTAGTCCACAG
Sequence 816
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Table 1

TGTTCTAACATGATTATATTCATGGTGTTACATAGGCCTCAATTTTTTCACAGAAAGATT
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AGATTAAGTCATCCAAGAAACATACAT
Sequence 817
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GGGTAACTCTTTCCCAATTTTTAACTTTTACATTACAAGTCATTTTCAGAGTAAAAAGTC
ATTTAACAAAGGCAGATAGAAAGGCCTCAAATCCNTGAGGACCAAAAATCCCAACACATT
TTCAAAAGGGAGAAAATTTCTTTAAACTTCATGGGAAAAGTATTTTTAACATAATAGAGA
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TTTCATATTATAAA
Sequence 818
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ANTTAANTTTTTNAANNNTNNTTTTTTTTTTTTTTTTNAATNTTTNTTNNTTTTATTAAAA
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TTTTTTAAA
Sequence 819
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CCCCTTTAAAAGAATCAGGTCAGAAATGCAATAACAATTAGACTAGACTGTTGCCCGTGT
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Sequence 820
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AATGATTGCACAATTATAGGATAGAAATTACTATCTTGTGCTCTAATTCAAATTGCTCTT
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ATCTTTGTTTCTTTCCTTAAAACTTAACA
Sequence 821
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CAAGGTTTGGGCCTGCCACAGCGGATTTCAAAAAGACAAAGCAATGCAAGCCACGTGTTC
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CAATGGGGTAAACCAGAGAGCAGAAAGCCCTTCTTTAAAATGAGCCTACCACTGCTTGGC
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TTATCTAAAATCTTTTTAATTTTTAAACAGTCACCTGATTT
Sequence 822
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ATTGTGCCTGTCCTCCCTTGACTGTCATGCATATAATCAGCATCTTTCCCACTAAGTGAA
GGGCCCAGACTCGAGCACAGGAGCACAGCACCCCTTAAACTCACGAGGGGCTGCATTCAC
ACCATCAGCAGGGAGATTACACTTGTGTCATTT
Sequence 823
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TACGTTTGTGTTCCTGGGAAGAATCTTGGACTCAGGCGTGGGCAGCTGGATGCCTGGGTT
CCTTAGGCTTCCTCCAGGCAATGTAGTTGCCTCTTTCTCTCCCCGCGTACATAGTAAGTG

Table 1

TATGATAGATGTTTGATTTGTAAATTACAAATATAAATTATCACCCCCATTTCCATTTAT
TTTCTTGATATATCAAAATGTGTTG
Sequence 824
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TTACAGGGTGAATCAATGATAATGATCTTTGCAGCTTTCTGGAGTTAAAAAGCATCAAAA
TTGGGAGATATTAGATGATGACATCTAAGTATTAAAATAAGGAGATATTAAATGATGACT
CCTAGAAATGAACCTGAATAAGGACTACCGCAATGTGTGTGGTGTGGGAAAGGACAGTTC
TTTTAATGGCTGGCTGACCCAGCCTCAATTTTCTTGCAGCTTCGCCGACACGAGGTGACC
ATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATA
Sequence 825
CCCTTAGCGTGGTCGCGGCCGAGGTACCTCTCATGGCTTTTTGGTTCCAGCANTGAGGGC
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GTNANGACAAATTTTGAGTTTTAACAAGGACAAAAAGTTGAAAGAAAAGGCACAGTTAAC
AAAAAAGGGTGGCTAGATTTATCTTGGGTGATGGAGGAAATGAGAGAGGAATGCTCTTGA
AAGGTGGTCTGTGGATCTGTCTGAATAG.AAGAGCACAGTNAGTATGCATTGCCGGAGAA
AACGTCCTTGAAGCTGCTTGTCTCATGTGTATGATGTG
Sequence 826
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CCTCTGTTTGGTGTGTGTATCACTTGCAGATGCTGTCTACCACCTTTTCAGTGACATCCT
AGAAGCTTCTCTATTACCACAGNAACTGGCTAACTANANATGATCTTTCCCTAATTTTCA
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AGGGAATATTC
Sequence 827
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TGAAAAATTGTTGATGTAAGATGGAGGCACATTTT
Sequence 828
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TACATTTTTTTT
Sequence 829
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ACAAAAAAAACCTTTAATT
Sequence 830
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TATTTGTTGTAGCTTGTATATGAACATAATTTTCTTTAGAGGTAGTCACTGTTCTCTCCA
GTATGACCCAGGTTTCTTGACTCTGAGTAATGCACCTTCTATAACTATCTAAATTTCTAT

Table 1

TGAAGCTTTTTGGATTATGAGTATGCTGACTTTTCACGATTGGCTGGTGCATGTTTAGAC
TTAAATGTCATATCCTTCATGTCTCAAAGCCAAAATAGTAACATCTCATCTCAGAACAGA
GCTGTGACCACATGCCAATATATGTGTCACAAAGTCTACATATGTTACATTCCTTGGAAG
TCTCCTTAAATGTTTCACA
Sequence 831
CCCTTGAGCGGCCGCCCGGGCAGGTACGCGGGCTGGAAAACTGAACGTGAAGTCACCACT
AGGCAAGCTGCCTGTAATTGAGCTTGCTTGTATATGACCAATCAACCTTTGCTTGTTGAA
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AATCTTTCTAGTCTAGAGCATGTGAACAGAACAGAAGGAAAATCAGGACTCAGTTTACTT
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CAATGGGCTTTCATTTGCTTTTTTGGGCCTTTTTGGCTTNAAANTCAAAGTGTNAAAAAG
AATTGCCATGGNTTTAAAAAAAAAAAAAAAA
Sequence 832
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GCGTATCTCCAAGATAATGCATGAACAGCCAGTAAAGATGAACGCAGATTATTGATGGAA
AGAACACACATGGAGAAGAGAAAAAGCAAGTCCACAGAGCTTTTAACATACACTCCCTCA
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CCAGCTTGAGAAACTATCCACT
Sequence 833
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ATTCACAAAATAAGAAATGGTATTTGGTCATTCTCTGAGTTCAATCTGTGCTCTAGTAAA
TATAACTTGNGAGGAAAAAGTAAAAAGGNCAAGAGTCTAATTCATTTTCAGTTTTTAA
Sequence 834
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CCTGAAGCCTGCTGGGTGGGGCATAGTATGAATACTTGCCCTCATCATCCCCATTTCACA
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Sequence 835
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Sequence 836
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GAGCTTGCTTTCCTCAGCTTCTTACCCTTAGTAAGACCACTTTAGTAGGACACTTAAGTA
TTTCAGTCAGCGGATTTGAATCTGACTTCTTGGATGCATCTGTATCAAAACATACCATTA
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Table 1

CAATAATTAATTTAATTTCAATAGCGATCCCCACCATTTATGTCCTAGGCATCTACACAA
TTGGTCTCTGAGCGAAAACACAGCCTTATCTGCAATAAAAGCCTCTGCTTTGCTTTGGCA
TGTTTTTACAATCCCGCGCA
Sequence 837
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TTAATAGGTTTTCTTAGCTTGACAACTCATTCTCTATATTCACNAACATCTCCTGACTTG
TTCCTTCAGTGGANATACCCTTTTCTAGCCAGAGTTGGCAAAAGTAGCAATAGCATGCAT
TGGCTTGTTTGANAGGCCCTGGGTGAGCCTTTGTTGCATAAAGTAGGAGGTCTGTTATTG
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CACAAAAGAGAACATTTCCAGATCCAAGAGAGTGTATGTAGAAACAGTGACAAGTTAGAA
AATCAACTTAGGTATCAGATAGCAGCCACAAAATATGTTCTGAGGAAAAATTCATAGCAA
TTTATAACAGCTGAAAAAAAGAGGGAGGATGCGGGAAGGTAGATTTTGTCAGAACTTACT
AGACTAAGGATTTATTGCATATTTTTTACTAATTAAATG
Sequence 838
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CAAAGGCCCCTAATCCACCTCCTCACCCGCGTACTTTTTTTTTTTTTTTTTTTTTTTTTNC
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TACAATTGGTTTTCAAAATCTCTTTGAATATTTTCTGGCTTATTACATGCAAATGACCAT
GAAAATATTTGGCATTTTAAAATTCTGAAACTCTGAATAGGCACTTGCATGAAGGAAAAC
AT
Sequence 839
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TGGTCTTGTAGTCGGTTTGGAATTTTCTAAGTCAGGGTGGGGTGGGGGGACTGTGCACGA
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ATTTCCCTCCTCGTTCCTATTCTTAGAAATAAGACTCTGACGCTCTCTTTTATACAGGCT
AGTCCCCTATAGGCATGTCATGGTGATTATTTGCAATCCTNCTGACTTTCCTAAGAAGAG
ATCANACTTAGCAGGGTTAGTC
Sequence 840
GTGGTCGCGGCCGAGGTACAAATAAATGTATCTTGGGTTAAGTGCTATAAAGGAAAAGAA
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ACTTCCAACTCTAAATCTCTGTCTCATTTCACCTCTTTGTAAATAATCATTGCTATTATG
TTAAATATCACAACTACTGTCATTTCTTGTTTACCCACTACATTCTAAGCTTGGTGCTGA
CATCTTTGTATTTATTATATAAAATTCTCAAAATTACTCTGCCCGTTAGGCTTTCTTATC
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GTTTTAAGCAAAAGGGGAAAAAAAATTCTCATTAACTCCAAGGATTATCATCAGGGAGTC
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CTTTTGTTAGATGGAGAAGGGCCAAAAAAAAAAAAAAAAAA
Sequence 841
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AACAATTATTTGTTAACTATTAAAGGGGTAATTATACTCTAAGCTTCCAGTTTTCAGTTA
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ATGGATTTCTGTTCCTTTGGTGCATTGGTTGTGTTTATTTTATGTGATCTTTTTTAGCTA
CAAGGTGGGAAAAATGACAGTGGTTTAGAAGATAAGAAGCACATGAATGTAAAGTAAAAT
ATGTGGAGATTTTTGGCCACTCTGTAAACTACTATCTGAAGTAGTTTTAAATATTTTAAG

Sequence 842

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTACAGTGGCGTGATCATAGCTCACTGCAACCTCCAC
CTCACAGGCTCAAGTGATCCTCCCACCACAGCTTCCAAATAGCTGGGACCACAGGTGCAA
GCCACCACACTTATTAATGTAGATTTCCTTTGTAGATGTAGATTTCTTTTACAAAGTGAC
AGCTTTTCAGAGCTAGTCCTATGTCTGCAGTTTCTCAGAATAACCAGCTCAAAATATGCC
AGAGAAGTATATTTTGGGGTGGCATATTCTAGTCTCCTCCAAGTCATATTTTGGGGTGGT
GTGTCCTGAGCCCCAACAAGATAGGTTTCATTTTTGAAAATTGCTCTTTCAGTCCCACTG
TTCATTCTCATAAGCCCAGGAATCACCACCTGTTGATTTCCTAGGCATCTTCTTGCTCAN
GGTAGTTAGATGTTTGGTGGGACTAGAAAATGCAANGGAGGGAGAAAAAGGAAAGGCTTG
GTGNATGTCAAAGATTTTTAA
Sequence 843
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTGCCTATTAATTGAT
TAGGAAAAATAGGTAGACCCTGAGTGAAAGTAGAAAAGAACCATTCTGGTAAAAATTCTG
AAAGTAGAAAAGAACCTTTAGCTTTAAAGGTATGTCTTAATAGAGCAGTGCTAAGACAGG
TGGTTAGGTATGTGAATGCATGCCACTTAGAAAAGAATATGAAGGAGAAGGGACCAAGAA
GGCAGATACATTGCCCCTGATAAAGAAGTCATTTTTCTCTCACCTTTACATAAATATCAN
GCCACTAAAAATCTAGGAGCACAAATAATGAAAG
Sequence 844
GAGCGGCCGCCCGGGCAGGTACAAGAGAACGGACGGCACTTACTGAGCCCATCGCAAATG
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AAGTAACACAAAGCAGGAAACTAACTCANATTTACTTGCCAAAGGTCACACAGTTAATAC
ATGGTGGAATCAGGACTCAAAATCANGCCTGTGTGACTCCAAAGTCCAGTGCTCTCTCCA
CTTTACCAGGTAACCTTCATAATACCGGATTGGAAATCAAACCTGTCACTTTACTTTTCT
ATGTCCCTGAGTGANTCACAACTTTTTCTTCANCCAGCTTTTTTCATT
Sequence 845
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ATAATAAATGTTCACTCTACTACTCAATAAATATTTGTTGAACAAATCAAAGCTGATCCC
TTTTTTCAAAATTTTTAATGTGACTCTTAGGGGATGGTGGATCCAGGAGAGAAGATTAGT
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GAGAAGAGAGAAATAGAGGAAAAGTTGCACAAACTCTTCAGCCAAGACCACCTAGTGATA
TATAAGGGATATGTT
Sequence 846
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ACTATTTCACAAAACAAAATGTAGCTTTCTTAAAATTTGTAGTTAAAATGTTTTCTTTGT
TTTCCCAATAAAATGTAAAGTTTAATATGTGATGGCTAAACTCCTAGGGGGATAAGGAGG
CGCTAGGAGAATAGGCAGGTTGGAAAAGGGTAGTCGGGACTTGTCCAGATTCTTGTGTGG
TAGTCTGGGTAGTCTGTATATTTACCATATGGGCTACAAGACACACACACACACACACAC
ACACACTCACACACACACACACACACACACACACCCTTGTGAGCATTTATTAATTCGCAG
TTGATGGTGCATAGTTTGGGGAGTGGGTAAAGGATATGTTACTTTTGTA
Sequence 847
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CTAAGCTTTTAAAAATACAGTACTGATCATTCTATTTCCCCCTNTATTGATCCCCACCTC
CAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGACTAATCAAACTA
Sequence 848
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CAATCTAATTGTTTTCTCAATCTTTGTAAACCAGTTTTAAGAGTCACCAGAAATCTGTAG
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CGGTAAAATACACCATAAATTATGACTGCTTTATCTGAATGCATGGGACACTTGCTACGA
TGGCGGGAATTATTACCAGGAGTTTAGGAGCCAGACATGGGTTCTGTATTTTTCATACAT
TGGTGATCAATTCAAATCTCTTTCCTTTGCANCCCAGGTTTGGTCAGTCTGGCCAGGAGT
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CCACCGAGTTAAACAACCTATTTAAATGCAAGACTATTGATTGGAAT
Sequence 849

Table 1

CCCTTAGCGTGGTCGCGGCCGAGGTCGGCCGAGGTACAAAAGTTCTGAAATAACACTATA
GGCTTAAGGAATAAGGGACCAGAAGTAGCCTGGTAGCCAGTGTATTTCTGGCTTTATACA
TTCCTTAGGAAAAAAAAAACTTTATAGATGTATTTAAGTAGAATTAAGGTTTACACAAATG
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ACGCAGATATTTATTTAGCAGCATGGTCTGCAGAAGTAGGAGGAGGTGACCAGATGTGAT
GGATTATGCCTGTAATTCCAC
Sequence 850
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ATAGAAAAAATATATATAATGTGAAGTCCACTCTACAAAAAGTGCTGGCATGTTGGGCTA
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ATTAAA
Sequence 851
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TTGCAGGATGCCTGGCCTCTGGGAACTGCTCCTGTCTCTGTGTGAATGTAGAAGTGAGGC
TCAAACTCTCTCTTAGGAAAATTTTCCCTTCCCACTGCCCATCCATTTCTGCTGACTCAA
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TGGCTCGTTAAAATGATTAGCTGGCAATACAGGTATGTTTGGACTGCTATTGGTGGTGAA
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TAAAAAAAAACAACTATATATGATTGAAAGAAATTTGAGATATTTTTGTTTC
Sequence 852
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CTGGTGACCGTGCCAAAGTCCTTCCTGCCTTGCAGAGAGGCCTNTCTTCGTCGAACATGG
GCCTCAGGAAAGACAGCCTGAATGCCACTACCCCAGGCTTGTGGAAGGTTCTGCATCAGT
GTGGCATTGTTGCGATAGCCCTCAGTTGATGCTTGTTTGTGGTGTTGGGAGGCAGGAACT
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GGTCACCTGATGGC
Sequence 853
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AAACATCAGAGTTGATTATTTAGCACTTTCTCAGGATTCTAAGGCAATANGCCTAANTTC
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TGCTGCTTCTCCATTCTGTTTTCAAAGAACATTACAAAAATAAACCAGTGNGTTCTCTAA
CAGTTCTAAAAACAGNTTG
Sequence 854
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AGCTTAGAGTCAGATTTCCTAGGTTCAGATCCAAGCATNACTACTTATTTTCTTTAAGAA
CTTGGGCATCTGTAAACCAGGGATAATATCTTCTTCAAAGGGCTGNTGNGAAGATTCAAC
AAGGTAATACATAT
Sequence 855
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CCTCAAGTGATCCACCTGCCTTGGCCTTCCAAAGTGCTGGGATTATAGGTATGAGCCACC
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TTATCCATAAACAGACATGTCTGAGCACAGAAGATCATGTTAATGAAAGATTATTGAAAG
GTACCTGCCCGGGCGGCCGCTCGAAAG
Sequence 856
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TCAAACTCAGTGTATATAAGAATGGCTAAGTGACCATTAGTCATGTGAAAAGCTTAACAA

Table 1

CTATTAAGCTCTTATTTTCTTACTAAAAAACAATTTTAAGTTCTTTCAAGGCTATAGTTA
CGCTTTACATAAGAGGCCCTATTACCCACTAATTCTTAAAATTTCTACCTACTTAAAATT
TCTTTAGACATTTCCAAAGGTTAGTAAAGGAAGACATAAGATATGCTTACTTAAATCCTT
GCTGGTTCCATGCCTGGCCATACAT
Sequence 857
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TTATCCAAATCTCTCATTTATGAATATGGAATATAAATATGCTAAATTGATTATGTCATG
AATAGACTTCTTTTTTGCATAACAATGTTTGGAGTTTCTCACCTTTCTCCTNNCCTTNTT
TTTCT
Sequence 858
CCCTTAGCGTGGTCGCGGCCGAGGTACAAATGTGAGTTCTTCTCCAGACCATCAATATAG
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ACAAACATGGACTTGTTACAACATCCCAGAGTGAAATCTGAATGTGGTCAAGAAAGTTCA
GAAACAATAAGAGTGATGCAATGCATACCACAACTCAGGCCCAGTGCAAAAGTCAGGCCC
CAGCCCTTCCCATATAAGGGACTTGGTCATTTGAAAAATCAAAACCCAAAAGGAACAACT
ATAGGGACCTGTAATCAATTAGAATATTC
Sequence 859
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CAGCTGGCCTTTTCCCTCAAAACATGGATAATCTTCAAACCTCCCTGAACAGGTGGAAAT
GCGTCTTTCCTCTAAGCCAAGTTCTCAGTCCACATTAGTCCATACTTGGCTACAGAATTG
ACGTTTGTGGCCACAATCCTACTAGAAATGACCTTTGGGTAATATCCTTATCTTGTTGAT
CTAGTTAGGGTCAAGTAAA
Sequence 860
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AAATATAGATGAACAATGAAGCATAAACAAAATTTTAATATCTTACAGGCTAAAATATTT
AGAAATGAAAGACAACAATAGCATATAAGTTAAGAAAGGGGGTAAAAAGAATCAAGAGCA
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AAATTAACAATGTATGCTGCCATTTC
Sequence 861
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TGAGCAGGCATTTTAAAAAATGGCTTTCATTGATGGAGAGGTAAAAGTGAAATGGCTTTG
TTGTATTTATATTATAAAAGGCCATTTCCCAAATCTAGAATTTATTACTAAAAATCAAGT
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ATATTTTCAATGTGATTACTCAC
Sequence 862
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GGAATATAATTTGGAAGGAATAACGTTGTTGAAAAACATCCTCTACAGACAATATGAACA
ATGCCTTAGTCATCTATTGATTATGACAATATACTCTTGAACAAATTGTTTTCGGTTCTG
GTTTCTGTGGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 863
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TGCTTTGTCCAAACCCAGTTGCAGGAATTTATGTCTTAAAGTAAACCATCGTATGATAAT
TTCCCCTGAAAATGTGCCTATTAAAAAAAAATAGGATATGATGGGAGGCAGACATAAACA
TTCTGGTCAATTTATTGGTGTTATTATTTATTTCAGTTAATAAACTGCCCTTTCGCTATG
CTTCACTTTCCACGTGTTTAGGCAG
Sequence 864
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AGAGTGAACATACTGCTTGTAGCTAAAACATTACAGGAGACCTTAAAAAGGGGTATAATT
GGTCCCTATGTGAAATGAACCTGACATATTTTTATAAATTATTTGTGCATGACTATCTTT
TGNTGATAGCACTAGGAAGACTTNTAACGTTTAAATACTTTATTTGCCCTCAATTACTAT
TTAAAAGTCCTATAATTTTAAGTAATTTTACAGCTGACAAAGATAAATATTTTTTTCTTT

Table 1

TAGTTTTTCTAATGTCTTGGAGGTAAAGTGGAAATGGCCTGTTTTGACACATAATTTCTA
GAACTTGGAGTTAATTTTGATCAGTTCCATTTTGGGT
Sequence 865
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GGTATTAAATCAGCAAGGTCCCCATCCCAGAAAAATGTGCAGTTTGTCCAATGGGAAAGA
TGCANAGACAGTTTCAGTTAATATACTAAGTGCTAAAGATTGGGATGTGCACAAGAAGCT
GGAGGTAAAAATTCTGGAAAACTGAACGTGAAGTCACCACTAGGCAAGCTGCCTGTAATT
GAGCTTGCTTGTATATGACCAATCAACCTTTGCTTGTTGAAGGATTAGTTATCTAGTTTC
CTCCTTTTCTTTTTTGGAATTTGGTCTTTTAAGGTCTTGATAATCTTTCTAGTCTAGAGC
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GTTGCTGCAGTTCAGGGGAGGTTAAAGTTGCTGGGCTCCACTCTCTTATTAGCATGGATG
CTTAAAGAACTTCAGGG
Sequence 866
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AAAAAGTTTTAACGANNTCTACNGTTATTGAATNAAANTACATATAGCGNGATTCTTATT
ACTTGAAATTAGGAGGAGAAAGAATTTTTTGAGGTAAATTNGAAAAGACATAAAATAGAC
TA
Sequence 867
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CACTAAATATTCTCCCTAGAACATATGGATTTTGAATAATTTAGCTAATTATAAAAATAA
CTTCCCTAATGGTCCTTTGGGCTCTTTTAAGGTTTTGCTGGTATATGTTCAGGGGATGAA
CCACTTAAGGCTCTTTGACCACCATACTGNCCATACTGCCATACTGGCATACCTGNTTTT
AAAAAAAAA
Sequence 868
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ACAAGAATTATGATAGTTCATTGAAAAAGGTTGAGAATTCAGAACTTGTCAGTTTCCACC
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Sequence 869
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TTGGGGCCCCCCCNCCNTTTTTT
Sequence 870
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GACAAAGCAAATGCAAACTTATCCTTCCAAACCCTGATAATTGGTAATACCAAATAACTG
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Table 1

AAAAACT
Sequence 871
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TTCCTATAGAGGCAATATCACTTTTAGGATGGATGGGTCTAAAAGGATCATATTTAAGTT
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TATTTGTCTCTCCTAAATAACCAGTATGGAATTATAGAAAGAAAGGTGGGGAGAATAGTC
CGTGTGATCTNCTGGGCAGCATTAAAGCCTGTTCCATCCAGCCCCTGACTATTTTGGTCT
TTCTTTGCCTTTGAAGGCCCAGAAGACATTTNCATTCCTTCGAAGNTTTTATGGTCTATA
CCCCTCTCTTGCCTNCATATTNTTTTGCAAGNGGGGGCCAGAATTTTTTTGGATTCCCNT
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CCCCTTNTNCCCCCCCGGGGGGCCCCGGGGGGNCCCCNCNTTTTTTTTGNAAAAAAAANN
GGGGGGGNCCCCCAAAAAAAA
Sequence 872
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ACAACAACNACNAAAAACAAAACAAAACAAAAAACAAGAATGACCAAATACAGAAATTAT
TA
Sequence 873
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CCTCGCTNGGAGCNTCAGTGGTCCCATGGTGGGCAAAGGAACCCAGGTTTNG
Sequence 874
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Sequence 875
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CAGGGCC
Sequence 876
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Table 1

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TNTGGGCAATNTCAAAGNNATTCAANGAAAAAAAAAAGGG
Sequence 877
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Sequence 878
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TAGT
Sequence 879
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GAGGTAGAAAACAAGTGCCACAGTAGA
Sequence 880
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Sequence 881
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TACATTCATATTTNAGTTTTTTGCCT
Sequence 882
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TTGGCCCCATCTTTCAATTTCAG
Sequence 883
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Table 1

GATAGCCAGCTACATGTGTAGTTTGATCATTCAGTTTAACCGTTTTATCACTGTTGATAT
GAACATTGAGTACCTCGGCCCGCGACCACGCTAAGGG
Sequence 884
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TAGGAGATGGTTTGGAAAACATCAAGCAGCTCAGTTTCTTGGGGTGGTCCAGGAGAAAGA
AGCTCAAACAACATTCAGTGATAACACTTAAAANNATCAAAAATTT
Sequence 885
CCCTTAGCGTGGTCGCGGCCGAGGTACAATAAACAAGACAGTGCCTGCTTGTGACCAGGG
GCTGGGCCTCTTCATAGCTCTTTTCCCTGCCTTTTGTCTTCAGAGTTGATCTGCTTCTTA
CACATTCACTTTTTCAGAGTTTGCTATCTTAGAAGCAAGGATCATTTTTAATTGGTTTGT
TTACTTCAAAGTCCCACTCATCAGAGGCAGNTGTTTCGCTTATATTTGGCTCAACTACTT
TNTCTGCTTGGTTTAGTAACACTAATGTTTACTAACATTAAAATGAAACCAGTTTTGCAG
CTAGCATCTATTGACCAAATATAATTATTTATTTCAAACTGTATATTCCAAAATTTAAAC
ATATTCAATGCTTATTGAACATCTAAACATATANCCTTAATGAATAANGGGAAAATATAA
CCATCTGGTTTTTGGATCTGAAAGCCACAACCCACCTGCTAGANTANTTTGGGGAAAGGC
TTTTTANTTCCAAGTTCAAAGGNTGAATTCTCCCGAGGGNNGNNGGGGGNCTTCCCTTCT
NAACCAGCAANAAAACCTNGCNCCAGTTTGGGATTTTGGGNGGAAAATAAACCCNAATGA
NGCATTTTACTTTCCTTTTTT
Sequence 886
CCCTTAGCGTGGTCGCGGCCGAGGTACATATGGCTCGGCAAAGGGGGACTGGATTAATAA
ATTCTGGTAATATAGTAAGGACAAAATAAATGTAAAAAAGATAGAAGTAAATGGAGAACA
TCAACATGAACGCGTGCTCCTTTGAGTAGAAAGTAATTTTTCTGCTTTGTCACTCAAATA
GCTGGCAGACCTGACATCACCCTGCCTCTGCTTCCATGCTCTAAAACTTTCCTGGGCCTC
AGATTTGGATGCTAATATGATTTTCCACTTAGTGGATAAGAGCTCCCTGGAGAAGGGCTC
ATTCTTGGATGGACAACAGAATTAGAGCCTGAGTTCTAAGAGCTTAATAAAACAAAAG
Sequence 887
CCCTTCGAGCGGCCGCCCGGGCAGGTACCCGATGAAAGTTTAAATCTAATCAACAGTATT
ATGCACTGGTTGAAGAAAACCAGGATTAAGACGGAGGATAGTCAGCATGGAATCTAANAA
GGGAAAAGTCCGNTAACTATATGTGTTCATNAGATTCTAAAGCTGTTAAGGGAGAAAGAC
CCTGAGTCTAATGAATATAAACTTTAAATTTAAAGAAAAACATGNTCTGTTATAGAAAAG
TGGGCTTTTAANTTTTGTAAAG
Sequence 888
CCCTTAGCGTGGTCGCGGCCCGAGGTACCATTAACCGTCTTTTAAAAAATTATTATTAGT
TTCAGTGCTGTTTCTTGAGGGAGCACCGGTGGTGCAGGTCAGGTTTGTCTTCTNAAT
Sequence 889
CCCTTAGCGTGGTCGCGGCCGAGGTACTAAACAGGCCAGATATATTCTCTCATTAACTTA
TTGCCTAGCAGAGAAGACCAACATTTTTAAAAGTTTATACATATAGTTAATTTCTATTAT
GATTATATGATACAAATGGAAAGTGCTATGAAAATGTGGAACAAAAGAGAATAATCTGTC
TGAACAGTCAAAGAAGACTTCTGGGAGATGACATCTGAGCTAAAGGTTGAACAAGGAATT
GGAAAACAGCTGGCATGTGCAAAAGACTTGAANACTGAAGGAGTTAGCCTTTAAAAAAAT
GAAGAAAGTTCTATTTGGCCAGAGCAGAGTTTCAAATAGTGCCTCACAGGCCACGTTAAA
GACCTGAGGCCTTTATTCTAGGAGAATAGGGAGCTGCTCAAGGAATTTAACTTGANAAGT
GACAAAGATCAGATTTGCAATTGCCTTTCAAGGTGGTAGGTTACAAGGGAGTTGGGTCTC
TTGACCCTTTGCAAATTATACCCCATTTCTTAACCTAAGAAATGGG
Sequence 890
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTGCCTTGCAAAATTATATTACAAGAAGAAG
CACACTTGTTATAGAAGTGCTGAATTGTATGGAACCTAAATCTGTCAAGTTACCTGTCTT
TCAGGTCCGTCTCCCCACCTCCCAGACCTCATTATATTATCCCGAAAAGAACACGATCTC
TTTAAGGCTAGGCAAGTATTGCGCTGATGAGCCAGGGACTGCCCACCAATTGGCAGGCCC
ATTGGGTGATAAATGTCCAAGGACCTCTAGGCTGACGACACATTTTTCATCATTAATCCA
GTCTATTGTAACCAGGGCCACTCACATTGATTCGGACTAGGGGGCATCATCTGCTGTTAA
AGAGGGTGATGACTCGCTAAAAATGAGGG

Table 1

Sequence 891
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACTTCATGGCTAAGCATGTGCGGATGGAA
CCGGTCTTCCTGGGCTTACATCTTTGCTTTGCCTCTTCTTTCCTGTGATGAGTCTTGGGG
TAGGCCTCAAAGGCTGAATCTTCAATATAAATACAACAGTGAATGAACAACAAATGGTTA
TTTTAAAGATCTATCTTGGATGGCTATTTAATTTCACTAAACCCCAGGTTGCTCACCTGT
TGACTGGAACAAACAATAGTCCCTTCTTCATGCGGGCATGGTGAGGGTTTTAACCCCGCA
TTGTCCACAAAGACCGCTTAAATTATAGTAGATGCTCAGCAAATCTGAGCTATTATTTTT
ATCACGACTGTCAGAGGTCAGATCAGGCTTCGGGGTCAGACACACCTGGGTTCAAATCCC
AGCAGGGCCACTTACTGTTGGAGCCGGGGCAAAGTCAGTTATTCTCCCTGAGGGTCAGTT
TTCTCATCCCTAAAAATTCC
Sequence 892
CCCTTCGAGCGGCCGCCCGGGCAGGTACTACAGAACAGGAACAATCTGCCATGTGTGTTT
ACAACTTCAGAAAGCCCTGGAATGACAGTTGCCAGGGCAGTTCTTTGAATTTGCAGGTCA
GAATTAGTGGATGATGAATTTTTTTCACACATGGTCAACTCTGTGCCACCTGCTACAAGA
TGTTGGAACAGGTATATTTATTTATTTAATGATGATCAATGATTCTTCCAACATCAGGGA
ACATCAGGGAAATCAGCTAGTATATGCTCTTTTTGAGGATTTTCAGCTCCAAATCCTGAA
AGCATTCATGAAACTACATAAATTACTTTTGTTAAGCAAATCATCATAAGTAAATCCAGT
CATATGAATCTGGAAGGATTTGCTGGTGGGCACTAACACTGACCACATGTTTCAAGTGTG
GGCAAGTTTACCATCCATCACGGATTTTGTGCTTGGTGAATTGTAGGGAGTGAAAGAGAG
AAGGATGTTTGGCCCAGTTGTCTTTTTTACCTATATCTGAAATTCTTACTTAGTCAAAGA
ACAAAACATTTAGACATTTCATTTCCTTTTGGGGGTTTTAAGTGATACATGTTTAAAAAT
TGTATATTTTAGAAGAAAATTGTTTTTATTATATATAATTTATTAAAATTCNGGNGGAGA
AGACCAAATTTTATCCTGAGNAAAANATTTAAATTTGAAGNTTAGGTTGGCTTTTTTAAN
ACCCNCCGGCCNAACCCCAAC
Sequence 893
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAGCATTAAAAAAGTCCTACAAATTATTAGA
GAGAAAATACAGGTTGCACGCAAAGCATAAAGAATGAGAATGGCATAAGACATCTTAACA
GTGCCACAGAAACTAAAAAGTAGTTCTGAGTAAAAATGAACTATTTACCCAGCCAAACCG
TTAATTAGGTATAAAGGTAGAGTTAAGACATTTATAGACATACAAGATATTAAGATTACT
GAGTCAATTGATATTCAACAGGGGTGCAAATGGAGAAAAAGTCTTTTCAACAAATAGTGG
TGGGACAAATGGATAGCCACATGCAAAAGAACATATATATAAGAGCTAAAACCATAATGC
TTTTAGAAGAAAATATAGGGTTTATCTTCATGACCTTGAATTTGACAAAGGATTCTTGGA
CATGACACCAAAAGCACATGCAACAAAAGAAAAATTGGAGTGATATG
Sequence 894
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTCACACAGCACATCAGTGGCTACATGTGAG
CTCAGACCTGGGTCTGCTGCTGTCTGTCTTCCCAATATCCATGACCTTGACTGATGCAGG
TGTCCAGGGATACGTCCATCCCCGTCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTC
CGAGGAGACAGAAGGGAGTGTCGGACACCATGACGAGAGCTTGGCAGAATAAATAACTTC
TTTAAACAATTTTACGGCATGAAGAAATCTGGACCAGTTTATTAAATGGGATTTCTGCCA
CAAACCTTGGAAGAATCACATCATC
Sequence 895
CCCTTAGCGTGGTCGCGGCCGAGGTACAGGTCACACAGCACATCAGTGGCTACATGTGAG
CTCAGACCTGGGTCTGCTGCTGTCTGTCTTCCCAATATCCATGACCTTGACTGATGCAGG
TGTCCAGGGATACGTCCATCCCCGTCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTC
CGAGGAGACAGAAGGGAGTGTCGGACACCATGACGAGAGCTTGGCAGAATAAATAACTTC
TTTAAACAATTTTACGGCATGAAGAAATCTGGACCAGTTTATTAAATGGGATTTCTGCCA
CAAACCTTGGAAGAATCACATCATC
Sequence 896
CCCTTAGCGTGGTCGCGGCGAGGTACCTTGAGCTGCCTCAGCACTCTTTTGCCATTCGTG
CTAGAAACAGCCAAAGCCAGACAACCAAATTACAGATGCTTAAATGTTAATGCCAGACAC
CAAGGCTCCGTGAACTTCCCTGTTGAACATCTGACCCCGACTACTTGAGGACATGAAACC
TAACTGTGCAGCTAATTACACCTTCCAAGGGCAATGACATCGGGTCCTATGATTTTATTC
AGGAAAGCAATAAGGCAATCGGGGTCACTGTGAACATCATTTGAAGGGAAGTAACTTCTT
AGCTTTATTCCACAAATGGTCTAT
Sequence 897
CCCTTAGCGTGGTCGCGGCCGAGGTACCGGTGTAGTGTATAGAATGGTTTGTATCAAACT

Table 1

AGATCTACATTACTTTACTAGAAATATAGGGCAATAATAAAATTTCCAAAGCCAAACTGA
ACGATAATATATATTTCTTTAGAAAGTCTCAGAAAACCCATTCCTGAATGACAAAACGGA
GAGATAACTTACAACTAGGTGATATCTGAAGTTAAATTTTCTTGGTTATCTATTTCAAAA
ATTCACAACTATTCTGCACTAAAATGTTTCACTGGGTCAGGCACAGTGGCTCATGCCTGT
AATCCCAACACGTTGGCAACCTGAGGCAAGAGG
Sequence 898
CCCCTTCGAGCGGCCGGCCCGGGCAGGGTACCNCGGGGTNGGACTCTNTGGTTTTTNAAA
ACCTTATGAACCATTAACTTGGGAACCCCGGCAAAANTAAGCCTNGGGGGGCTTGAGGGG
ACTTTTANGANNNAACCNTTTAAACATTTGGTNTNNTTNAAAAAAAAATTNCAGGGTTTN
CCGTNCCTTTTCCAAAGGGGGGAAAAANGCNCNAACNTTTTTTTTTTTTTTTTTC
Sequence 899
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGACAGATGCCTGGGTAACCATGTCCAATGT
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TCCGCTGGTAAGAAATCCGCCACACAAGAAAGCACTGACATTTGGAGCCTCATCAGGTTC
AGAGTTGAAAGTGAAATAAAGGATAATAATCTTTGTCTTATTTTCTTTGTTTTAATGTTT
CCCAACTTACGTTAGGACAATGTCAACAAAGACAGATGTCCCTAATAGTAATTGCAGGAC
ATGTGTTTTCTCATTCCTATC
Sequence 900
CCCTTTGAGCGGCCGCCCGGGCAGGTACATTGGAGGGGGCCATATCCAGGACCTGTGATG
TGTATAGGCAGACCAGACTGGTAGGGAAGAAAAGCAGAGATATCAAGTGGGGGACATGTG
TTTGCCCTGGGGCTCTATTGGCCTGGAATTTTGTGGTAGGAGGAAGGCACAAAAAGTAGA
CTGGGATTACAGGCGTGTGCCACCGCGCCCGGCCTAAAGTGTGTTTTATAATAAAACCTC
AATCTGAAACATTTTAATAAAACCTTTAGATGACTAGATTTATGTTTATTTTGGATTTAT
GTTTATATGAATAAAAAAAGAAAAAAGACGAG
Sequence 901
CCCTTAGCGTGGTCGCGGCCGAGGTACCTATGAGATGCATTTGAAAACTTACCTTGTTTA
TATGTTTCTTCTGTTGCAATTTCTTCCATTACCTGGGAATAGCTGCTTTGGACGGCAAAC
CAAGCAATGCCCTTTCACAGCTGTGGGATGAATGGGGAAAGAAGTCTTGGTAAGGAAGCA
ATTCAGAGAACATGGGAGCATCTCATGGCAGCAGTCACAATTTTGTGTTGCGTAATATTT
CAGGAACTTGCAACCCTGATAACTTGTGCCTGCCTGTCTGTAGGCCTTTAATGATGTTTT
ATTGAATTTTGG
Sequence 902
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AAGAAAATCACACTTCTAAACACAAATTAACCATTTCAGTATTTAATTGCTCCTAAAAGG
TGTATTCTACTTCATTAAATGTAAGAGAAAAGGTTACCTACATTACGCAGTTTAAGAAAC
AGGATAAACTTTAGCATATAAACCAGTCTTGATTACAATTTCACACTTTCAACCATCTTA
TTTATACCTCTACATTAGATAATCTTTAAATTTCCATCATAAGGTTTTCCCATGGTTAAC
CTNCCATATAAAATTTTGGTAATCCTGCCC
Sequence 903
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGGTGACAGGAGAGAGCTCATGTGACCCGAGT
CTGGGTGGTCTCAGGCATGGTATAAAGAACTAGGCCAACCAACTGCACTAGACATAGAAA
CTAGCTGAATAAACTCATCCACTCCGATTTCATTTCAGGTATCTCATGAGAAACTAGAGG
ACAAAAACAATTCCAAAATTAACAAAACAAAGTTTACTCTAGCCATCAGTGCCAATGAAC
ATAAATGACTGCCTGAGAGTTATATTAACAAAATAATTAATTCAGACGAATTAAGGAATT
AAACCAGCTATGGGAAATATACACTCTATACTTAGATGCACATT
Sequence 904
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TAGAGATAAAGAGTGAAGTTACTAGAAAAAGGTGACTAGGACTCTGTTTATGAAGAAAGG
TTAGTATTTAAATCATGAAAAAAAGTAAGAATACTTAATTATTCAAGTAACTTAAAATTG
TAATTCAGAATGGCTTTTATGTATCTAAAACAATCTGGGCTGCTATAAAAATTCAGTCAA
CTTCTAAACTTCCAAACACAAAATAGTTATACTCAGTCTAAGAATATCCGACCTACCGTG
CAGGACCAGAGGGCTCATCTC
Sequence 905
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAAATAAAATAAAATTAAAACAAATCATTT
TTAGAGATAAAGAGTGAAGTTACTGGAAAAAGGTGACTAGGGACTCTGTTTATGAAGAAA
GGTTAGTATTTAAATCATGAAAAAAAGTAAGAATACTTAATTATTCAAGTAACTTAAAAT

Table 1

TGTAATTCAGAATGGCTTTTTATGTATCTAAAACAATCTGGGGCTGCTATAAAAATTCAG
TCAACTTCTAAACTTCCAAACACAAAATAGTTATACTCAGTCTAAGAATATCCGACCTAC
CGTGCAGGACCAGAGGGCTCATCTCTTGCCGAGCTTAATACAGTTT
Sequence 906
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTGCTTTAAATGCATACTAAGCTGTGAATGA
CTGATATCAGAGACTTTCTTGGAAGTAGGTTTCATAGGATGGAGGACAAATGAAACTTTA
TGGGCGAAGAAAGAAGGGTCAGTTGGGTGGTGCATTGAAATAAGTGGTTCCAAAAGCAAA
CTAGGTCAACTTTTTAACTGGCTAGTGAAAATGAGATTCCTCAGGATACAAAAGCAAGGA
GAAGACAGGAATAAATCAGGACTCCAACAGGCAGAACAGGATTTATTTAGGGCATGCAAT
GTGGAGGGCCCTAATGGGAACATGACAGTGT
Sequence 907
CCCTTAGCGTGGTCGCGGCCGAGGTACAAATTGCATTGTCAATTTATATTTGTTTCCCCA
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GTTGAAGTTCTTTTGAAATGAATTGAAGAATGTGAATAATAGTTCTAGTTCTTCGGGATA
ATGGAAAGCTAATAAGGTTTATGCTAGAGGCTCTTACTGCTGGGACTCTCTTCTTGTTTT
TGGTTTTTAGGAAAAAAGCTAGAAAATCCAACTTCAGCTAGAGTAACAGTAGTAACTGAC
TTGAAAGTATGTCAAAACAAAAACTGTTAA
Sequence 908
CCCTTAGCGTGGTCGCGGCCGAGGTACCTATGAGATGCATTTGAAAACTTACCTTGTTTA
TATGTTTCTTCTGTTGCAATTTCTTCCATTACCTGGAATAGCTGCTTTGGACGGCAAACC
AAGCAATGCCCTTTCACAGCTGTGGGATGAATGGGGAAAGAAGTCTTGGTAAGGAAGCAA
TTCAGAGAACATGGAAGCATCTCATGGCAGCAGTCACAATTTTGTGTTGCGTAATATTTC
AGGAACTTGCAACCCTGATAACTTGTGCCTGCCTGTCTGTAGGCCTTTAATGATGTTTTA
TTGAATTTTGGT
Sequence 909
CCCTTCGAGCGGCCGCCCGGGCAGGTACCCTCTTCTCAATTTTGCTATGAACTTAAAACT
GCTCTTAAAAAAATATTTTTTTTAAAAAAGGAGGGNGTTATTATCAGAGATCCCATAGAC
CTTAAAGGATAATGAAAGAATGCTATGGGATAACCTTCATGCTAAAAACTTCAACAACTT
AGAAGTATGAAATGAATGAACTNTCTCCAAAAAAAATACAAGTTACCAAAATTGACATGA
ATAATAACAGAAAATNTNGANTAACGCTCTAACTATTAAAGGAACGTGAAGTTTGTCAAA
AGCTTCCCCAAAATAAAATTCCAGGACCAGATGG
Sequence 910
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GTTTCTTAGACCTTCAATGCTTCTTGGCTTTCCTCACTGCTAGTTATAATTCAGTTTTCT
CAGGTCTAAGTCATTCATCACTCTTTTGTCTGCTTTTCAGCTTCCAAAAATTCATTGCTA
TTATCTCCTCTCCTGTTTTCCCTATTGGTGTGTTTGTNTCTTTTTCTTTAAAAAAATTCC
TTTGTGG
Sequence 911
CCCTTAGCGTGGTCGCGGCCGAGGTACAACCTAGCCAGCTGCACAGCAGCTCTCCAAGAA
AAAGGTGTATATTAGACAGATTCAATTATTCATCTTGTGATTATGAGTAGTAACCAAATT
GTCTATGTAATTTTCTTATGGTGAACTACCCAAAGCAAGGCCTCACCTTAGGCTACCAGC
TTGACTCTTAAGTGGACAGAAAGAGCCAAAGGCTAAAAGGTTTGTGAGAAACCTCATGAG
CACTGAGTGTTCTAGTTCCAGATGAAAACCGGTTTCAGGTATGAAGCAAGAGGGAGTGCT
AATTGGTAGAAGTAATTACATCTT
Sequence 912
CCCTTAGCGGCCGCCCGGGCAGGTACAACAGAGCACAATGCTTAGATTTGGGTGGATTTG
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AGGACCACAAAAATTTAGACCAAAGTATCTTGTAAATTCTACCTGGTGAAAGTTTGATAT
AGCACACATATGACTTTTCTATATTATTTTCTGTTTTGAGTTTAGTAGTAAGCAGATGGT
TTGTATTTTCTTTAGTTGCAACTAAGTGATCAGTTTCATGATTTCTCTTACTATGAAACA
TTTTTTTTTTTTTTCTTAACAGTTATCTT
Sequence 913
CCCTTTCGAGCGGCCGCCTGGGCAGGTACCACAAAGTTATTGCCTACATCCAGGTCAAGA
AGATCTTCTACTGTATTTTCTTCTAAGAGCTTTTACATATAGGTCAATGATCAATCTAAA
ATTAAGAGTTGTGCAATCATTAACTCTAGCTTTAGACTGGTATACTAATTGGTTTGTATA
CGAACTGGGTTAAAGGCATAGGACACATGCAGGCTGTGTTCATTTCACAGCAGGGCTCTG

Table 1

TAATTAGGCAATAATTACTTACCATCATACCTAGTGAGGCAATATGGGAGAAACAAAACA
GGCCATACAGCTTCACTATTATTCCTACT
Sequence 914
NNCACCCCTAGCGTGGNCGCGGCCGAGGTACTTGAGGACCAAGCCACAGAGCAAGCGCTA
AAAAAAAAGTTAACTAGAACCTTACCACTNTTNCACGCACCCCAATTNCATAAAATGTAT
CAGNAAAAAAAAACAATNATCTAAAGANAAAAAGNAAAGAAAAANNATNNANCACATAG
GNAACNGGGTGTCAACTAGGNAACNGACCTATANNAANNNAGGAAGANAGNGNCTNCCTT
CCTCAATNNNCAGANNNACGGAGGGGAGGCTCAAAAGGCCCGAGAGGCTCNCTACAAGGA
GAAAG
Sequence 915
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGAAATGGTAAATATATGAGTAAATATAACAC
ACTTTTTTCTTTTAAAATTTTATTTAAAAGGTAACACTTTGCAGCAAAATAATTAACAAT
GTATTGTGGGTTATATAGTAGTAAGATGTTTGACATAAATTACATAAATAATTGGAGCAG
GGAAATAGAAGTGTGTTGTTGAAATGGTTTGATATTATATATGAAGTGGTATATTATTAT
TTCAAGGTAGCCTTGATAAGTTAAAGGTTACATATTGNAAACCCTACAATAATCATTACA
AAATAAAGAGATATAACAGNAAG
Sequence 916
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCATAGAGGTCCAGACCCCTTGCGTCTGGCAT
TCCTTTGGTCTATAATTCAGTAAACTCTGCTAAAAAGGAAACGAGACTAGCTTGCTGTGG
CCCCTTAAGCGACCCAGGGTAGCTTGTGATGGTTCAGATTATGATTTGTTCTAGAGCTTT
TCCAGAGGCAGATGTTGAGGAGTTTATCCTATTTGNCCCCTNCCCTTTAAACAAACAAAA
GTGCCGGCTGGACGCANTGGCTCATGCTGGTAATCCCANCNTTNTGAGAGGCTNAGGCAG
GCGG
Sequence 917
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGCCTGGCATGCATCTTCTCGATGGTCTGTT
ATCTTGTGGGAATGACATTCGTTAAGTTGTTTTCTGTGTGCATCCCACCCAAATAAAGAA
TGTTTCATCAGCAAAGTGAATTGCCGTATAGTCATCAGACTCTAGAAATAAATTATCAAC
GATGACTGCAGTGGGTGAGGCTGTTTGTTTATCACATCACTTGAGAACAGAGTAAAGTGA
GTTTCATATTTTCCTGAGTCTTGAATTCTCATTTTAGACATCTGTTCAGAAGCTTTCTAA
GCCATGGAGTATTCTAAATGAGC
Sequence 918
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TCATGGCAGTATGAAATGTGTCCCTGATTCCCTCCGACCTGCCACAGAATACTGAAACAG
TGGCCGTGGGAAGAAATACCAGATGGTATGCATATGGCTTTGGGAACAGCTTTCAGCAGT
GGTCACTTGTCTTTTTTTAATGCATTTCAAAATGTGTTTGGTTAGCAAAAAATAATGAGA
TAATTCCCTCAAATAAATG
Sequence 919
CCCTTAGCGTGGTCGCGGCCGAGGTACAACAATTTATCCATTCCTTTAGCAATAGTTGGA
CACTTAGAATGTAAAACTGTTCAAACAAATTGGTATATTGGAGTTTGGGTAGAAAGAAGG
GCCGTTGGAAGAGGAGGAAAAGAGGGTGAGATGATACATTAATATAAATTACTGAAAGGT
GGTGTTCACATTTAGAATTTTTTTTTTAAGTTGCATGTTTAGGATTTTAGTGCTCAGGAG
GAAAGAAGGCCAGTGTTGCCCTTCCAGACCATCGCTGCCATTTCCCTGTAATATATCGTG
TGTAGAGGAACCTAATGCCTGCA
Sequence 920
CCCTTAGCGTGGTCGCGGCCGAGGTACTCGCTATTTCTAGTTCAAAATCACAGATTTTCA
GATTGAAAAAATTTCAATCCACTTATTTTTCAAATGAGATAACTGGGACAAAGAGAAATT
CCATGACTTGCCCAAGATTACCTACAGTTTAACTGTCAGCGGGGCTTAAAACCACAATCC
ACATCTCCTGACTCCCAATCCTTTCACTTAAAACAAACAAGCAAACAAACAAAAAAGATT
TCTAATAAAGTGGAATAATTNTAAGAAAGGCAAGTATCACTATTTTAC
Sequence 921
CCCTTAGCGTGGTCGCGGCCGAGGTACTCACATGTAAACTTCTACTTTCCCCTTCAGATT
ACAGCAACCATCATGCCAAAGCTATACACTCTCAGGGAATCCCTGTGGATTTCACTGATG
ACCACTTGACCAACTATCATAAAGATCAAGGCCAGGGGTTCTCAAACTCTCAACATTTGT
GTGCTCATCTCCCCTTCACCCAGAGACTCCCCAGGGCTGCTGGGCCACACTTTGGTTTGT
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Table 1

AGATTTTTAAATATTAAAAAAAAGAAAAAGAAAGA
Sequence 922
CCCTTAGCGTGGTCGCGGCCGAGGTACATACAGTATGCACTCCCTTCTCTGTGTTTTTTG
TCTGAGTTGATGATTTGGAGCTCAAAGAGCTAGCGGAGGGAAAAGCTGAAGCCATTCAAA
CACATAATGAGAATTGGAGATGTAAAAGAAGGCTGAGTTCTAGGAGTTGCAACAACTTAG
GAGATAACAGAACCAATTCGGAATGAGCAGGAATTGTAGGAATGCAGGCGAGGACTAGAA
GAATCAGCTACATGCTGTTTACTGGCAAAGCAGGAGAAATGTGACTGAGGACAGTATGCC
ACTGAAAACTGATGAAAGAGGAGGGAGACAGGAGG
Sequence 923
CCCTTAGCGTGGTCGCGGCCGAGGTACTGTTGTCTCATGCTCTCTTTCTGTTAATAGCAC
CTCAATTCTACTCTGGGGGACATTCCTCCTCTCTTTTTGGTCTGGAATGTCCCCTGGCTT
CAGGGACAGCTCAACATGGGCCTGGACAGTCAAATTCCATCCCCAAGCTTGGGACTCAGG
GAGACCATCCAGTGACTTGTTCCTGAAGTGCTGGGAAGGCAGAGCNTCCTTTCTGCGGGG
TGCTGAGTGATGGGACGACAGNGTGGAGCTACTGNGCTCTCCAAGCCGGNGCCCAGGACC
AGCCTGCCTGAGAACGAAGCCAGC
Sequence 924
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTGCCTTGCAAAATTATATTACAAGAAGAAG
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TCAGGTCCGTCTCCCCACCTCCCAGACCTCATTATATTATCCCGAAAAGAACACGATCTC
TTTAAGGCTAGGCAAGTATTGCGCTGATGAGCCAGGGACTGCCCACCAATTGGCAGGCCC
ATTGGGTGATAAATGTCCAAGGACCTCTAGGCTGACGACACATTTTTCATCATTAATCCA
GCCTATTGTAACCAGGGCCACTCACATTGAT
Sequence 925
CCCTTAGCGTGGTCGCGGCCCGAGGTACCTACTGTGTTGAGCCCTCTTCCATCTCCTGTA
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TGAAGTATCCCGATTGAAACGGAGATCTAAAGATCTGAATTGCCTTTATCCCAGAAAAAG
ACTTGTGAAATCTGAAAGTTCAGAGTCTCTTCTTTCTCAGACAANTGGTAATAGTAATCA
CTATCATCATCATGTGACATCCANAAAGCCACAAACAGAGCGGTCCTTACCAGTGACTTG
TCCATTGGTTCCAATTCCTAGC
Sequence 926
CCCTTAGCGTGGTCGCGGCCGAGGTACCCAAACACAAGATTGCTAATAGACTGCTAATAA
TAGAACTTAATAAATGAAATAATTTATTTCATTTATTGTTGCTTGGAATACAGAAAGTGC
TTAGTAAATATTGAATGAATCAACAAAGTACCTCCCAATATAGAGAAATCACTTCTGAAA
AGGATAAAACCAAGTTGATCCTATTCAATCGAAGGCATCTTTTGGGGCTGTTACAGTTAT
TTCCTTTATTTGAAGAAGGAATATGATATACCTACTTTGTTCCAAGTCACTGCTTATAAT
GTGCTAATGGTACCT
Sequence 927
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGTGAAGACAGCTACACCTGGTTTCCTCCCTC
ATGCCTTGATCCCCAGAACTGCTACCTTCACACGGCTGGAGCACTCCCAAGCTGTGAATG
TCATCTCAACAACCTCAGCCAGAGTGTCAATTTCTGTGAGAGAACAAAGATTTGGGGCAC
TTTCAAAATTAATGAAAGGTTTACAAATGACCTTTTGAATTCATCTTCTGCTATATACTC
CAAATATGCAAATGGAATTGAAATTCAACTTAAAAAAGCATATGAAAGAATTCAAGGTTT
TGAGTCGGTTCAGGTCACCCAATTTCGAA
Sequence 928
CCCTTAGCGTGGTCGCGGCCGAGGTACAAGAAAGAAAACAAATACCAAGTATTTACAGAT
CCAGAGAAAGTTCACAAGAATGGGAGGATGCCAGTTCCAATGCTTTGTAAAGTCAAAAAT
AGCCACATTGCAAAACAAACAAAAAAAAACGAGAACGTTCCCGAGTGTGCCTCCAAAACA
TAAAGGAGAAAATCATACAGAAAAACCTCATGTAAGGGTTGGAACTTGAGCAACCAGCTA
TCCAAATACAGAGGGGAATCCTCGCTTAGCTAGGGCATGGCCTGAGAGAAGCCCCTTCCT
GCTTTCAGAGCCTACAAGTAGTCCCCA
Sequence 929
CCCTTAGCGTGGTCGCGGCCGAGGTACTTAAGCAATAAATCTGAGCAATTATCAGGTTAT
TTTATTGCATTTCTAATGAGTTCTTCTAAAAAAAGTCAATCAATTATCACTGCTATATAT
GTTCTGTGTGTAAGGAGTGCTTGAGAGTCTTTAATTGTAACATTTATTAAATAAGAATAA
GAGGACATTTTTAAAGGAATTAAAGGAACATTAATTCCTTCATAAATGTATAGTGCTTAA
GCTCTGCTTTAAAAGGTCTTTCCATGTGCTCTTGGGTAACCACTTAGGGCTGAATTCATA

Table 1

GTATAAATATCAATAAATGTTGCAATCACAA
Sequence 930
CCCTTAGCGTGGTCNCGGCCGAGGTACGCGGGTGGGAAAGGGAGGATGACTCACTTACTC
TGAAATCTGGGCCCAGGAAGGACCTCTCCCATCCTTGGAGCCTCCTCATTCTCCTGTCTC
TCACNNGTCCCCCCACCTCTACCATGATGTCCTCATTCTGGGAACCCCGAGCAGGGATAG
TGGCTTGGGCCCTTCNTCTGGCTTTTCTCCCCACNCTTTGCTCCACTTCTAACATTTTTC
TNCCTTCATCTNACATGAAAGGGACAANGGGTTAACCCCAAGNAGGGAGGGCAGAAAACA
ANGNNCCCCACATCCTGGCTNTGCCTTCTGAC
Sequence 931
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCAGGGATTTANAGACAGGGTCTGGCTCTTT
TGCCCAGGCTGGAGTGCAGTGGAACAATCATGGCTCACTGCAGCCTCACCCTCCTGGGCT
CAAGAGATCCTNCCACCTCAGTCTCCCTAATAGGTAGAACTACAGGTGCACACCACCACG
CCTGGCTAATTTAAAAATTTTTTTTATAGANACAAGGTCTCACTATGTTGCCCACACTGG
TAAAGTATTTTTAAATTTGAGACATGAATAATGATGCAAATCATCCTTTNTATGGGTCTG
ATTCTGTTCTGTTACCTTATTCAAGGACTAA
Sequence 932
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGNAT
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GATCATCCGCCTTGGCCTCCCAAGTGCTGGAATTACAGGCATGAGCCACCGTATNTGGCC
ANANAAATTTTTTAATATAAATTTTTTCAGTTACCACTTAAAGGGAAATATGATTAAAAA
AACTAAATAAAGAAGAGCTTTAGTAAAACCATGCCCTCTTGCTAATCTATTAANAGTCAA
ATCTGAA
Sequence 933
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CCATGGGGAGGGACAGAAGGAAATAGGATGGAAAGGGGTTGAGGGACTTCAACTGTATTT
GTGATGTTTTAGTTCTTTAAAACAAAAATCTAAATGACATTTGAAATATGAAACAAACGC
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TGGTCTCTGCA
Sequence 934
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GGATATAGGGAGTGGATAGCTATTATTAATTGCAGATTATTTTGGAAGGAAAAACACACA
GAGAATTATGTATCTTTCAGTGTAAATGTTAGTTCTAAAAACAATCATATTATTTACAAA
GCTGCAGTTATAGAACACAATTCTGATTTCTGCCTCACCCCCACGGTTAATACTGTAAAA
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CTAAAACATAAAAATGTTTAGGCCAGGCGT
Sequence 935
CCCTTAGCGTGGTCGCGGCCGAGGTACCTAATTCATAAGATAAGGATTAAATGAATTAAA
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AAATGTTGTTGTTACTGTTATGGAATTTATCACAAATATGTAATTATATGTTTCGTAGTG
ATTATTCATCACCCCTACTGGACTCTAAGGTCTGTGAGGATATGTCTATTTGGTTTACCA
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AGTGAATACATAAAGGTT
Sequence 936
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CAGGAGGTTGTGGGAACATATAGACAGTGACCAAACTTTTAATGAATACAGGAAGATTTT
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GTGATAATAATCTTTTTATCATAAAATTTTAAGTGTGGTAGAGAATAAAAGTTTTGAATT
AAATGTTGAATGAAATGTGTTAT
Sequence 937
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CTCAGGGGACAGATGGTCCCTAAGGTGCAAAAGAATGAACTGGTGCTGATATATGACTGA
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Table 1

TACTTTTTCATTTTTTTTTTTACAGTCAAA
Sequence 938
CCCTTAGCGTGGTCGCGGCCGAGGTACCAAGTATACTTCACCAGATATCTATAGAACATT
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TCTCCGGGATAGACCATATGTTAAGTCATAAAACGAGTTTCAATAAATTTAAAAGGACTG
ATATCATACCAAGTATGCTCTCTGACCAGAATGGAATGAAATTAGAAATCAATAACAGAA
GAAAATTTGGGAAATTCACAAATATGTAGAAATTAAAAAACACACTCCTTAAACAACCAG
TGGGTCAGAAAAGAAATCACAAGG
Sequence 939
CTTCCATACTCTTTTAATTGGATATGCCAGTGTGTNTCANTAATTTCCAGTGGCTGTAAA
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AGTGATCTCTTAGAGGTTTCCAAAGTTATGAGTTTGAGTTTACAAGTGCAGTTTTTTTCC
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ATAATTGCATATAATAAAACAGGTTCTTGACTGTTCTTTT
Sequence 940
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GTTGGTCGAATGCCTCCAAAGCCCTCGACCTTCCCACTATACTTCACGCATCTCTAGAGA
AGAGACAGAAGTAGCCAGGATGAAGGTCTTCAGGTTTAAGAAGAACTATGAAAAAGCAAA
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CTATAGGTAAGATATCAGA
Sequence 941
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GACGGAAAAATTTGATATCAAAGGAAGTATCAAAACCCTTGATGTGGTTAAGAGCATGGA
TAGTGAAACTAACCTCTGATGTATGGTGAGAGAGCAAAAGAGAAAGGATTGCAAAGAAAC
TGGAATGTAGAGGATGAACATATTGGTAATAATAATACTGGTGGAATTGTTATTCAGGAA
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ACATGGTAGAAGATATCAAATATAAAAA
Sequence 942
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CTGCATTTCTGCTGCTTATTGGCCATGTATTTATTGGCCATTTGCCGTCTGCTGTGAAAT
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TCTGATGATTTTTATTGT
Sequence 943
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TTAGGAAAC
Sequence 944
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AAGTATAGGTATTTACAAATAGATAAACTATATTCTTAGATGAGAATACTTAATACCCAC
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ATGGCACCTATAGTCACAGCTACTCAGAAGGCTGAGGCAGGAGAAGCACCTGAGCCCAGG
AGTTTGAGGCTCTAGTGAGCTAT
Sequence 945
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TTGAATGAATAAATGTATATAGATAGAAAGTAGAGACCTTGATAAAGTCAAACTCCTTGC
CTTTACAAGTGTGTGTTCAGCAGCCATGCAAGGGAGATGCCCATCTGGCAGTGGCCCAGG
GCAAGGTGTCAGAGCCCTAGTGGCAGGGAGATGGCATCCACATATGAGGGAGGGTGACAT
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Table 1

Sequence 946
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGCATATTTAATGAATTATTTTATAAATTGC
TGTTGTGAAGCATTTGTGAATGACCTGCCTCCTAGCTTTCAATGCTATTGCCCAGGCTNG
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AGCATTTCCTGGGAGGTTTCTTTTTCTGGTTATGAAAATAATATATGCTTATGGGGAAAA
ATTGGAAAATAGAAACNAGTATCTAGAAGAAAAATCACTCATAATTCCANCACCCTGTTA
ATACTTTGTCTTTTCTTACAGTTTCTAATA
Sequence 947
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGTAGATGAGAACTACTTATTTAGAGTGGCAG
AGCATGCTATAGAAACAAAATATGAGTAATTCTAACTGTAGTTATGTTATATTAGCATAG
TGAGATAGTAACATTAATAGAATTCCTTAGGTGGAATTTCTTTAATGC
Sequence 948
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CTTTTATTGCAACTGTTTTATGATACAGTTTTGCATTGTATGTGTTTACTTTTTAAAGAA
GCATTTCCTGGGAGGTTTCTTTTTCTGGTTATGAAAATAATATATGCTTATGGGGAAAAA
TTGGAAAATAGAAACAAGTATCTAGAAGAAAAATCACTCATAATTCCAGCACCCTGTTAA
TACTTTGTCTTTTCTTACAGT
Sequence 949
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TCAAGGTAGCTCGGAGAGACGGTGTCTACTTATTCACCACATCATGAGATCACCTCAAAC
TGAGCAGGCAGCCAATGAAAACCGTGAGCTTTCTTTACATTAACTTTCTGAAAGTCATTT
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TATTTAAAACACT
Sequence 950
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TAAAAGGTCTGCACCCACATATGCAAATAAATA
Sequence 951
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NAANATATGTTTTCACGTCTTTAACCANTGTTTTTCATAGTGNAAGTCAGGCCTTTCTCC
TTTGATCTAAGTGGAACCAAGAGGTTAGATACTCCCTTTNCTTTAGTTATATAATGGGCT
TCATGTAACT
Sequence 952
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TGCAGGTCAAGGGGCTAAGAAAATTGCAACACTAGAAAACCAACAAACTTAGGTTGTTCT
AACATACATACACAAATACAGGAGGGACGTTTATGGGTCACATCTGCGAAACATTTTTTC
CCAAAAAGCTGAATTTT
Sequence 953
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AAAACATGACCCCTCCATCCAGAACCAAACTAAACTCAGGAGTGATTAGAATCACCTGTG
GGCATTTTCCCCCAAACCACCCATACTCTGTAGATTCTGATAAGCGCTCTTAAAGAAGCT
ACAGCTCTTCCCCATTCCCTATCTGAAAGCAAGGAACCACTGGCTTTGGTCAGGAAACAG
GCATACAACATCAGATGTGATTATAA
Sequence 954
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GTGCTATTTTGTTNCTCCTACATTTACTCCATAGTAAGCTNTTGTTTGAGAAAAAAAATG
CCAGTTTGGTGCGTAGTAGATACGCAGAGGCCTGNGAAAGGGACNGATGACNCCATTACC
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Table 1

TACA
Sequence 955
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CATAGCACCTCCATTGACCCACATGGGGGCCTGCCTTGGGCTTCATCAGCCCTTTGGAGT
CTCAGATCCCTCACCTGTTAAAGGAGAGTAATACTACCCACTTACCTTTTTGGGTTGTTG
TGAAACACACATAAGACAGTATTAGGAGAAGTAAGGTCTGAGGGCTGGGCTTTGGACCCA
GCGGCCCCTAGGTAGAGGCCTGTTGAATTGGATGACAGTGAACTTTGCAGCATTTCCTAA
CCTCAGAAGTTCAAGA
Sequence 956
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TGGATGTGTGCAGGTGACATAATTTCAGGGGATAAGGTAAAAATTAGATGAAGCCCAAGC
AAATATTCTTAAAAAGAAAAACTTAGGATTTTTTTTTACAAAAGTTAACTTAAAATGCAT
TATCTAGAATAATGTTATAAATCAACGTATAGAGACGTTAGTGAATAGTTCCCTTCATTA
GGATGTTGAAGGAATATGGTTTCAATATTCAACAAATGTCGTGATGCCTATAAATTTTTC
TACAAACAAGAGTATTGT
Sequence 957
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GATTAATGTGTATATACTAGTTCTGTTACTAAGGAGGGATGTTAAATTAATCCCTAGCTG
TAATTGTGCATTAGTTTGTCTCTTTTCAGCTGTTCTAGCTCCATAAATTTTTGGAGCTGT
TAGGTGCATATACGTTTAGGATTATTTTGTCTTCTTGGTGAACTAGACCTTTTATCATTA
GGAAACTGTCCATATAACCAC
Sequence 958
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CTGAATTCAGTAACCTGGGTCATGGTCCAATTTTGCTCACTACTTCATATCTTTTATGTA
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ATTATTCAAATGTAGCTATTTAACGGTCAGTAACAATGCCTAGAAACCTAT
Sequence 959
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TCCCACCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGATGTCCAGCTTAGGTTCCAG
CTNTTAAAANANTTGTCAGTGTGGTGGGCGAGGTGGGTCACATACACATATAATTATAAG
GTAAAAAATCACAACTACTACAAGAAAGGTGCAAACATTTATGAGAAAACCAAAGAAGGG

Sequence 960
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TATAGCCAACCTTGGTGGCCTAATAGAGAGGAAAGTAGGGAATAGCTTCACCTTCCTTCT
CTAATCTTCTGCTAGTATCCCTATTAATTTAGCCTAATTAGAAGCTGGAAGGTAGGAGAG
CCTCCATGGGCCAAAAAAGCTGTTGTAGAGAACATGGATCCTTGAGGGGGGTAAATGGGC
AGATAATTCTAGCCACAGATTG
Sequence 961
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CCTCCATGGGCAAAAAGCTGTGTAGAGAACATGGATCCTGAGGGGGTAAATGG
Sequence 962
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CAAGCTTGTGCTTCTGGATGGTTGCTTTGTCAGTGAACACTTGGATTTGGAAAATACAGC
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AACAACAAAATTAGGATGGTAGTGAAATGGAACTAAATCAAATGCAAGGTTTTAGTTTAA

Table 1

TANAACAATGTCATCCTTTAATAATCTTTAAAAGAAGAACAACTAAATAACCCAATNACA
AAATTTGAAAATTAGGGTCAAACCT
Sequence 963
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CAAGCTTGTGCTTCTGGATGGTTGCTTTGTCAGTGAACACTTGGATTTGGAAAATACAGC
ACCTGGGTTGGTTTTGAGAGAAAATGGTTTCAACTTTATAATTACAGTTTTAACCACCAC
AACAACAAAATTAGGATGGTAGTGAAATGGAACTAAATCAAATGCAAGGTTTTAGTTTAA
TAGAACAATGTCATCCTTTAATAATCTTTAAAGAAGAACAACTAAATAACCCAATAACAA
AATTGAAATA
Sequence 964
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AACTGCTGAATTACCATACAGGGAAGAATGAATTCAAGAAAATTCCCATGCAAGATAGGC
TCTTAAAAAAATAAATTTACACAAGAAAATCAGCACTGTAAAGGTAATTGATAAGCCCAAT
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AATGATG
Sequence 965
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GGCTATAGAAAAAACAATACTTATGAAAAAACCAATTGGAAATTTTTAGATGGAAAAGCC
TGAAAGTAAAAAATTCAACACATGGTCTAAAAGAATAAACTGCACACAGCTTGAAGGGAA
AATTAGTTAATTTTACCNAAGAAA
Sequence 966
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CATGAAAGA
Sequence 967
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CATGAAAGATACAAAAATAAAATCAAACTTCTAAAGATGAGAAACTGTAGTGTTTGGAGG
GGAAAAA
Sequence 968
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CACAATTGT
Sequence 969
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TACAGTCAGCTGACGTCTGGCACCGCCTGTGCTGGTGTGCGCTAGCCTACTCACTCCCTC
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Table 1

TTTACCTTCCTAAATTAATTCTCAAGTAGTCCTGGGAGCTGTATTTATTTTAAACAT
Sequence 970
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TAAGTTTTTGGTAGAAAACTAGCCCANTNGAAGTCATGTGGGTTTGGGATTNTTCTTTGT
ANGANAGGNTCCTAATTACTAATNAGCTTTTCAAAATAN
Sequence 971
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GGTTATAACCTTTTTCTATTCTCTGCAACAGTGGATATAGGATTGGAGTTATTTTTTTCT
TAAGTTTTTGGTAGAAACTAGCCAGTGAAGTCATGTGGGTTTGGATTTTCTTTGTAGGAA
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CTTCCTGTGTCAATTTTGTTGTCTTTTTCTATAAATTTGTTCATCTATAATTTTAATATT
TTTGGTATAATTTTTTTCAAAAATAATCTTGTATTTATTTTACAAGGACAGGGATCTTTA

Sequence 972
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GCAGATCATTCCCCATTCANCCCTGGGTATGGGACTGAACTGTGTACCTTGCCCGGGGCG
GGCCCGCTTCGAAAAAGGGGCGAAATTCCAGCNACACTGGGGCGGGCCGGTTTACTTAGT
GGGATTCCCGAGNCTTCGGGTTACCCCAA
Sequence 973
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CATTCACAAAGNGTATGTCACTTAAATACCTCAAAATTTCCCTGTTATACATGCAGATCA
TTCCCCATTCAGCCCTGGTATGGACTGAACTGTGTACCTGCCCGGGCGGCCGCTCGAAAG
GG
Sequence 974
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CACAATCTTGACCAGTANCAGTTGAAANGGGAGTTTAAGGTGGGGGTGA
Sequence 975
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CTCTGTTGTTTTCACTTAGTATTACTTTAACTATTAGGGCTTCTTTTTTGGTTNCATATT
AAATTTGTAAAATAAAATTT
Sequence 976
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TTAGTTNGAAAAGGGAGNAGGTCCTTT
Sequence 977
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ACCAATTCATATGGACCTTCAAAATTAGTCTTATAAAATTTTTATGGATATTGGNATTAT
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GATTTCTTGCCATTTNCCTTTTGGNTTT
Sequence 978
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TCAAAAAATGAGCTAGGAGTAAAGTATCTGCTCCAGAATCTACCCCCATCCCAGAAAGAG

Table 1

CAACCCAACTGTGTCCTGAGTGGCTCTTAGAGTTTAAGACTCTGAATGAATGCCTAAATT
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Sequence 979
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GAGCAGTAGACCAGGAGTCAGACAGTCGAGGATCTCATTCTAAATTTGAAGGTGAATAGC
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TCATAATAGCTACTCCTGCCTAACTCATANGTTGTTGAGAAAATGAAGTGATT
Sequence 980
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AAGAAATTCCCCACAAGCTCTGCAAAATAAGTTCTGTCAATCAAATCTTACATGATGCAT
TAACTGAGCTATTTTAAAATACTACCATGGAATTCATCTTTAAAGGGTGACCTTTGTAAA
AG
Sequence 981
CCCTTAGCGTGGTCGCGGCCGAGGTACAGTATTGTTGACTGGCTAACAGAGGACCAATTA
ATAAGCCAAAGAAATGGCTCTTTAACAATGAACATTTCTGCCATCAACTGACAGATCCCA
GGAATAAATGTTTTCCAGTGAGGAGACTTCTCTGGTTTTCAGAACACCTCTGGCTGCCCC
TGCCCACCCCATAGAAGGGCTATCCCTCCAGGTCAGGTTAGCATCATCACCTAGAGCCAA
CAAGTCAAGGAGGTGATGGTTTGCCTTTGACATCTCTACCCAGACCAGACTCCACTGGAG
AAGACTCTCCCTTTTTTCATCACTGCCCTACCTAGTTAGGTTGGTCCTGC
Sequence 982
CCCTTAGCGTGGTCGCGGCCGAGGTACTTAGATCAGATGGATTGAAACATGACAGCCCCA
TTTCATCTGGCCGGTTAAGGTCCTCATGGAATGAAAAACACTTTCGGGCACTCTCCTATG
AGAGAGAGAATGGGTTTCTTTAATTGCCAGATTGTCTGAACACAGCCTCAGCTACTTCTA
GGAATAAGACGAAGCAGTGAGGAAGTTGCCAGTTGAGTGATTCTTGGGGAAAAAAATTAG
CATTCAGTGCCAGCTCTCTAAAGTGTGGATTCTGGATTCTGGTAGAAGCCAGTAAAGAAA
CGTTTTTCTCTGGAGTGGAAGCCTAGTAAGATTTATTT
Sequence 983
CCCTTAGCGTGGTCGCGGCCGAGGTACAGTGACATTTCAAGACATGGCCCAATGCACAAG
CAACTTCCCAAAGCTGTAATTCACGAGATTCCTCAGGGTCCTCTAAGCTCCTTGAGGGCA
GAAACTTATCTTTGTATTACAGCTAGCCTTCAATCAGTAGGTGTTGAGCTGATTTTCTTT
TTCTTTTTTAAACTCAGAAGTTAAGTTCCAGCTTCAGTGGCTATGCCCAGATGGTCTGAT
TCTGAAGGACAAGAGAATTCAGNTGGCATAAGCCCTGTGCTTGGCATGTAGTANGTTTCT
CAGTAAACTTTANCTGGCGGGA
Sequence 984
GAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTAGTAAAGATGGGGTTTTGCC
ATGTTGGCTAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACTTCGGCCTCCC
AAAGTGCTGAAATTACAGGTGTGAGCCACCGCGCCCGGCCGAGGACACTATTTTTTTGCT
TTGGAAGAAATGAATCCTAGTTTTGGTTCAGAAACTGTCAACAGCATTGTGCCTCTTCTA
TGACTACTAAATTTCAAGCAAAGAGAGCTGAGTTGGGGGTAAAAGCAGGGCTATTCCCCG
CCTTCAGACAATGCTTGTCCCTTATCAAGGGCAGACTGCTGTCTGG
Sequence 985
CCCTTAGCGTGGTCGCGGCCGAGGTACTTACTTAATTTTTTTTTTTTTTTTTTAGTAGAGA
TGAGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCTG
CCTCAGCCTCCCAAAGTGTTGGGATTACAGGAGTGAGCCACCGCACCCAGCCTGTGTGTG
TTTTTTTACTTAAAAATTTTTAAATTTAAATTTAAATGTTTAATTGACAAATAATTTTAT
ATATGGGGTATAATGTGATGTTTTGATGTATACATTGTTGTATACGTTGTAATTGTATAC
ATTGGGGTTGTATACATTGGGATGTATACCATTGAAATTATTTGNATCCAGAAAATTAA
Sequence 986
CCCTTAGCGTGGTCGCGGCCGAGGTACATGGAATACATAATTTTGAAATGGAGTCAGGGC
TTTCCTAATGATCCATTTTGTAATTCACCTAACAGCTGAGGGAAGGTCCAGAGAAGGAAG

Table 1

AACTCAAGGTTAGTAGACAAACTTGATATTGAGTTGCACTGGCTGCCTTCTCTTTTTGGT
CCCCTAAAGAGTATTTATCATCTTAGATTCAGCTTAAGTTGTGGACAAATATCAAGGGGA
AAAGTATTTACAGTTAACGTTGGAATCACACGGTTTTCCGGGGTTGTGCCTCTTTACCCT
TCAACTTTGGTGGTTTCTAAAGAGGGACCGATTATTAGTTGCTTTCACTAAGGAAGGGGA
AG

Sequence 987
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGGCCTAGAAAATATTTTTTTTTTTGAAATGG
AGTCTCACTGTGTCGCCCAGGCTGGAGTGCAGTGGCNCAAATCTTCNTCTNAAAAAAAAA
AAAAACAAAACAAAAATAAACTTTACTCAAATATCACTTTCTGTTAAATGTTCTTAATTC
CTTCAATCATCCCCCTCTTCTAACTNTNACAGCACTTTCTTCCACTACGGCACGCATTAC
ACGCCAACTACTCACCAGTTCACGTTTTCCGCCCTNTNTCCCACTTGCCCAATCACAGAN
TTCCTAAAGAACCAGGACTATGTTCTACTAGTCTTTGTAGCCACTGCACT

Sequence 988
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTCCTGTTTCTACAAATTTATCTTATAATAAT
TTGTCAAATGTTGAGTGCACAGATTTATTCATTGCAGCATTTGGTTTTTCATATCAAAAG
ATGGGAAACATTGTGCAAACAATGCCCATCAGTAGTGGATTGATTAAATAAATTAGGTAT
ATCCAATAATTGAATATTATGCAAGTATATAAAAAATAAGAATCATGAATATGGAAAGAT
TTCGAAAATATATTGCTAAGATTAAAAAAAAGGAAGGGGCAGAAGAAAATAAGTTGGGTA
AAAAAAACCCCAGAAATGTTTACTAATAATTATATTTAAAAACTCATAGGATAAACAAGG
AAGGGTAATGAAATAATTAAT

Sequence 989
CCCTTAGNNTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTAGAN
ACAGGGTCTCACACTTTGTTGCCAGGGCTGGTCTNGAATTNCTTGGACTCAANCAATCCT
CCCGTGTTAGCCTCCCAAATTGCTAGGGTTATAGGTGTGAGCCACCCTGCCCAGCCTATG
TTTATTTCAGATGTTCAAAACAACAAACAAAAATAACACACTNGAAAAAATGATCAGAGA
ATACGTGTTAAATGAGAAATNGTTCAGGGCTTTTATAAATTTGTGACCTCCACCCTTCCC
CTTANTCCTTTTTCTCCATAAACTCTAATTNCAAATTTTACTACCACAGCAAAAAAGAGG

Sequence 990
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGTGATTGTCTGTGTTGAGACTATTACAGAGC
TCCAAAAATTAAAATAAAAATAATAATTTTACAGAAATACATATTTGCATTGGAATATTT
AAGAAAGTTGAGTTTGGATGCCACAAGATTATTGGAGTNATAGGNAGCTGGGCACAGTGG
CTCACACCTGTAATCCTAGCACTTTGGG

Sequence 991
CCCTTAGCGTGGTCGCGGCCGCGGTACCCTAAAACTTAAAGTATAATAATAATAAAATTA
AAAAAACCAAAAACAAAGATTAACAGAAAACAAAACANCAAAAAAACTCCCAGCATATAC
ATTGAGTCATTTGCAGGTTTGGGAGGGGGGGAAATGCTTTTTTGTATTAGGAGAAAGGGA
AGCTTTCATTTTAAATGGCTATATTACTTAAAGTTTGCANTAAATATTTATTACTTTC

Sequence 992
TGCTCGCTGGACAGAGGGCAACCCAACACTCTAGCCTAAAGCCCCGTGACACCTGCAGCA
GGTGCTTGCCCACGCNTTGCACCCGTTCCCGAANTAAAAAGTCGCCGGTCCTANAAGGCG
NCGAGNTCTTGGTNGACCTTTGNGCANCCCCACCCGTTGCCAGTCTTGAATGNGGTTACC
CCANAGNCGCCNCAGGCTGACATGGGAAAGGATGTTCTTTGGGAAAAAAAAAAATGGAAC
CCCGGTGGGTAGNCCCTTGNGGGGCNTGGGNAGCCCCCCGGANGGGGTTCCCCGNCNGT
T
TGGCCGGGGCNCAAAATTCANAAGNCAAGGGTTGGGGNATCCCCGNGGGGAACCTTGGG
G

Sequence 993
ATGCAGAATTCGCCCTTTGAGCGGCCGCCCGGGCAGGTACCCCATCAGAGTGTTTCTCTT
GGCTTNCCTGTATGTAAACCTTACCTAATACTTTCAGTCACCACTCTTTCTGTGTTCATT
TCCCTTTTAAGNCAAAAAANGGGANGNAAGTAAGTTGGNNATTTGGNGTTTCAAAGNGNC
CAATTGNCTTTTGNCTTTTTTCACA

Sequence 994
CCCTTAGCGTGGTCGCGGCCGAGGTACCAAGTTGTTCTCAAACTTTCATGTTTGTGTATA
CAAATCAGCTGAGGCCTTCACTAAACTACAGATTCCATGGCCTGGCCCTCAGAGATTTTG
ACTCAACAGGTCTGAGTTGGGACTAGAAATATGCATTGCTAATAGGCACCCTGACAATTC

Table 1

CGATGTAGGTGGTCCTTAGAACATATTTTGAGAAATATATTCTGTAGTCTGGCAGATAAA
GAATTCTTAACAAGGAGGTCCTGCCCGGGCGGCCGNTCGAAAGGGCGA
Sequence 995
CCCTTAGCGTGGTCGCGGCCGAGGTACCATCATCTGTTTCCCTCTGGTTATAAATCTTTA
ATGAAAACGGATTTAAAAAGTCACATTATGATGCTCGAAGCTCTGACCTCTCATCACAAT
GAGAAGCAAAAGACATGCCATAAAGATGATATTTCCCACAGGAACGATATTAGAATTATG
TGATGCAATCTCATCCAAGGTCATGGTATCAAACCAGACACAGCTAAAAATGTATCATAA
TAGCAAGGATACAGTAGCAAGGATGGGCCTCAATAAACATTTAAAGTGGAAAAATTCTTC
TCTAACTCATATCAAGTACCTGCCCGGGCGGC
Sequence 996
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCAAAATAGATAAGGATCCTGTTTTTTGAAAT
GAACCCCAGTTGCGCCTTAGGCATTGTGAGTTGGCTCATTTCAAGCCAGTTGTAATATGG
TTTTTTATTCTCTAAATTTCGGGACCTGATGCTAAGGAATGTGAATATACAGTTAGGTTC
CTGCGAACCCTGTGTTGGTTCAAAAAGGCTGGTGGAGGGAAATTTATGACACTAAATGCT
TATATTAGAAAAGAGGAAAATTGGCCGAGCACGGTGGCTCATGCCTGTAATCCCAGCATT
TTGGGAGGCCGAGCCAGGTGGAT
Sequence 997
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AATTGCAAGTAGACTTTTCAAAATTAAATTCACTTACTTCTATTCCCAACTCAATCTAGA
ATATTATTGGTGATAGTGAAAAGACCAGACAGATGACATTACTTCCAAATTTTACCAATC
TAATTGTTTTTACTCACACCTGTNGATGTCACTTTAAAAATGTGAATATTAATTTCTTCA
AAACTACTCCAATTTAAGTAATGAGTTAGAGCTTTGGCAACCATTAAGGCTCTCTTTTCC
CAACTCTAACAATATGTGGTAATGTCTTCCCTGACTTCATTTTATGTTTACACAAAATCA
AAGGTTATATTTAAAGGGTTTTCTACATTTTTTTGGGATATTTACCTCCTTGNAATTTAG
NNTTATATGTCTGGATTACAAAAACATATNATATTCAAAGAATTTNTAACACTTAGAGGT
AGAAGTGAAATTACAGGTTGAAGAATTATTTAAA
Sequence 998
CCCTTAGCGTGGTCGCGGCCGAGGTACGTGTTTTACTTGGTGCTGTAGGTAATGCTAATT
CATGATAAATTTTGAGAACCACTCTAGGGTAGTATGTTTCCAACAGTTTAGGTCATGAGC
AACCTTGAGAAATACACTTTTAATCATGACTCAGCACACACACTCACATGCACGTGTGAC
TTAGACGTTCCATGAAACAATGCTTATCTTACAGTGTGTTTTCTGCTCTGGTATTTTTAC
TTATATTCTATTAAATAGATATGTGTGTATAAACTTATTGATATAAAAATGTGGTCATGA
TCCACTAAAGTGATTTTACAAGCCACTAATGG
Sequence 999
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAACTTGGGTTNTCCTTTTTNATNATTCTGN
AAAATNANAAAAACCNAAANCCTGTTNATNTAGGGTTTTNATGGNTANAGTTGNANAAAA
CTGNNTTTTGTNAGTTTNAANAAGNCCATTTNAATGAGTNAAATTTTTNAAAANCCTCNA
AANCNAACAAANCTGNAAAAAAGTAGGGGNGGGGGTNAAATGGTTNATTTNAAATGTTTG
CCTTCANTANCATGAGAGGG
Sequence 1000
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAACTGAATATTTATTTAAAAAAGCATTAAT
TTATCTATCTATATAACTAAATCTATCAAATATTCTTTAAAACACGAACCAAAGTTAATC
TGAAACTCTTCCTGTGAAAAAAGTCATGTATTATATGCCTTCAACACAGAATTTGTCATT
ATTTCCTGTGGCATTATACTATGCCCTTTGTCATATGCTTTTTTTCCCATAGAGCATTTT
TTCCCATAGAACTTTGTATTCCTCCACTTCTACCACCTTTCTTTGAAGAACTCTTATTTA
CCATTTCTTGGACTAAATTAGGAA
Sequence 1001
CCCTTAGCGTGGTCGCGGCCGAGGTACCCAGAATATGGTATATCTCTTCATTTATTTAGC
TCTTTTTAAATTTGTTTTGGTAATATTCTGTGATTTTTTTTTTTTTTTTTTGGTATGGAGG
TCTTACATCTTTTGTAAAATTTATTCCTAATACTTTGGATTTTGACATTATCATAAAAGA
AAATTATTTCACTGACTTTTCCAGTTTGCTGCTGGCCTAAACATATANTTAATTNTTTAT
ATTTTAATCTTGTATCCTATNACTTTGCTAAATTCATATA
Sequence 1002
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACTTGGCATTAATTAGATTGTGATCATAAG
TCAAAATGTCATTGGTTATAAAGTGGTCATCAGACCATGCAGACTATTACTAATATTGGT

Table 1

TATGTTTTAGTTTATTGCAGTGAAAATACAAAATTTAAAAGTTATTGTAGAGAATTATCA
TACCCCCCAAAAAGTGTCATTGGTCCTCCAGGACTCTGTAGTCCCCATCCAAGAAAGACT
GTGATAATTGTCAAGGGGTTAGTATGGTCTGAGCATGGTTGATGGTGCTCTGTCATTCTG
GTATTAAACAACCTGCCAAATGTCTTGATTACATGTCCTAAAAAAGTGAGGGGAAGAAGT
GTAGGACAAATGCAAAATAAAATAACACATTTAGCTATACTTTTAAGTATTTTTTATT
Sequence 1003
CCCTTAGCGTGGTCGCGGCCGAGGTACATCTGTTTCTGAAAGCATTTTTCACTGAACCAA
TTTTCTATACCTTTTTCTTGTATTCTTTTCCTTAGCTTTTGTTTATATGGTTGCTATATT
TTTCAAGCCTCATACCAGTCATATAAAACCATGATAAAACTTCATCAAAGCATACTTGGG
CAAATTTCAATTATCAAGTAAAATTGTAAAGAAAAATTTTTTACTAGTTTGGAAATAGAT
CTACATGTTTGATTTTCTTTCCTTCCTCCCTCCTTTGTTTCTTGTCTTTCTCTCCCCTTT
CCTAAAAAGTTAATGGCTATCATTATCTTCACCAAATTAGTGTTTGGTATACCCATAA
Sequence 1004
CCCTTAGCGTGGTCGCGGCCGAGGTACTCCTGAACTTAAAAGTTGAACAACAAAAAAAGA
AGGAAAATGCGTTAATACCTTATTGTAATTATTATTTTTTGGAAGACTATTTTTTATATT
CAGAAGAAGTGTCAGAGTCAGCAGAAAGGGATTATTTCTCCATTTACCTACAACAATGGT
TTTAAATGACTGGATAGATAGAAATCTCTTTCAACTTAACTGCTTAGCACATTGCATTTT
TCTCTGTTTCAAGTTAGTTTTCCAAAGGATTACTGACTTTTTACCTAATTTGCTAAGGGA
TGTCAGGCCTTAATGACATATTTCTCCTCAAATAAAGGATACAACATGC
Sequence 1005
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCGGTATTACAGCGCCACCCACTGGCTAGAAG
TCCTCATAGCACATATGAGATGTAGCCATAAAATAGATGAATTCTTGAAATANGGAATAT
AACACTTGACTATTCTGATTCAGNAGAACATAAAAAATGTTCTAACAAAACAGAACCAGA
CACATTTATATNTATTTCTACAAGTNAACAGAATATCTATTAGA
Sequence 1006
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATAGTTCTGCTTGCATTGGTCCCATTACAAT
CCTGTCTAAATCCTGAAGTAAAAATGAATACCATAGTGAAGAAATTACTTGTGCATGTGA
AAGAGGCTGGTCCAACTCCTTAATTGCAACAGGGATTTGATTCTTCTACTAGTAGTTAGG
AAAGGTTGCATTAATATTCAGTAGTTAAAATGTGCGATTCTAAATTTTTTGTAATTTCCC
ATGAGAGAATAAATTTTTTCAAAAATATTCCCAGTAGGTGAATGGCTTTAATACATGGTA
TCTGTGAAGATGGCAAATAAAATGAC
Sequence 1007
NTNTTNGNNNAATNCNCNNTTAGCGNGGTCGAGGGGCGNGGNNCATNTAAAANGTGATGC
TAATACTTTAAAATGTGTTAAGATATATGATTTAAAAAGCATTGTNAATTGTATACTGCA
GTGTCGTCTACATGGCATTTGGACAGGACANTAATTGTAAAACATAAANAGTGCNAATTG
TTACACTTACATATGAATAGCTGAAATGNGCAACAGTGGACGCAANTTTTTTNGTTCTTC
AAGTTTTANTAATTACCCCAANAANACCTATTTAACNAGGCTGATNCTAACNTGGGGGAT
ATTTAATGGNTTTCTTATTAATTTGGACCNAAAAANTCTTTTTGGAATTAANCTTGGGCN
ANTTCGCAACCAAAACCAAATTTTAAT
Sequence 1008
CCCTTAGCGTGGTCGCGGCCGAGGTACACTGGCTCACCTCTCAGGGCTTTGCTCCTTGGG
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TTGTAAATTTCCACTAACTGAAGATTGTAGAGGAAAAAAAAAAACATCTTATCGAATTCC
TGCTCTTATAGCTGATTTTAGCTATTAGGAAAACATCCCAAGTTGAGCTTTTCTATTCCT
AGAATTTCAGATTTCTTTCCTTTTTAAAAATTTTATCTCCTTTTATAGTAGTAAAAATAT
TTTCCTTTTTTTTTTGGAATGGGAGGTCTTAAGCTCAGTGTCAAAAATAAAATCATTTT
Sequence 1009
CCCTTCGAGCGGCCGCCCGGGCAGGTACCTTCTTGCCTACAGCGTTTAGCTCCGTTTGTT
TTGCATAAAGATCTGTTTTCTGACTTCGCATGAGGGGTAGATGTTCAGCTTATTCTCACT
ATGTAAATTACTTAGTAAATAATAGGAAGAGATGTTGAAATACAAACTTTCTGCCACCAG
ACCTTCACTCTATTGCAGTCATTTTCTCCCACTCTCCCCCCTCTCTCCCACTTCCTCTGA
GGATTACCTTCCCCTCTCTCANCATTCCTCTGTCAGTGGCTTTTTTTTTCCTTTGGCATG
CAAACATGCTCAAGTCTGTCTTATA
Sequence 1010
CCCTTAGCGTGGTCGCNTNTCGAGGTACTCTTTTCAGATGAAAGTGTTCGGTCACCTGGA
ACCTGTGAGTATGTGGTTTTTGATCTGTGACTAAACTGTCCCCATTTCCCAGTTTCTCTG

Table 1

CTCCGTCAAATATCAACATTTTACCAGGTTTCTCTGTTGTTGCCAAACCTGTCATTTTTA
TTTGGTGTGGCTTCTTGGGAAACTTCCATGGCCCATTTGATGGGAATCAAACAGTGAAAA
CAAGGACAGATGCACCAGAGGTGGCATCAGGAACAAATGGGTCATAAGAACTTACCTTGG
CAGCAGCCCCAGAATGGTNAGGAGGAAAGGCACTNTAAGGTATCAGAAGGTAGAAAGGAN
AGGTTGGATNATAGNAATGGGGGAAAGGG
Sequence 1011
CCCTTNTNNTGGTCGCGGCCGAGGTACTGAGACACTGGATCCTAAGAAAATCAGAGTTAT
AGCTAGTGGCAGTTATCAAGGGAATGCAGAGGTTTCTGTATTCTGAGCATGTTCCTGTAA
TAGGATAGATAGGCGATGTGGCAGCAACAACTCCCAATTCGTAATGTCTTAAAACAAAAA
CAAGTTTTATTTCCCATTTATGCCATGTTTCCAGCACAGTTTCTCAGAGGGCTGTGCTCC
ATGCATTTACTCAAGGTCTGGGAATGATCATGGCTACACTATCTTGCAGCCACCATATTT
GGAACCTGTTGCCACTCTGATGGCAGCAGAGAACAAAAGAAA
Sequence 1012
CCCTTTCGAGCGGCCNTTTNNGGCAGGTACGGGCTTTTTTGTTCTTGTGCAGTAACAGTG
AGGGCATGATTAGCCATCTTTGCCAGCTGATGTCTTGTTGGACACCTGCCTTGTTACCAC
TCTAACAGGCCCGTGTCAGCAGCTCCGCTTCCTCCTGACAAGCTGCGAGCACAGGGGACA
GCACAATCTGAAACTCTTACNGATACCAACAGCAACAAAAATGAAAGCAGTTATGGTGGG
CAAGCATTAATCTAAAATTTTTTTTAA
Sequence 1013
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACGCGGGGGGTCTCACCATGTTGGCCAGGCC
G
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TAAGCAGGAGCCACCGCGCCCAGCCTATTTTGTTTCTTAAATTTTTTTGTTTTTCAGTCA
CCACAATTTCACCATGCATAAATCACAACGGTTAACAATTTAGCATCTTTGCCTTCTTTT
CCTGTGCACTTACGTTTTTATGTAGCCAAGATCACACGTTGCATTTTGCTGCTTTCCTTA
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TCATTTTTAGTAACTGTGTAATATTATATCATAAAGTTAAAACATAATTTGTCATTCAAT
TGTTGAAATTTTTAGGTTACGTATATTTTCTCTTATAAATATGTAAATATGTTTATAAAA
AGTTATATACAGTTTTTTATAAATCTTTGTGCATACTTTATACTGGTTCCTTAGCATAGA
GACTGTGGGAATAGGATTTCTTGAAAAAANGTAAAAAGTGTGAGTATGCATATATACCTG
GTACATATATGTTATTATTATAAANGGTAATATTCTTTTTTTTTTGGAGAAAGAANTCTC
ACTGNACTTCANNCTGGGGTAAAAGTGAGACCCCTGTCTNAAACCAACCGGAAAAAAAA
Sequence 1014
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTATTCAGACAAGAGTTCTGACTCTCATGCTT
GAGGATAAGATTATACATTTCAGTATTACATTGAAGATATTTCATTTTTAACCAGACTAA
CTTAGTATATTGTTATTTTTAATGTGACCAAAGAAATATTTTCATAGAAGCTAATGCTGA
GTCTTTTGATAATTTGCCGTATCTTAGTCAATCCCAAAAAATTTATTTTCTACTATTTAC
ATATTATCCTAGTGGATATTACATTACTTACTGAAGCCTTTGGTTCTATGTTTCATCTAC
TCAGACTTAATTCAGGAAGAGCTTCATCCAGATGTTTTGTTTATTTGTTTCTCGATTACA
TGTATGAGATTTCAGAATTTATGAGATCATAGGTCAAGTGAAAGGTCACAGTTGAGAGGT
CAAGTAAGAAGCTAAAATTTGTGAAACCAAAGAAATGACAGGACAGTGCCAAATGAAAGG
TCAAAAGTCAAGTGACAGACTCAGTACCTCGGCCCGCGACCACGCTAAGGG
Sequence 1015
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CTGTTGCTCAGGATGGTCTCGAACTCCTGAGCTCAAGCAATTTGCCGGAGCTCAAGTCTC
AGCCTCCCAAAGTGCTGGGATTACATGAGCCATCGCACTCTGCTGTTTCTGAATTTTTTA
AACAAATAAATATCAAGCAATCAGATGCCAAAAATTACAAAAGAAAATCAGTATCAAAAA
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GAGGCGGGCAGATCACGAGGTCAGGAAATCGAGACCATCCTGGCTAGCACGGTGAAACCC
CGTCTCTACTAAAAGTACCTCGGCCCGCGACCACGCTAAAGGG
Sequence 1016
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CGGAAAATGCTGACTATATCTTTTGGTTGCTTTGGAACACTATCTCCTCACAACAGTCCT
TGTCTACAGAAATGGGAAAGGGAAGGACACATTTTGGTTTCTGCAACATGGCAACATTCG
TAAAACCAGAAATGATGTGTGACAAGAAACTAAAGAACTGGACGAAATTCACTTCCATTC

Table 1

ACCCTGGTTAAAGCTTCCTTGAATCAGAGATAAGAAACAACATGAAAAATCTATTCCTTT
TAGAAAACAAGTCTTTAACCCAGAGGTTGGTTTATTTTGAAAAGGAATTAGACTCTGGGC
CCACATACCGCTCGTTCAAAATATAATGCTGTGGTTTCAACTCCTGCTAAATGTTGCTGT
GACTTTTAAGCAGAGAACTTCTAAAAGGAAGTAACCTAGGGAGGGGCTGATATAACTCAG
ACATCAATAATTCATTTTATTGGAAATAGGAGTAGTAGTATGAAATGCTAGCANACTGTT
TCATTTGCAGGGAGGCATTTTCTA
Sequence 1017
CCCTTAGCGTGGTCGCGGCCGAGGTACAATTCAACTATCATTCTGGTTGCGGTGGAAGAT
GGAGACTGGCTATAAGGTAGAAATATGGTTTGGGGTCTTGGATATAGTCATGGGTTGCTT
TGAAGGACTGGTGACAAAGTTTGGACTTTACCTTGCAGACAGTGGGGAGCCATTGAAGAT
TTTTTTGAGCAGGAGTGCAGGAATCAAAGCAAATTAAATTTAAAAAAATTTAAATTAAGG
CTAGCAGGATTCAGTTTTCAAACTGGCCAGCTGTGGACTAAATCCAGCCTACAGATACAT
CTTGTTTGACCAGCAGAGAGGCTTCAAAGTCTTCAATACATTGCCAACACTTAAAAATGA
GAAGATTAAATATAAAATTTCAAGTTTCCATCATCTTTTTAAATATTAGGAGTTCCAGCA
ATGCCGGGCCTTTTCCCCCGCATGATCACTGAGCTGGATCTCATGTTTAAAGCAAGCTGT
GCTCCCCGCTGCAGCTCTCTCGGTTCTCTTTTCTTTTACCTACTGACCCCCATATNCATT
TTTAAAGATTTTTTAATTTTTATGGATACATAATACTTGNNCCTGCCC
Sequence 1018
CCCTTGAGCGGCCGCCCGGGCAGGTACGCGGGTCCCTTATTTTCTGGTGTTTACTTGGGA
TGCATCAGTGAACAAAACAAAGGTATCTGTCCTTATGAAATTTATATCATAGCAGAGGAA
GACTGGAAATGAATAAATAAATAAAGAATGGAGTTTGTTGGAAGGTAATAAGTTCTGTGG
AAACAAGGAAAACCAAGGCATGGAGGTTTGGAGTGCTAAAGTGAAGGTGTGAGAACAGAT
TGCTCTTGCTCAGTTTTCTGTCTTCTTTTGTTTAGGAAATTGTCATTCTCTGTATGCTTC
ATTATAATATATACAATAAATATGAATTGTTATAATTTAAGATAAATTATATAAATATAA
ATTATAA
Sequence 1019
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAGTTACTCCTTGCCCATAGACGTGTTTGA
CCTAGAAAAATTTCTTATACGCAACAGATATTCATAGAAATATATATTAAAATAAAGCTT
GAAGGGTGAATTAAATAAATATTTACTTGGAAGCTACAGTGGGTGAATTAAACAAATATT
TACTTGGAAGCTACTTTATAGCCACTGGGCTGGATTTCATATACAGAGTTCTTGCCCTTG
GGAGTTNTACAACTGCTTAACACTTTGTCTATGCTAGAATACA
Sequence 1020
CCCTTAGCGTGGTCGCGGCCGAGGTACCTAATGCTTTCAGCCCAGGAGCAGAAAGAGAAG
TGGGCTCTTTGCTTTGAGAGTCTCTGAAAATTTTCAATACCCTGGGACAAATTAAATGAG
GTAGATCCTTCTTTGAATTTGTTAATAAAGCATGCTTGTTTTGTCTCCATAAAACAGGCT
TTGACCATTAAGGTTTATATTTTAAATGGGTAAATTTTATTGTAATACACTAATTTTAAG
AAAAGAATTAACTCATGGCTTAAAAGCAAAAACCAGACCTTGGATTTCACCCATAACTTT
AAGGCTGGTCATTTTAACCCTGATTTGACACACTCTTATTATGGTGTCTTTTCTCCTTAT
TTGGCTAAATATTTCTGACCATCATAGCAATCTTTTCTATAAAGGAAGCAGGCAAGAGAG
CTAGAGTGAAAATGTTAAAAACAAAACAAAAAAGACAGCATACTGGCTACCAGTTTTTCT
TAATTAAGATGATCTGTTTTCGCAATTGCGTAAATTAGAATAAAATGTTATTTAACTCAA
GGATATTTCTTCACTGAAAGAAAACT
Sequence 1021
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTACAGTCTTAAGATATCCATACACCCCCAC
ATCCGTCCTTTGTGCTAGAAGATTACTGAANATTTAATTCCATTTATGTCATTGGATTTG
TAAAAAACCCCTTCTGGATTCAAAGATGAAGGCCTCACTTACTTTATTTTTGTCATTTTC
ACAGACCCCTTATGTAAATGCCTCAAGAGTAAAGAATCTTGCTCAAGTGATTTTTGTATC
TCCAATGGCTAACAAGGAGCCTGACATAGAAGTAGCTGCTTGGTAAATATGTGTTCATTC
ATTCAACAAATACCCCCCAAGGGACCTCGGGCCGGGGACCACCGCTAAGGGCGAAATTCC
AGCACACTGGGCGGGCCGGTTACTAAGTGGATCTCGAGCTCGGTACCAAGCTTGGCCGTA
ATCATGGTCATAG
Sequence 1022
CCCTTAGCGTGGTCGCGGCCCGAGGTACCGTGTGGGCCACTAATACATAAGCATCTGTGT
TGGCTGGGGGTAGGTGTAGGGGGTGCTTGGGGAGAGATTTAAACAAACCCTTTCCTCTAC
TTGCAACATCTCTTAAAAGCTTGTCATCATGTTACTTCCTATTTCTTTAGAGTTCATTTG
TTTAAGACGGAAACGTGCTTCATCTTGTTCGCTTTTTCTGCATTCTTTGTAAACTTAATA

Table 1

TTCTAATTANCCCCAACACGGAAAAGAATGTAACACAACTGTCTTAGTTGTGCCATAGAG
TTAGAATCTATCTATTAACATGTTTTAGGTNATAACAAGAAAAATAATAAAAACAAACCT
ATTATGAGAAGCTGCCCATGCCAATAAATTTTGAAACATTACCAGGAAATATAAAAGGAA
NG
Sequence 1023
CCCTTCGAGCGGCCGCCCGGGCAGGTACATATATTTCAAACAACATTTTCTAAATTAATT
AATGTTTTCACTCATAATTATGTGTTCTTCCCACTTCTATATTCTCTATTTGGGGAAATA
ATCCCATCAACCACCCAACGGCCCAAACCAGGAACCTGAAACTAACCATATTTCCCTCCC
ATTGCACATAAATTAACTTCTAATCCTACCTACTTATCTTTGAATCCACTCTTCTATTTG
CAGTGGCAATACTTAGGGCTTNCCTTACTTTTTACCAGGACTATTACTAGAGCTNCCTAA
ATGCTTTCTATCTGTAGGCTTACTCTTCTGCATTTCTAT
Sequence 1024
CCCTTAGCGTGGTCGCGGCCGAGGTACCCACAATGGAAAGATGATCTTCCTGCATTGTGA
AGGTTGTTCTCATCAACCAAGCCTGCAATGACTAGACATTCTAAAGAGAAGAGTGATGGC
AATGGAAAGAGGACACATCCGCTTGCCAGGTCACTTCTATCAGTTGATGACATGCCATAT
TGTTATGGCTAGGTCAGCTTTCCACAAGTATGCACATGCAAAATAGAACTTGGGAAAAAA
ATCTTTGATTTGGCCCTTTACCAAGTGGATCAGGTGTGTCAGAGTTCAAGTTGAGCAAAG
GTCAGAGTTTAA
Sequence 1025
CCCTTAGCGTGGTCGCGGCCGAGGTACTTGTTTCTCCCCTTCGGACCACTCTCCCCACTA
GACAGCTGTATGGCCGGCTCCCTCACTCTCCTCAGGTCTATCAGAGGGTGGCCACTGACC
TCATTGTCTCAAACATTATATAGAACACACACGCACCCATGCACGCACACCGTCGTTCTT
CATCCGCCTGGTTCCGTGCACTATTCCAGGACCTACAGCAGTGCCTAGAACACAGAACAT
CCATTAGCAACATTTGTTTAATGAATTTATAGTGCCTAAACCTGCACAACTCTGACTTTG
CCTTGCTATTAGAAAATGCAAGGCCAGGCGCGGTGGCTCACACCTGTAATCCCAGCACTT
TGAGAGGCCGAGGTGGGCGGATCACTTGAGGTCAGGAGTTCAAGACAAGCCTGGCCAACA
TGGCGAAACCTNTTCTTTACTAAAAAT
Sequence 1026
CCCTTAGCGTGGTCGCGGCCGAGGTACTGAGGCTAATGGTCTTAGTTGGGATAAGGAGAG
TGGGGAAGGGGCAGGGGGAGATGATGAAATTCATTTATCCTCTGTGATGCTATGGAAGAA
CAATTAAGATCATGTTTCCTACTTGATTTTAGTTGCTAGTCATTTCTTAATCTAAGCACC
CCCTATAATTTACCTATGTCATCATGCAAAATCACCATCGGTAATAATGTGGGGGCGGGG
GAAGTCTATACAAGAATATTAAGGCCCTGTGCGTGAGCATGTCTATAGTTAAAGACTTAA
TGAGAAAGCATCAAATTGTGGTGCAAACAGCTGAAAGTAGAAGTAAATCACAACGTAATA
AGATGCAACTTTGGAGGAGCTCAAAGCAACANATACGTTTTTTATCCAAAAAGGAGTAAA
AGAAAAAATCGCNACGGCAGTTCCTTCAGATAATCAACNGATGATTTCATTTGANAACCA
TAATTAACTAGCGTTGTTTGTAAAATAACTTTTTTCATTTATACNTTTTAATGNTTATTA
A
Sequence 1027
CCCTTAGCGTGGTCGCGGCCGAGGTACTAATTCTTTTCCTCTTTCCTAGACCGATTCTAG
TTTGTTGCCTTCCCTTTCCTCGGAAACCCCAAGTTTGTGGATGCTGCAGACACTCTGTGC
CCCCCTGCATGCTGGGTGCCTGGCCAGCTGCCAGGGCATAAAGACAGAGACGATGTGGCC
TTTGTCCTTAAGAATGAGGTTTGAAAGCCCCAGTTCTTCCATGTTAGGTGATTTCTTGCA
GCTCTTGGTATCTGCAGAATTAGTGTGAATGCTTAAAAAATATTAACAGCTTT
Sequence 1028
CCCTTAGCGTGGTCGCGGCCGAGGTACTATGGGTGTAGTGTTACTATTACAGTTAATCCG
TCCTTTGTGTGAAGCTGTTAAATGCAGTGAGGATTGGAGCACTGTCCACTGAATCTCTGT
GCAACAACTTACTCGGTGTGGCAGGGGTNTCCNGGTGTCTGGCTCTGATCTTGGTCGCTG
GATAGNCGNCTGTNTNTCTTTAGGTGCCCAAGGCGACGGC
Sequence 1029
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAAACATTTAGACTCCTTTGTGCCTTNTGG
AATGGGAATTGCTTAAGCTGTCCTGAAAAAATNGCCTTTAACATCTGTTNGATTGAGATT
TGTGATACATAGAAGTTGGGAGGAAGATGTCGGAAAGCCCTAAGAGAGCTACTTGCCAAC
CCCACCATNAGGTCTNCCTCAGTGTTCCTAGTCAGGACAGACGAGGCCGAGTCTGAAATT
ACGATAAGNCTTTGAATGCAGCATAAACAGACC
Sequence 1030

Table 1

CCCTTTGAGCGGCCGCCCGGGCAGGTACTTTGACCTGTATGTAAACTCTAGTTACTTTGG
TCTTCTCAGGCTCTTGACTCTTTCACAATTAAAGTAGTCTTTGAGGCTCAGCNCTGCTTT
CCTCATAGCTATGCTATTGGCCTGGACACTCAAGGGAGTATAAGCTNGAGGCAAACATGG
ACTCATTTGTNTTTCTAACTTTCAGGGGATTATTTGNCCATCATTGCCTGATGTCCAGTG
TCT
Sequence 1031
CCCTTAGCGTGGTCGCGGCCGAGGTACCATTGTTTTGTTCAAAATCACAATTTAAATACT
TCGTGATTTTAGAAATAATTGGAGCCACCGTTTTCACCATTAAGGTGAGTGATTGTTCAG
ATACATTTGGCACTGTCCATAGGTTTATGGCTTCCAACTTGTTTAAGACCATTCCCAGAG
TGAGAGCTGATTTGCCATGGTTATGAAGCTTTCAGGATATAAACTATAAGAATGACAAAC
TACAGCAGTTGAAAATGTGTCTTCAGATACTCACTTGCAACTCCCATTTATGTCTCTAGG
GATTGAGAAATGAGGATCGAGGGACCAAATCTGGCTTGGTCAGTAAGAGTGTAGGTAACA
TATAAATATTAATGTTCGTTGNAGTTAGTGTGGTACCTGCCCGGGCGGCC
Sequence 1032
CCCTTAGCGTGGTCGCGGCCGAGGTACAGTGGTGTGATCGCAGCTCACTGCAGCCTCAAC
CTCCCGGGCCCAAGCAATCCTCCCACCTCAGCCTCCCCAGTAGCTGTGTTCCAAAGAAAT
TTATTTATAAAACAGGTGTTGGGCTGGACTTGACCCGTGGGCCACAGTTTGTCAACTGCC
ATTCTGTAAGCTTAACATGTGTTAATTACTGCAATCTGAATAACAATGCTATGATATAGA
CACTGTGTTCCTTTTAATAGACAAAGGAACCCAGGCACAGAAGGATTGACTAATATGACC
AAAGTCACACTGCCAGTGAGTAGCAAGCCTGAGCTCTGAACCATGACAGTTCACATCTTC
CACGACAGCAGCTTCTCAATGCTCTTTGGAGGGACCAGAGCCCAGGCAGTAGCAACGGCT
ATGAGGTGGTGAGACATGACCAGCAGATAAGCCCTGGGCAATGGTCCAGAGCTGGAGGGA
GTGGAGAACTAGCCATTTGTGACTTTGTGAACAATCCCTGGGGGAGTCTGGAAATTA
Sequence 1033
CCCTTAGCGTGGTCGCGGCCGAGGTACTAGATTGGGTGTGTGTATTAAGAGAAAGACAGG
AGTCAAAGATAGTTCCAAAACTTTTGAACAGAACACTGGATGAATACTGTTTACTGAGAT
GGGGAACACTTAGAGAAAAATGCATTTGGAAAGCAGAAATACGATCAAGACTTCCATTTT
TGATACATTAAGCTTGGTATGTTTAATTCATAGCTATATAGAGGTATTAAATTGGCAGGA
CAAAATCATAGCTAGAGATAAAAATTTAGAGTTCACCAGTGTAAAGATGATATTTGATGG
CACAGGATGGACTTTCTTCTGGGATTTGAGTATACATAG
Sequence 1034
TCGCCCCGCGTCCGNGNACGCGTGGGCAGGCATTANTTNNNGCCCAGTTTATGAGTGTGA
GCATACCACAGTACTGATTACTGTGAAGCTGAGNCCCATTTTATATGTTNATTGATGTTT
AAGATTTTCTGTTCAACAAATTGTTCATTTTCTTTGCCCGTNTTTTCTTTNTGAGTAATN
CTTTGTATATTCNGGATGTTGATCATTATGGATTATAAAA
Sequence 1035
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCATTTAACTGAGTGAAAGCTTTACAATTGAG
GGGTTACTCATTAGCAGGACCTGGGTTTTGTTTTTAATCTCATTAACCCCTTGTTACCCA
TTTGATAACAAAGACTTCAAGGAAGAATTTGCTCAAAAATCTCTGGGAGACAGTAATAGC
TTCTTGGGCCTGACTGATAAACTTTTTGCCTCCAGCAATGGAAATGTGGGAAAATTCCAG
ATGCTAAATGATCTGGCTTGGACCCAGCAGGTTGAGGTAGTGGAGCCTTTCGATTGAGGC
ACAGCCCAGGACTGCTGCAAGGGAGAGGCACAACAGAT
Sequence 1036
AGTCGACCACGCGTCCGGTTCGAGCGGTACCACGAGGACGCACATATGCTGGACACTCAG
TACCGCATGCATGAGGGCATCTGTGCCTTCCCCTCTGTGGCGTTCTACAAGAGCAAGCTG
AAGACGTGGCAGGGCCTGAGGAGGCCGCCCAGTGTCCTGGGCCACGCTGGCAAGGAGAG
C
TGTCCTGTCATCTTTGGCCACGTGCAGGGCCACGAGCGGAGCCTGCTGGTGTCCACGGAC
GAAGGGAATGAGAACTNCAAGGCCAACCTGGAGGAGGTGGCTGAGGTGGTCCGTATCACC
AAGCAGCTGACCCTGGGGAGGACCGTATAGCCCCAGGACATCNNCGTCCTCACGCCCTAC
AACGCGCAGGCCTNTGAAGATCATCAAGGCCCTTCGGCGAGAGGGCATCGCCGGGGTGGC
CGTGTCCTCCATCACCAAGAGCCAGGGGAGCGAGTGGCGCTATGTGCTGGTGAGCACCGT
CCCGCACCTGTGCCAAGAGCGACCTGNACCANCNGGCCACCAAGAGCTGGCTCAAGAAGT
TTCTGGGCTTCGTTGTGGACCCCAACCAAAGTGAACGTTGGCTTTCAACGCCGNCCCAAG
ANGGGCTCTGNCTGATCNGAGGACCACCTTCTTNTTGCGCTTGTTGCCCCCTTTGGCCGT
AANCNTNCTGGACNTTTTGCGAGGNTTAAAAAAACCTTTTTCCCTGGCCGGCCAGGTGCC

Table 1

CCTTNTTCAGGAAGGCCAATNTGCCTTTCTGAAAAGNCTTTTCACCTGCAAGNTGCCAGG
ACTGGGANGGGAAAGTTNAGGGCCCCCC
Sequence 1037
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCATTTAACTGAGTGAAAGCTTTACAATTGAG
GGGTTACTCATTANCAGGACCTGGGTTTTGTTTTTAATCTCATTAACCCCTTGTTACCCA
TTTGATAACAAAGACTTCAAGGAAGAATTTGCTCAAAAATCTCTGGGAGACAGTAATAGC
TTCTTGGGCCTGACTGATAAACTTTTTGCCTCCAGCAATGGAAATGTGGGAAAATTCCAG
ATGCTAAATGATCTGGCTTGGACCCAGCAGGTTGAGGTAGTGG
Sequence 1038
CCCTTTCGAGCGGCCGNNCGGGCAGGTACTTTGACTATTTTTTAGCAACAAATTACTTTT
GACACACAGCACAATTGATTTAACACTTCCAATTTTGGAACTATTGGATAAATAATGATG
GGATTTAAATAAAGCAATCCGATTCTACTATTACAGCATAGGGTCTCTTGTAGTCCTCTT
AGTAAAAACTATTGTGACACTTCCTTCTTTCTCCAAATATTCGGCCTGGAAAGACCTAAA
TACAATGCAGGGATTGAATCAAATTCACACATTTTTTTTCCTACGGAAACAACAACCTTT
CTTGCTTATATTTAACAAAAACTAGTATAGATTCCCTTTATATTAATAGTTATATGGTAT
TTTTTTCTCAGAGTAGAAATCAGGTTTATAGGCTAAAGAATATAGGCTAATTT
Sequence 1039
CCCTTAGCGTGGTCGCGGCCGAGGTACTTAGATCAGATGGATTGAAACATGACAGCCCCA
TTTCATCTGGCCGGTTAAGGTCCTCATGGAATGAAAAACACTTTCGGGCACTCTCCTATG
AGAGAGAGAATGGGTTTCTTTAATTGCCAGATTGTCTGAACACAGCCTCAGCTACTTCTA
GGAATAAGACGAAGCAGTGAGGAAGTTGCCAGTTGAGTGATTCTTGGGGAAAAAAATTAG
CATTCAGTGCCAGCTCTCTAAAGTGTGGATTCTGGATTCTGGTAGAAGCCAGTAAAGAAA
CGTTTTCTCTGGAGTGGAAGCTAGTAAGATTTATTCTGTGGTGATGAAGCCATCTGAAAC
CTTACAAGCAGTGTGGTTGTATCAGCATATGGGAGCTGACTGCCTCAGGACTTTGGAAGC
CTGCTTCTCTGTGCCTCANCCGGAACTCAGGTTACTCAGTAGTCATTTGCTAATTTCTGA
GAACGCANCACTCCTGAAGGGGATAGAAAGCATGAACAATACCC
Sequence 1040
CCCTTTCGAGCGGCCGCCCGGGCAGGACTCTTATCAACTGTTTTATAGATGAGAAAACAT
TAGCCACAGCTTAGCTTATTTGAAGTCACAATAATATTAACTAAGTAAGAGCAAAAGCCA
AGATTCAAATGTAGATTATTTTACTACAGACTGAGAAACGAATTAAACTAGGAGCCTAAG
ATACTTTCTGGAATTGAAATGATACATTATATATACCTATAAAGATAATTGGCTATAGCT
TCCTAAACTACAAATTGTCATAAAAATGACTTCTGTCCTATATCAATTAGAAACTGGTAT
TAAAATTGAGTATTATAAGACAATAGAATGT
Sequence 1041
CCCTTCGAGCGGCCGCCCGGGCAGGTACTGCAGGGCCCAAGAGCATACAAAGCTAGTTAT
TTGGATCCAAAGTTGGTCAAGTGTGCAGTGTTTAGACATCATGATCTAGGCAAACAGAAT
TCCTGGCCTGAAATATGTCACTAGTTAGAAACATTAGAAGCTTTCAGGTAAATAAATATA
AAAAACCAGTCAACCGTATTCTTATTTCTTCGTCAGAGAATCATGTGTCGTTTGGTTTAA
CTTCCTGCTGGATTCTGGATGGGAGTTGTTGAACATATTAATCTCATTATTTTCTGTAGA
GGACAGGTTGTCCCCCCTTCCTCATTAGCG
Sequence 1042
CCCTTAGCGTGGTCGCGGCCGAGGTACCCTGCTTTGATTATTTCCGAATCCAGTGGGTAG
AGAAGGTAAAGGCAAGGGCTCACTGGATATTTTTAAATTGTAGGGATGTCCTTTGCTCTG
GGTCAATTTTAGGATCAAATATAAAAGCACCTATAGCTCAGAGTATCTTCTAACATAAAA
CTTCTGAGATACCAGAAATTTTCCAAAACATGGTATAAACAGTATGAAACACTGGGTAGA
TAAAAGCTTTCTCTAAATCTTAAAGTGCTCAAATATCATGACCTGATTTTTTAGTTTTAG
AAATCAGATATTTTTCTATTCCATATCTTAAACTTT
Sequence 1043
CCCTTAGCGTGGTCGCGGCCGAGGTACCCGTTTGTCCATGGCTATTCCAAATACCCCCAT
GTTTATTTAAAATGTATATATAATCAGTTACATAAAAAGAGGTATGCTTAAATTCTCATG
ACTCTATGGTTGGACCTCTGTGGTTGGAGCAGGCAATAGAAATGTCTGTAATTCATTTAA
AAAAAAAAGTGACTTTCCTACCTTTAGATAGTGAGGACAATCTGTTAACTCTTTGTGTTG
ATAAAAGCAAACATTTCAGGGCACGGTGAAAGAAATCTCTACCATGTATAAGGTTATATA
TATACCAGAAGCAGTGGAGTTAGGACCAAATTAAGATTTGA
Sequence 1044
CCCTTAGCGTGGTCGCGGCCGAGGTACATAATGTAATTGTTACATATAATTGTTGTATAC

Table 1

CATAACTTACTATTTTTTCTTTTTTATTTTTATATATAATTTTTTTTTGGTTTGTTTGTT
TGTTTTTTAATAAACTGTTATCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAANGTCCC
TGCCCGGGCGGCCGCTCNAAAGGG
Sequence 1045
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTTTCCTGGGTTGTGAATCTTGGAGGTTGCCC
TGTCAGACTGGTGAGATCCCAGTTTAGCTGTGCTAGCTAAAGCAAGGAGAACAGAGAGAG
CCATAGATACTTTTGCTTAGTAAAATCTTTCTTTGAGGGTAGGGACTGGAGTATGGAACC
TTTTCAGAGGAATGAGAGGGGCTTGTGACGAAAGGGTAGAGGAGGGAATACCTCCCTGCA
AAATCTTACACAACTAACTAATGTCATAAGGCCGAGGATGAGAAAGTAGCACTTAACTGT
TTCATCCTCATCACACATAAAGCATTCC
Sequence 1046
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGCACTTTCAAAGTAGTGGAATATAAATCTT
TCCATTTAACAGCAACATTCAAATATTTCCCATTCTGCTTATTATTCCTCTCTGAAGGTG
ATACATAGAAATATAGGAGCAAACACAGCAATGCAGGCGCTCTATGATCTGGTTTGCTCA
CATAGATCTTAAAAGGAGAAGAATGAGGGATTTGCCTACAACCCACAGCCAATCTATGTG
GACACAAAGGGTGACTTCTTCCTTCTATTACGTTCCTTGAGGTAGAAATGGTAAACTAGC
ATGACCTCGAATCATAATTTAATATCATTCTA
Sequence 1047
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATTATTGGTAGTATCTCAGAATCCTGCTTAG
CTTTTGAGATAAACCAAGTCATGATATTTTGGGTAATATGGCCATAGGTATCATGCAAGA
TTGAACTGCCCAGTATTTGCCTTTTTCAATATTTACTTTGTAAGAACCTGACACTGTAGG
TCCTCACCACACCAAAACCTGCAACATAAACTTCAATTTTGGGCAACTCATAGACCAAAA
AAGCTAAACAAAACAAAAAGGAAAAAACCCTCTATATACAATCACCCTGCTTGTCTACAT
TTAATTTGCTTCATTCAAAATAAGCA
Sequence 1048
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAACACTTTAAAAAGTGAATTNTAAGCTATGT
GAATATCTCAATAAAAACATTTTTTAAATAAAAACAATTCCCAAAGGCCTGGAAATTCAG
GAACATAATTCAAAATAATTTATGGATCAAAAAATAAATCATATAAAGATCTGAGAACTA
CAATGTAAAAATATAGAAAAAAGTCATAACAATATTAGANAAAAATTTGAGCTGGATAAC
AAAAATAGTACCTCNGCCNCGACCACNCTAAGGGCGAATTCCAGCACACTGGCNGN
Sequence 1049
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTATAAACAAAGGCATCATAAATAGATATAA
AGCCAGAAGAAAAGGGATCTAAAGTAGACAGAGAAGATAGGCTGACTCTCCAGTTGCAGA
TTTTCATTATCAGCTCATCACACCACCGAAACTCTCTGGTGATTTGCTATCCACATCCAT
GGCGTTTGGTGGCCCTAAAGATTGTAACGGCCCCCATCCTCTTGGTTAAAATGGCAGGTG
TGTTGACAAGAACTGTCTTAGGTACCTCG
Sequence 1050
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTCTCATCTCCAAATCAACTAGACTCTTATG
TTAAGAATACTAACAAGAAAAAATCCAAACCCCCAATAGAAAAATCCCCAACAACAACAT
ATACCCTTAAACACAAGAATTGTATTATTCAATGAAAGCAATACAAGTAAACACAACAGT
TACCTTGGCTATTTTTTCAATGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1051
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCCATCTCTTCCATTCTGGGAATCTGGGAAAC
TAAGCCTGTAACTTGTAGCTTGTAGAATGAATGATGGAGTAGAATAAATAAGAAAGGAAT
ATATCATTAAATGCACAGGTTAAATAAATAAAAATCTATTAATAAAGAGCCTAAAGAAAG
AAAGATGACATTTCAGCACATATTGGGTGAAATAAGTTGTTTAGTCCAGCACTTCTCAAT
TTTTAGTGGATATGTGAATTGCCTATTAAAATGCAAATTTTAAATTAGTTAATCTGGGTT
GGACCTGAGTCTGCGTTTCCAACAAGCTCCCAGGTGATGT
Sequence 1052
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGTATAGCTATATACTCATATTTTTATT
TTTATGTAAAATTTCCAAAATGCTTAATATGGCAGTATAATAATTATAACTAGATTTACT
TCAAAACATAGACATAAAGAAGATTACATGCCTGTAGAAGTTCATTGAATTAGGAATCAC
ATGCTATTTATTTTAGCAGATATCTTCTTAATTAAATGTTTGACCCATGTGAAGTCATTT
AACAGATCTGTTACGCATTATTCACATATGCAAAATAATCTATATGATCTGAATACCATT
TCCATCTTTAAAATTACATATTCC
Sequence 1053

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATCAAAAAAAGACAAAAAAGAAATGGTGTT
AAAAGCCACAGTAAACATAAACCTCATATCAAGTATAAAACCACACACACTTTGCTCTTC
ATCCGGACAATGCCCAAAATTATACTGAGGTATTGGGGTGGGCTGATACCTTCAAACAGG
GAGAGAGGGACCATGTTCAGGAGGTGTATTCCTCGATTTAGGTGGTGACTGAATTTTTTT
TTTTAAGACAGGGTCTCACTCTGTCACCCAGGCTGGAATGCAGTGACGTGATCTCGGCTC
ACTGCAGCATCAACCTCCTGG
Sequence 1054
CCCTTCGAGCGGCCGCCCGGGCAGGTACAATGAAAATTACAAAATACTGTTGAGAGAAAT
TAAAGAAGACAAATAAATGAAAAGAGACGGAACATGTTTTCGCTTGTAAAACTCAGTAGG
ATTAAGATCTCTTCTCTCCCACGACTCTATAGCTTTAAAGCAATCAAAATCANACTGGTT
TTGTCTGAACGTTTTTGAATAAGTCAATGGCTTATTTCAAAATTCATATGAAATTTCAAA
TGCCAAAGANTAGGCAAAATATTTCAGAAAAGAAGAAAGATTGAGGATTTGCAATAACCT
GACTTCAAAACTCACTAGAAGAACGAGGCCAGACTGCCCAGGGG
Sequence 1055
CCCTTAGCGTGGTCGCGGCCGAGGTACCCACCACGTTCATGTCTCCTCTAGCCAACTATA
AAGTTATTAACACAAGAACCCTGTCTTATTCATCACAGTATCACCCACAGGGGCTGAGAC
AGTGCTTACACAGAAATGGCCCTTGATAAAATATGGGCTGAATGAATGAACATATGAATT
TGACACTTTGAGAACTAAATTAAAAGTTATTTCTACTAGCATTTTTAACACAAGAACTAT
TGAGATTACTTATATATTAGTAGTAAAATGTTTGCTTTATTCATTTTGATTGCAAAACTT
ATAATGAACTCAGTGAACCTTGNCCCACCTTTTT
Sequence 1056
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATTAACTCACTGACTTACTCTGGGTTGCTAT
TGTATTAAAATTCTGTATAGACATTACGTAGCCTCAGAGTTGAATTTGGACTGCCCTTAA
AATAAAAAATTCTTAAATCTTTAGTGTGGTGTCTATTAATTTTTATGATGATTTACAAGT
TGGAAATGATTACTTTGCAAGTCATAGTTTACTTTGAAGTTAATAAGAGTGATTACAGTA
AAGGAAAAATGCCATATATGGCATTGTTCTTAACAGCTTATGAAATTTGGAAAACGATAT
TTTAGAAAGCTTTCTCTTGNTGGCTGGAATGAAGTGGAGACCCTGCT
Sequence 1057
CCCTTCGAGCGGCCGCCCGGGCAGGTACAGCTTGTTCAGGATATTTCTTCTATTTTTCCT
TTGAGTTCTTGTTCATATTCTAGTTAATTTCTAGTAGTTCTTAATGTATTTTAACCAATA
GACTTTTGTCTTCCTTCTGCTTATGTATTCCTCGTAAATGCTTTTTGTGACTTGTCTAAG
TATAAACAACTTTACTATTAGCTGTAAAATTTTCATTTTTAGTATGTCATCAATCTTTTT
TTGTGNTTTAGTATGATTAAATGGTTTTTCACTTGGAAAGATATTGAATAGTCTACTTCA
TTGATTTTTTTTTTAAAGTCATTTTCATTTTTT
Sequence 1058
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTATACCAGAGTTAAATTGCCTGTGTTCTTTT
CTGCCATTAACTGGCTTTGGGTTGGGAAATTCAGATAATTCCACTTTTCCAACTTTAAAA
TGAGATCTCATTCAAAACAAAATTGCCCACAACCATTTGGAATATGTGTTTAAATTAGAC
AGTAATGCTTTGGAAAGTGGAATTAAACATTTCAGAATAATAGCTGTTAGGCCGGGCTCA
ATGGCTCACGCCTGTAGGGAGGCTGAGGCAGGTGGATCACCTGAGGTCAGGAGTTCGAGA
CCAGCCTGGCCAACATGTTAAAACCCTATCTCTATTAAAAATACAAAAATGAGGCATGGT
TGGCAGGTGCCCGTTGTCCCAGCTACTTAGGAGGCTGAGGCAGGAGAATTGCTTGAACCA
GGGAGGTGGAGGTTGCANTAAAGCTGAGATTGCGCCAGTGCACTCTAACTTGGGCAACAA
GAGTGAGATTCTGTCTCAAAAAATAATAATAATTAAAAAATAATAGTTGGTAGATTGAAC
ATAGAAAACACGTTTTGTAGATAAAAANTGGCCAAGTNTTAGCCACCTTTGACAATTTTT
TAAAA
Sequence 1059
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTAACAAATTAAAAACAAATTTTAATTTAAA
ATATTTTAGAAATTTTACTTAATACATTTATTTAATGAAGGCTGCTTTTAAGAACTTTAA
ATCCTCACGTAAACACCACCACCTGCAAAGTATTAATATCAACTTTTTCAACAAAATGCC
TGCTATGTATAAGCTACTGAAAGAAGACAAAAATTAATAAAATGTGTCCCTCCTCTTAGA
TATCTATAATCTAGGAAAATGAACACATTCTTTTCAGACACTAAACTCCATAAGAACAGG
CATCAGATCTATCTTATTTACCACCACATCCTGAGAATGGAGCACAGTGCCTGACACATA
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AGCAAATATCTCTTAAAAAGAACAGACTTTTAAAGTTAACAAGCAAGTGATGTGTTATTC
AGTAGCAAATAAGATTGTTTCCTAATGTCATAATTCAATTTT

Table 1

Sequence 1060
CCCTTCGAGCGGCCGCCCGGGCAGGTACAGTTACCAAAACCCATCCAACTAAAAATTTAA
GCTTTTTGCATTTTAGTGGATGCAAATTGTGTCTTAGTAAGAAGAACATACAAAAACTAA
GAAAGATAATGTTGAAGAAAATAACAAAGCTTAAGGACTTAAACTATTACCATCAAGACA
TGTATAACTACAGTAATTTTAAAAACTGTTTTCTTGCATAAGTATAGAGAAATGTACCTC
GGCCGCGACCACGCTAAGGG
Sequence 1061
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTACGCTTTATGATCTTGAATATTTTCAGNGT
NTAAGGAATCTCTTCCTTCTTTGATCTCCACTGCATGAAGAACTCTGTTGCAGGTGTTAA
CAAGGAAGTTTTGAAATACAAAGCCAGAACCTGCCCCCCAAAGATCTGACAGTAGTANAA
GGAGATCCATTTTGAAGAAGGTATAATGGCAACC
Sequence 1062
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTAACAAATTAAAAACAAATTTTAATTTAAA
ATATTTTAGAAATTTTACTTAATACATTTATTTAATGAAGGCTGCTTTTAAGAACTTTAA
ATCCTCACGTAAACACCACCACCTGCAAAGTATTAATATCAACTTTTTCAACAAAATGCC
TGCTATGTATAAGCTACTGAAAGAAGACAAAAATTAATAAAATGTGTCCCTCCTCTTAGA
TATCTATAATCTANGAAAATGAACA
Sequence 1063
CCCTTTCNAGCGGCCGCCCGGGCAGGTACACAAATTCTAGGNAATCTAAATTATTTAAAT
GTCTAGAATTTTTTTTCTTTTATGAACCANATCACATTTCTGGACATGCTAACCATTAAA
ACGGNGAAGCTTCAGCTTGGTTGTTATTCTTCCATTAAACTGTTTCAGAAACATTCAGGC
GGCAGATAACTCATTTGGATTGTTAAGAAACACCAGGTTTTCCAGATGCTACATTAACAC
CTCATAGAAGTGGTCTTTCATATGTATGTTATGNATGATGTNAACCATAATATATATGGN
TAAAATTTTAGTAGGAGTTATCCTTTGCTTTTTATAATTTCCAGTTTTNNCGNNAACGTA
ATTCCTTTTTTCGGATTCATTTTTTAGGTAAAAATGGTTCCCCATTANTTTAAAGGATAA
AAATAAAGTCTTACTTTTGAGTCTTTTAAGNCGTNNATTTTNGCCANTNNTGTTCCCGTT
GGAACNAGAAAGGTNNTAAANCCNTAAATTTTTGGAAATTAAAACNGCCNTTTNAAAGNN
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NNAANGGGGGGGGGNNGTACCCGNGGGNTTATTNAAACCTTTAGNANGNTTTTNTTTTNT
TCTGGCTTTAAAAATTANTGGNNTTTTGCNNTAAGGGCCAGGAAACCNTAGGGTTTTGGA
AAAANCNAAAANTGGCCTTNGGGGGCTTNTTCNAAACCCGGGGCNCCAAAAAANAAAAAA
AAAAAA
Sequence 1064
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTACTACAAGCAGCAAAAGGAAGCTCTAGAA
CAAGGAATTAAACACAGTGTTTGTTTCCAATCGCAGAAGAGGCCATGAGCACCATATGTG
TGTCAGGCTTATCATCTGAACCAAAGAAAGGCCAATCCTTCACCTTTCTTATGACTCTTA
TAGGCTGCAATATTTCACTTGGCCATAAACAACTTAATATCTCACACCTAGTAGTATTCA
GTGACACAGAAAGGGAAAGAGAAAGGATGAAGAAAAGAGGAAAGAGAAATAATTTNCCCA
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GNAAGTGGAGGATGGA
Sequence 1065
CCCTTAGCGTGGTCGCGGCCGAGGTACATTGAAACAATATAGTAGTCTTCCCCTTTACAA
AGCTGAATTAAAGTAAAAGTGTGTGTTGGGAATAATAGGGGAATGTGGATTGTAGCTGTT
TAATAAAGATTTAGATACATATAAAATTGCTTAAGGCCAGGCGCTGTGGCTTACGCCTAT
AATCCCAGCACTTTGGGAGGCTGANGTGGGTGGATCACCTGAGATCAGGAGTTCGAGACC
ACCCTGTTCAACATGGTGAAACCCCATCTGTACCTGCCCGGCGGCCGCTCGAAAGG
Sequence 1066
CCCTTAGCGTGGTCGCGGGCGNGGTACCCACATGATCCCAAAGAGGAGGGGCCCTGTAGA
AACAAGAACCAACCAACANAAAGCAGTGNCTACAGGCACCATGACAACAAAAGGAGTTTT
AAAGTGCATCTTCAAATAGCACACAATTTTCCAATTTAAATAGTTTGGAATGAATCAAAN
GGGAANAAAGCATTANTTAGATACAACTGAATTTCTCAAAAGTATATTANCACAGCCTAC
AAATAAATCCTTAAATGTA
Sequence 1067
CCCTTAGCGGCCGCCCGGGCAGGTACCCTCCGTGACTTTTCAGGGTCTCCTGGTTGAATG
AATTTGCANAAGGATTAAAATGTGTGTTCTTATTTGTGCTTTGTATTCTCCCATAANTAG
TGTGTTGGAGGCTATTAGAATAGCTGAGAGGGTAAAACATAAACACATACGTANGAGCCT

Table 1

GACATAAACACATAGGTAGGAGCCTGCCATAAGCACCGTAGGTAAGAACTAAAAGGGTGT
GTTTCCATTTCANGNGGTCCAGNCCTTCCTTNCATACTCTNAGATGACAAAAACACAAAG
TTGCTGGAGCTCACACAACTAATGACTAAANCCAGAAAGTTTGGACATGGAGAAACATTT
TT
Sequence 1068
CCCTTAGCGTGGTCGCGGCCCGAGGTACTATATTAGTGTAGCAATTTTCCAAAAGCCATT
CATCTTAGAGGGCTAAATGATTTTACCTTATCAATTCCTCCTGTGAAAAAATATCTCTAA
AGAGGTTTTCTGCTGGAAAATATTGTTGCTGTCACATTGATATGCCAACAAAAGCTAAGC
AGGGAAGTCAGGCCAAGAAATATCTNCCTGCAAGAGAAGGCATCGCACATGTATCTCTCC
ATGCTATTTAAAATTTGCATTCTGCAACATAGAAGGGATAGGCCATGCTGCAGAAGCCAG
GTCCAGGAAAACTGCTTTCTTTGGCCNTTACACATCCTTTTTGGAGAAGATGCTGGTGAA
AGCAGCAACTACCATCTGCCTCCTGTTGACTTAAGTGCAACAGGTGGAAGGGANGAAGGA
AGGGCATCGCAAACATCATTCTATTATCTCAACCTTGCTTTTCTCGG
Sequence 1069
CCCTTAGCGTGGTCGCGGCCGAGGTACCCTGCTTTGATTATTTCCGAATCCAGTGGGTAG
AGAAGGTAAAGGCAAGGGCTCACTGGATATTTTTAAATTGTAGGGATGTCCTTTGCTCTG
GGTCAATTTTAGGATCAAATATAAAAGCACCTATAGCTCAGAGTATCTTCTAACATAAAA
CTTCTGAGATACCAGAAATTTTCCAAAACATGGTATAAACAGTATGAAACACTGGGTAGA
TAAAAGCTTTCTCTAAATCTTAAAGTGCTCAAATATCATGACCTGATTTTTTAGTTTTAG
AAATCAGATATTTTTCTATTCCATATCTTAAACTTTCATGTTAAATTCTAGTTCTGACAA
TGTAGGGTTCTATTTTTTTCAGGTGATTGTTGGGAGCGTATAGAAGCATATATAAATATG
GAATATGTGTTTCTTTTTTCCCCTTCTGAAAGAAAGTCAAGCCTCTAATCAAATAGATTG
ATGCTTCAGAAACTTAACAGAATATTATCTGCAATTTGGCATAAATGCATTTTTCTTGGG
GAAGTTTCCATGGTCAAAATTATTAGTCATTGCAAAACAGAAAAGTTTGACACCTGGAAA
TGCAGACCCTTTTGCTT
Sequence 1070
CCCTTTGAGCGGCCGCCCGGGCAGGTACATTATATTAATGAAATTTATCTAGTCCTTGCA
AACTTGTGCCTATTGATTTTCATTAGTGTAAACTAAAGAGAGAAACTTCACACTGACATT
TATAATTGTAAGAACTAAGAACCAACCATCAGCTTTTCTATGCCAATCCATGCCCTTCAG
GAAGTTCTTGAGGCCTTGAGGTTGCTAGTTTAGTAAATTGCTTACTGGGACATTAAAGCA
GCTACATTTTTGGAAAGANGGAGAATTAAGTTTTTGGTG
Sequence 1071
CCCTTAGCGTGGCCGCGGCCGAGGTACCAAAACTGAAAAAAGATTGTGTATCCAAACATT
ATTTCACATAAAATGTATTTTGATAAAGTAAATTCCCAAACCATGGTGCTCAGAGGTTGT
AACAGTCCATGTAAGTTGAAGAAAAAGAGTTATCAATCAATACGTGACTATCAATCATTT
ATTTAATCATTATTTAGTTTTCACATATCTAGAAATTTCAGTAGAAGAACCAGCCCTTCA
TAAANGTGGCCATTCCCTATACCTGCCATCGATTACATTATTTTACT
Sequence 1072
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTTT
CACTCTTGTTGCCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACCACAACCTCTGCC
TCCCGGGTTCAAGAGATTCTCCCGCCTCAGCCTCTTGAGTAGCTGGGATTACAGGCATGT
GCCACCATGCCTGGTTAATTTTGTATTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCC
GGCTGGTCTCGAACTCCCGACTTCAGGTGATCCTCCTGCCTTGGCCTCCAAAAGTGTCAG
GATTACAGGCGTGAGCCACCACGCCCTGCTTAAGTTTTAATAAGATCTCTTGGCAACTTT
TTACGACTGGCAACTTAGGTCTCACAAACACAGAAAAGCTTGTCTTTAAGTATATTGTCT
TTGAAAAGTTAATACACTCTCTAAATGCTCCATTTAAAATGATTTACTTTATAAATGCAT
GCACTGAGAGAAAAGATATTTGAATGATATACACCACAATGTTAAATTAACTGNGATTGT
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AAAC
Sequence 1073
CCCTTAGCGTGGTCGCGGCCGAGGTACCTATTGTATCAGAAAAATGCTAATTAATTTTTT
GCACATAAAGGGCATTTTAAACTTGGTTTTATTCTTTGTGATAAATATGGATGATGAATG
GTAATGTTAAACAGAATTCAAAAGTTATCAGTTTGGCTAGCCAGACACAGTAGTATATGC
CTATAGTCCTAGCTACCCAGGAGGCTGAGGCCAGAGGAGCCCGGAAGTTCACGTTTAGCC
TGGGCAGCATAGTGAGACACTGTCTTTTATAAAAACAACAGCAAAAATGATCAGTTTGGG
ATAGTAAGACAAATGGCTTTCTTTTGTTAGGAATTTCTCTATTTAAAGGACTTTTAGGCC

Table 1

TAGAGTGGTGGCTTACGCTTGTAATCCCAGCACTTTGGGAGGCCAATTGCAGGAGAATCA
CTTGAGGCCAGGAGTTGGGGACCAACCTGGGCAAAGTANGGGAGACCCTGTCTTTNCAAA
AAAAATTCAAAAAATTAGCCCAGTGAGGGGGGNGCTTGCCTGNGGGTCCTAGCCACCTGG
GAAGGCTTGGGGGTGGGAANAATTACTTGGGCCCANGAATTTGANGGTGTAGTNGAGCCT
TTGATNCCCCGTNAACCGAGTANAAGACCCTTNTTTTNTTNAAAAACTTTAAANTTNAAC
NTTTTTTA
Sequence 1074
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGGTCACTCTGCCCCAGCTCTCCAAAGGCATC
AAGATCCGACTGCTAGGAGCCCCGGCTTCTTCCCTGACCTGCCCGTCTCCTACACCCTCT
GGTCCTGCTCCACACTGGTCTAATAACTGGTGTTCCACATTCCTCTAACGTGCACAACAC
AGTCCTGCCCCCGTGCTTTTCACCTCCTGTCCATTCCTCTTATAACG
Sequence 1075
GATATCTGCAGAATTCGCCCTTCGAGCGGCCGCCCGGGCAGGTACTCTTCAAAGAGGATA
AACTTAAAGAAAATGACTAGATACACATCAAATTAAGCTGCTGAAAACCAAAAACAAAGA
AAAAATTTTTGAAAGCAGCTAGAAAAAAATTACACACCACACAGAGGGGAATAAGGTTTA
CATTACAAAGATTTTTCACCAGAAATCAGAGAAGTGAAAAGACAGCTAAATGGCATCATT
GAGGTGCTCAAGGAAGCAAGCATCTACTCGGAATTATATATCCACCTAAAATATCCTTTA
GGAATGAAAGTAAAATAAATACATTCTCAAAGAAAAACAAAGAGAATGTATCCCCAGCAG
ACTGATCTGCTAGAAAAGCTAAGGTCAACATTAGGCTGAAAGGAAATGCTGCATCTTCAG
GAATGAAGAAAGAGCAATAGAAACAATAAATATATAGGAAAACACAAAATAC
Sequence 1076
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTCACTGATTTATGGCAAGTCAGCCAATCCA
TCAGTGCTCAAAGCTCCTTGTATTGTCAGGNATGNNTNNCATTATTTGTCACTCATTCAG
AATTAAACTGCCAACTAGTAGCATTTGTTTTGTGTCTGATAGATTCTTCATGCAGAAAGA
ATAAGTAAAATGAGATGGGACACAAATCTGAGTATAGCATTGTCATTACTTTTTGCTGCA
CAGATTACTTGCAAGAAATATTCTAGTCTGGGGCATAACAAAATCCACAAATTCCAGATT
TAAAAAAGTAGGTCTATATAAAGCCTTATTTAATATTTGGTATATTTTTTTAGGTACCTCA
TTGGGNGNNCCTTTATNATGCCAAGGCATTTTTTTGGGGATCCTGGGTTTCTTAATTAAAA
ATAGGAAGAAAATCTTAACATTCNCGTGGTGGATTAAGAAACNCCNCCCCACCCTNTTTT
TTGGATTAANGGNGNTTATTAAGTAAAAGCTTACCGTTNAAGTAAGCTTCCCGAAAAGAA
AATNTTTA
Sequence 1077
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAGTAACCATGACTTACTAGGTGTTATGATGA
AGGTGTATGTGTGTGTATATGTGTGCATGCATGTAGATAAGTGTGTGCATTTGCACACAT
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GGACTCTTAAGATTGTCTTGTAATTGTCTTTTTGTTGTTGTTGAAAATTAAGGGTGTATA
TTAAAGGTAGTTTTTACCCAGATCTTATATGTGTGATAGCTCACGTCTGTAATCAGAAAC
CTACTGTTTAATGGCCACCCAATTGCCATTAGCTTCCTAGAGGGTGATTTAATAAACTAT
CTTCTTTAAAACTCATTTAAAATTAAGAGACATGTTTGCATACAATGGATTAATGACGTT
TTCACACTAACCCCAAAAGTCTGCTTGCACTTTCTTTTGTAGGCCTAACATTCATTTCAT
ATGCATTGATTATTATTGTTGAACTTGCATTAATTACATCGNGCATATATGGACATACAA
TGTCATCTGCAGAAATTAAGGATTTTTTA
Sequence 1078
GAATTGGGCCCTCTANATCNTTCTCNACCGGNCGCCANTGTGATAATTCTCCTNTAATNN
GCCGCCCGGGCNGGTACAGACTTTNGTTCCTTTGCTTTTATTTTTTTTTTTTTTTGCATN
GATATGAATAGTTTCACTAATTCCATTCATGGTTCTGTAAACNTTCTTAAAACTTTGTTT
TATGGGATTATCAGAGTAACAAAATAATGTAGTCCCTTTATGGGACTATAAGTAACTTAA
TGCTTTTCTTTCCCTATTTCATATCCCCATATTTGGTGCAATAATTTAATTCA
Sequence 1079
CCCTTAGCGTGGTCGCGGCCCGAGGTACAGCTCACATTCATGGGGAGGAAAATCAGGGCC
TGTCTTTAGATAGGAGATGTATCAAAGAATTTGTGGACATATTTTAAAATCACAGCACTA
CTCTTGATGTACCTGCCCGGGCGGCCCGCTCGAAAGGG
Sequence 1080
TAGGGAGTCGACCACGCGTCCGCTGCCTCGCCCAATGGGCTCATAAACAAAGTGGCCATG
GTGGCAGGGATAGACTTTCTCAGCAACATGGACTTTCACTCACCAAGGCAGACCTGGCTA
CAGCCACTGCTGAGTGCCCCATTTTCCAGCAGCAGTGCCCAACACTGAGCCCTTGATATG

Table 1

GATCATTCCTTGGGTGATCACACAGCTACATGGTGGCAGATTGATTATATTGGACTTCTT
CCATCATGGAAAGGGCAGAGGTTTCTCCTCCCTGGAATGGACACTCCAGATATGAGTTTG
CCTATCCTACACGCAATGCTTCTGCTAAGACTACCATCTGTGGATTCACGGAATGC
Sequence 1081
CCCTTAGCGTGGTCGCGGCCGAGGTACACCGATGTGGCTGACATTTGGCTGGAGTCTGCT
AAGATGTTTTCTTATNCTGGATGGACGCAGACCTGTAACACCCTGTTTTTCATCTTCTCC
ACCATATTTTTCATCAGCCGCCTCATTGTTTTTCCTTTCTGGATTTTATATGGCACGCTG
ATCTTGCCTATGTATCACCTCGAGCCTTTCTTTTCATACATCTTCCTCAACCTACAGCTC
ATGATCTTGCANGTCCTTCACCTTTACTGGGGTTATTACATCTTGAAGATGCTCAACAAG
ATGTATATTCATGAAGAGCATTCCAGGATGTGAANGAGTGATGACCAAGGATTATGAAAA
GGAAGAGGAAGAAGGANNAAGAAAGAAG
Sequence 1082
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTNGCTGGTTA
ACAAATATTTTAATTCATTAAAATAAAACTTAAAAATTCATGCTTAGTCTACACAAGTTT
AACTTACTTTAGTCACTTAGTGAATTGTGAATTGGCTCCCATTAGTGGTCAGGANAATGT
ATTTGGTGTANAAACCAAATAAATCAAGCTATTATCGCCTTGTGAGTACCTCGGCCGCGA
CCACGCTAAGGG
Sequence 1083
CCCTTCGGCCGCCCGGGCAGGTACTGGGAAGTGCACTTGGACGAACAAAAAATAAAAAAA
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NNNTTGGAAAAAANAAAAAAGGAAACANNNANNGCGGGTTTTTTAATTTTNAANCATTNN
AAATTTTTTTTTAANNANNCCNTTNAANNNTNNNTGAAAATGTGANNTTTNNNNNGAATNG
ANCNTNNNTCTTNTNTGGNTGATTTTTTATGTGTTCCAAATNGTTTTTTTTTANNGAANA
AAAATTTTTTTTTNNGAAGNTANACNTNNATTNAAANNATTTATNCNTNNTAAAAATTNN
AANAAATTTTAAATNNTTAATGGNNTTNAAANTTTTAAAATTT
Sequence 1084
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GTGAACAAATGAACATGCCACATGTCAACAAACTGAACAAACATGGATTGTTAGTGACTT
ANAGGTGGAGGGAGGGCTAGAGAGAGGCTAGCTGTGTTGGTCTGCCAATCTCCTGTGTCC
CACACTGGCTACAAAAATACAACCACTGGGTAGGTAGGGCTCATCTAGAACCAAAATTAG
GAATAAGGATTGAGAAGAAAACTCAGCAAGGGTGATGAATGAGTTTCAGCTCATTGCTGG
AGTTAGCTGAAGAATGAATAGGACACAGTGGATGAAGGAACAANGCTATTCCNGGGACCT
TTTGAAG
Sequence 1085
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TACCACCTAACAAATTGGAGGAAATGAAAAGACGAATCAACAACATTTTGGAGAAAAAAT
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TGAAATCAAAATTGGATATTTGGAACATTAAATATGGGAGCAGAGAATCTGTGGAATTAT
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CTTTTCAAAAATGTGGAGAAATTTATAAGAATTTGGCTGGAGAATGTCAGAATATTAATA
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AGTCCACTCTACAAAAAGTGCTGGCATGTTGGGCTACTTATGTGGAAAACCTTCGCTTAC
TAAGGGCTTGCTTTGAGGAGACCAAGAAAGGAAGAAATTAAAGAGGTACCTGNCCCGGGC
GGGNCCGNTCTAAAAGGGC
Sequence 1086
CCCTTCGAGCGGCCGCCCGGGCAGGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTTTGAGAC
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GAACAGTAAGTAGATTCATTTTGTAAACAGACAAGCTTACAAGTTTTCTCAAATATGAAA
GTCATACTAAACTGGGAGACTGTTAACTTCTTGATGGGGTTAATCTCTAATATGAAGCCA
CAGTCATAGCTAACTACAAATTACATATACAATGCCAAAAATAT
Sequence 1087
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTAC
CCAGAAGGGCAGACTTCAACCCAGAAACAACTGTGAATTGTGATGGAGAGATGGCTCTA
GTATCTGAACAACGAAATTATACTTATAGACTACTTTCTTTTCACAGAACAAATGAGCTT

Table 1

TCTTGGCTTTTAACAAAATTATCATTGAAAACTACAAAATTAAGATCACCCATAATCCCA
GCATTCAGAGGGTTAATCTTTTGTTTAAAATCCTTCCAAAAGTCTTAAATGTGTTTATAT
GCCTTTTGGAAAAAAAATTTATTTTATAATCATTTNGGATTTACAGAAAATTGACAAAGA
TAGTACCTCGGCNCGCGACCACGCTAANGGCGAATTCC
Sequence 1088
CCCTTNCNAGCGGCCGCCCGGGCAGGTACATCCTTTTGCATGCTCAAGAGCCCATTCTTT
TCATCATTCGGAAGCAACAGCGGCAGTCCCCTGCCCAAGTTATCCCACTAGCTGATTGCT
ATATCATTGCTGGAGTGATCTATCAGGCACCAGACTTGGGATCAAGTTATAAACTCTAGA
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TCCAGTAATCAAACTAGAGCTCCTCTGCCTTGTGTAAGTTGCTATAAAGTATTGACTATT
AGAATGTCTTGAACTTTGGTTACTGTGAGCCAAGTCGGTGCTCAAAGTATATTTCATAGT
CTCAATTATATAGTAATTTAAGTTCTGAAAAATAGGTTCTGGCTTTGCTATGGAAATATT
TTGNGAGTATTTACTTTGGAA
Sequence 1089
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACATATCCCTATCTACTATGTAAAGACAAAAA
GGCAAATGAAATGATGTAATACAATGAACTCCTCAGAAAATAAGCTCTGTAAAATCTCAG
ACTGCCTGTTTATCATATGCTAGAGTAAACTTACATTCCTTTCTTGTTAGAGAAAAATGA
TGGTAAAATCCATGCATTAATCAAAACTAAAAACATGAAAAGGCAAGCCAACTACAAGAG
AAATACAGTTGGCCCTTGAACAACACAGATTTGAACTACATGAGTCCGTGTACCTCGGCC
GCGACCACGCTAAGGGCGAAT
Sequence 1090
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCGTGCAGAAGAAGCTACCAAACAGCAAATAT
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CTGTTTGGGGTGCCCCCCTCCCCCTTNCGACCTAAGTGCTGCCAAGG
Sequence 1091
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTGCAGTTTTCTAAGGGCTCTTAGTGCTTTT
AACTAGAAAGGGGTTTTTCGTTTGTTTGTTTGTTTTAAAAGGGTCCTTAGTGCCTCTTAC
TCCCTTCCTGTAAAATCCTGTGTAAAATGACAAAAGTGCACAATTGATCATTGTAAGTTC
TAGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1092
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGATCTAAAGTTGGGGTGGGAAGGAAGG
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GTATAATCCTGTGAATATACTAAAACATTGAGTTGTGCACTTTACATGAGTGAATTGTGT
GGTATGTGAATTTATATCTCAATAAAGCTATTTTTAAAACGAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAGGTNCCTCGGCCGCGACCACNCTAAGGG
Sequence 1093
CCCTTAGCGTGGTCGCGGCCGAGGTACCAGGTCACCTGTATCTTGATCACCAGAGAGCAC
ACCAGCCTGGACAGCAGCACCATACGCTACAGCTTCATCTGGGTTTATGCCACGGGATGG
TTCCTTGCCATTGAAGAACTCTTTAACCAGTTGCTGAATCTTTGGAATTCGAGTCGAGCC
ACCAACAAGAACAATTTCATCAACCCGCGTACATGCTAAGACTTCACCAGTCAAAGCGAA
CTACTATACTCAATTGATCCAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACA
GCGCAATCCTATTCTAGAGTCC
Sequence 1094
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATGCCAAAGACTTCGCCATAACTTTTCAAGT
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GGGTTGAGAAGACAAAACACTGTTAACTTCATTATACCTTTGACAAAGTAATATTATGTG
ACATGATGTGTTTTCCCCAAAATATTAGAGCTGCAGATTTAGCTGATTCAATTTATGGGA
CAATTTGTTATGTGATCTAACAATTTGGCATATAATCTAGAAAGCAGCTTTATGATCAAA
AATTGATTTTATATATATACATATAAAT
Sequence 1095
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAC
TTCAAAATAACATTTTTATTATATAAAAATGTAAAAATCCAGCAAAACCAGAAATACGGA
ATATATTTTTCTGGGCTTTCACATTTGTTGATTTTTATTCGCGATCTTTTTCAATACAAT
TTACACCCTCATCCCCATTTCCAGTCTGATTATACAAGNGCTAAGTGGCANAAAGGTCTG
GAATAAATACATCAAAAAGAAGAGGCAAAGCTGTGAAACTAAGTTGCA
Sequence 1096

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATCTGATACAAAATCTGAAAGAAAGAACAG
TCTTGTAATCTTTACATACTTGTAAAAGCATTTCTCAAATTTCAGCTTACTTTCAAAATA
AAGTTCTTACTGTCTAATATGCTCTCTTTAAATTTATTAAGTATTTTAAAAATACCCTGG
CTCTTTATCTAGTTTCAATCTAAGTATAGAAAAGCATTCTCTGTAAGGCTGTCTTAAAAA
AAAGAAAAAAAAAAAAAAAAAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1097
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATCTGCAGACATACTGAGTGTCACCGTTGAA
GAGAGTGGAGTGGCTTTTGTAAAGAAGTTCAGGTACATGTCCAGGGGCCCAGCCTCTGGG
CCCAGTAACTCAGCTACTCTTTGTGGCTTTCTTCATGGCTTTTTTTGTGGGCTGCCACGC
CCATCTTTATCACCAGAATGAGGAACTCCTGGAAGTTAACTGCACCATCAGTGTTGATAT
CCAACTCTTTGAACCAGACGTCTGCACCCTTTTTCCTGATATACTGAGGACACTCGGTCT
CTAGCAATTTCTTCAGGTCATCC
Sequence 1098
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTACCATTCCATACAATGGAATATTACCCGAT
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AAAGAAAATGCCAAAAGAAAAATGAGTTTTAGCTCAAATTTTTTTAAGAGGCCTAGCCTG
CTCAAGATATCCTGTTAAAAAAAAAANAAAAAAAAAACTCTTCCCATATCTAAGGTGAAA
ATAAAAAACATTTTTAAAAGTTNAATATAAAAGAATGAAATAATTTCAGGTCAAGTTTAT
TATACAGAAATTATATTAATGGGTGG
Sequence 1099
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGAGGTCTCCATTCAGTAGGTGGCCC
GGGATGAAGGCCGTGTTGGGGCTAAACCACACTCTGGAATTCTGTCAGCAAATTCCTCGC
TGTGTGAACTTGAGCAAGCCATTCACCTTTCTTAAGCCATTTTCTTGATATTTCACAGAG
CCTCACCAAGTATTCAACGAGAACATGTAAGTGAAATGCTTCACAAAATGCCTGGTAAAT
AATAGATGCTTAGAAAATGGTAGAGAGAGAAAAGAGCAGTCTCTGCCCTTTAATGTACCT
CGGCCGCGACCACGCTAAG
Sequence 1100
GGGGNCCCGGGGAAAAATNATTTTGGGGGGGGGGGNCCCCCCCCCTTTNCCTTTNANNA
NNTTAAAGGGCCCCNNTTGGGNCCCTTTCCCGGGAANGGCCCGGGGGGCCCCCCGGCC
C
CCCAGGTTNGGTTTGGGANTGGGGGNANTTANTTTCTTTGGCCAAGGAAAATTTTCCCGC
CCCCCTTTTTTTCCGGAAGGCCGGGGGCCCCGGCCCCCCG
Sequence 1101
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CATCCAAAGGCTTTGCCCAGTATGAGCTCTTTAAGTCCTCTGCCTTGGATGATACAATCA
CAGCATCACAAACTGCGATCGCTTTGGATATTTCCTGGAGTCCTGTGGATGAGATTCTTC
AAATCCCTCCACTCTCTTCAACTGCAACTCTGAATATTAAAGTGGAATCAGGAGAGCCCA
GAGGTCCTTTGAATCATCTCTACAGAGAACTGAAATTTCTTCTTGTTTTGGCTGATGGTT
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GTCAGGAATTTCTGAATGACTTAAATAAGCTGGATGGGATTTGGTGATTCT
Sequence 1102
GATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGTACGCGGGATTCCCCCAT
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AGTTAAATTTTGTGTAAGGTATGTTATACATGTGGAAGTTCATTTTTTTGCATGTAAATA
TCCAATTGTTTCAACACCATTGGTTGAAAAGACGGTATGTTCTCCTTTGAATGCTTCTGC
GCCTCAATTAAAATCAGTTTACTCTATCTGCATAAGTCTACTTCTGGGCTGTCTACTCTC
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ATAGTAAACCTTGAAATCATAATTCTATAGTAAGTCTAAAAAAATCACACAGGTTGGAAA
TGCACAATTAGTATGCTAANATCAGAGCAATCTTGTTGGTTCANAATGGTTTATGGGAGA
AATATTAGCNCAGTGNNCTTCACATGCCTCATTGATGATAACTGGAGCTTAATGTGAA
Sequence 1103
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTGTTAGCGTCTGCGTGTGTATGGAAAGTTGA
CAAAAAATGGCATGAAAAGATCATGATTGGATTTTCTTTTAAACCTGCCCTTCTGTAAAA
AATAGTTTATATATTTTTAAATTAGTAGGTATGTGTGGCTTCCTTTTTTCCTAACATTCC

Table 1

CAGCAAATTTTTGCTGCTAAGACTATCACTGTTAAAGTGAAAATTACAGGGAAAAATGTG
ATGAATATACCGTAACTCAAAATGTGATATTTTCTTAAAATCACTCTTTTATGCTTTAGG
AACTGGTTGGTCTCCACTTTGATTATTAGTGTAAAGAGCCTGAGTATACGTGGATTTCAT
TGTAAAATTTAACTCCTTGTCTTTTACTTGGGGCACCGGGGCCCCTGGAGGGCTTCCCTA
CTTTCCCCACTATGTTAACAGGTAAATNCTGATTTTATGCCTTTAGTTTGACTTATTTTT
ANCNAAATATTAGAAGTTATTGCTTTTAAAATGTTTAATGTGGGACTGAAATTTTCATCT
TTTNNTTNAGAAATCTATGAAGTGTATTCAAATAACGTGGCCTAAAGGCAAAGGNGGGG
TATTTTGGNAATTCTGAAATTGNTTTGGCATCTGGNCCAAAAACCTAAANTANTCCCCGT
GGCCCTTTTTTTTTTTTTTTTT
Sequence 1104
CCCTTTCGAGCGGNCGNCCGGGCAGGTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGG
T
ACTTGCAATGTTTTGACATTAAGAGAGAGACTATACATTCACAGAGGTTGGGAGCTTCTG
TCTAGCCTGTTGTCCAAAACTGCTTATAAAATTTAGCAACTAATTTTCACTTTTGACAAC
TATTTTAATTCTAGAAAATAGGTTTATAAAGATTTTCTTAAAGTGTTATCTATCCTTCCA
ATGACTTATTATAAATTTTAGAATGTATTTCTATAGGGTGGAAAAATCTCCTTTAGTCAG
AATTGAACAGTTTTCATGAAGAACATGTTACACCATGTAGAAACATGGGTACCTCGGCCG
NGACCACGCTAAGGG
Sequence 1105
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTAGCGTGGTCGCGGCCCGAGGNACT
TTTTTTTTTTTTTTTNTNTTTTTTTTTTATATGGCAATATTTATATTTATTTTTGCAATTCC
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AAAATGAAGGTTTTTNTATTTTCCACAAAAGTTAAA
Sequence 1106
CCCAATTGGGCCTTTNGATGCTGCTCGAGCGGCGCAGTGTGATGGATTCTGCAGAATTCG
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AGAACCATTGTTCTGAATGCTGCTTCCATTTGACAAAGTGCGTGATAATTTTTGAAAAGA
GAAGCAAACAATGGCGTCTCTTTTTATGTTCAAGCTTATAATGAAANTCTGTTTGTTGAC
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AA
Sequence 1107
GATATCTGCAGNNNTTCGCCCTTTCGAGCGGTCGNCCGGGCAGNTTCNTGAGATGTTACA
CTAGTATTTTGAAAAAGTATAAAAATGTGGCCGGNCGTGGTGACACATGCCTGTAATCTC
AGCCACTTGGGGAGGCCAAGGGCANGGAGAATCGCTTGGAACCTGGGAGGGCGGAGGTT
G
CAGTGAGCCAAGATGCAGCATTGCACTCCACCTGGGCAACAAGAGTGAAACTCTGTCTCA
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TGTCACTTACTGAGAAGCAAGAACCAATGAGTGAGCCCAAAGGAGTCTACTACCCATACC
TATTAAGGGTAGGGAAAGGGTTTAAGT
Sequence 1108
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CCCATGTTCTGGATCTGGGGACTGCAATATTACAGAAATATGCAAAAATAAGTTTAGTGC
TCAGAGATAAATAATTTTNCTTATTTCAATGCATCAATGCGCAAAAATTTCAATTCAAAA
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CCAACATTATACAAAAAATGTGTGGCACCGTGCACATACNTGTGCATATGTGTATGCAAT
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ATTATATACAAAACCTTTTATATAAAAAA
Sequence 1109
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CTGTTAACGAAACTCAAAAACAGAAATACCTATATTTTCTCGCTAAATCCAATTGTTACC
TATGATGAGTAAAGACACTAGATCTGCAGGTCCTAGTACAATCTATACATAAAAGGCCTT
CAGATTTGAGGCACAAAAAAAAAAGGGCAAAAAAAGAAAAAAAAGAAAAAAAAACCTTCT
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TTAACAAGAATTAAGAACACGATTGTCGGGGAACTCAGATGTTGGCAAAGCTTAAAAATA

Table 1

AAAAAACAAGGGCTGGGTGCAGTGGCTCANGCCTATAATCCCACACTTTGGGAGGCCGAN
GCAGGAGGATTGCTTAAGCCCAGGAGTTTGGGATCAGACTGGACAACAAAGTGAGACCCC
TATNCCTATCTTNTNCNAAAATTTTAAAAATTAGCTGGGCCCAGTGGTGGTGGTGCCTGT
AGCCCCAGCTACTTANGANGCTTAAATGGGAGGATCCCTTGAGTNCAGGANTTTGAAAA
TTGCNTGAGCCTTTGATCAAAACTTTACTTTAACCCTGGGGTGGACCANAACCAANGGGG
TTTTAAAAAAAAAAAAAAAGGGAAAAAAAANANAAAANGGGGAGGTTTCCCCCTTGGGCC
CCCCGGGGGGNCCGGGGGCCCCNGGNTTTTTTTGAAA
Sequence 1110
CCCTTAGCGTGGTCGCGGCCGAGGTACTGGGATTACAGGCGTGAGCCACCGCACCCAGCC
AAAACTGAATGCTTTTAAGAGCACCCAAGTCAACTCTTGAGTGCTTTGCTGCTTATAAAT
TTATTCCACCAGATACCCTANATCATCTCTCTCAAGTTCGAAGTTCCACAGATCTCTAGA
GCAGGGGCAGAATGCTCCCAGTCTCTTTGCTAAAGCATAGCAAAAATCACCTTTGCTGCT
CCAGTTCCCAATAAGTTCCTCATCTCTGTTGGAGACCACCTCAACCTGGACTTCATTGCC
ATATCAAGATCGGCATTTTGGCAAAGCCATTCAGCAAGTCTCTAGGAAGTTGCAAACTTT
CCCACATTTTCCTGTCTTCTTCTGCACCCTTCAAACTATTTCAACCTCTTCCTGGTACCT
AAGTTCCAAAGGTACTCCACATTTTCAGGTATGGTTACAGGAAGCAACCCGNTTNTACCG
GTACCTGCCCNGGGCGGGCGNTCGAAGGGCGAATTCCAACACACTGGGCGGGCGTTACTA

Sequence 1111
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTATGTTTTAATTTTTTGTAGAGAAGGGC
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CCTCAGCCTCCCAAAGTGCTAGAATTACAGGCGTCAGCCACCACGCCCAGCCTGNAGCCT
ATTTTTATAAATGAAGTTTTATNGGAACATANCCATGCCTGGNCATTTACATACGTCTAT
GGCTTCGTATGCCATATAGCAACAGAATATATTAAACATTTACTACCTGGCCCTTTGCAG
AAAATGTTTGACAGCTCCTGCTGNATAAACATAAAATCTGCCAAAAAATGCTGATATTAC
CCCACATGGAGAAACACTGGAACCCCTCTTCAGAAATCAGATGCCAATTTAAATATTACT
ATCAAGAGAAATACACTCTGATTTTTTTTTCCTATTCCCTTTCTTTTATTTTCTTTTTTG
AGACAAGGTCTTGGCTCCGNTGNCCAAGCTGGAATATGATGGNGCCATCATAGCTCACTA
TAACCTCNGATTNCTGGGCTCAAGTGATCCTCTTGGCTTANNCTCCTGAGTAGCTGGGAC
TATNGGCGTGGGCCCGCCCCACCCGGGCTAAATTT
Sequence 1112
GCGCTNGTGTTTCAATCCCTTACGCNCCGCAGCCNTGNTGATGGTCTAACCAAATTCTAG
TNCCTGCTACAATGGGATGGCCTGGGGGATTAATGGAACTTTGCCGGGACCAACTTATGA
TAAGTGGGAAAGCACTTTAGGGCTGATCCCATATANGTGGTGAACACTGCACTTNTGGCC
AAATGGACACGGAGGATAANCACCATNTGACACTGGGGGTGGTNCAGTTGGAGCTCTGGA
AGGAAAAGNCTTCCTGGGGTGGATCTCTAACAATATTAATACCTCNGCCGCACCCGCTAA
GGCGAATTCCAGCACACTTGCCGGCCGTTACTAGTGGATCGAGCTCGGTACCAAGCTTGG
C
Sequence 1113
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TCCACCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAG
GCAGGCACCACCACACCCGGCTAATTTTGTATTTTTAGTAGAAACGGGGTTTCTCCATGT
TGGTCAGTCTGGTTTCGAACTCCCAGCGTCAGGTCATCTGCCTGCCTCGGCCTCCCAAAG
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TAAGATTTGAGTATTATACTGGGATAGAACTGAAGTTGGGGGCTTAATTTGATCTATCAG
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TTAATTCCGTCATTTAANTTAGCCNAGTATGTTGATTTTTTTTTGGNGAAAGNGTACCTG
CCCCGGGCGGGCNGTTCGAAANGGG
Sequence 1114
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ACGACAAAGCACTGTTGCTGAGATACTGTGATTTATTTTCCTTAATGGGCAGTTTTTTTA
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Table 1

Sequence 1115
GTACAGAAGGGTTTCACCATGTTCACCACACTGGTCTCAAACTCCTGGTCTCAAGTGATC
CATCTGCCTCAGCCTCCCAAAGCACTAGGATTACAGACTTGAGCCACCGCACCCTGTCCC
ATCACTTTATATTTTCAAGAAGGTGGTGAGGGTGTGTTGGTGCCTGGGGTCTCTAGCTGA
AGAAAAGGGAAATTTTTCTATCTCTGGTAATGTCTTTATGGATATAAACCTCAGTTAACT
GGAATAGCTATGGAATGTATGCTTCTGGTTAACTAAAAATTAACCAGTAAACACTCTGTA
NTAACCATTACAGAAAATACTTCTGCTTTAAAAAAGTACCTGCCCNGGCGGGCCGCTCGA
AAAGGG
Sequence 1116
TNTCTGCANAATTCGCCCTTAGCGTGGTCGCGGCCCGANGTACCATCCCAAGGACACAAG
TTTCCAGGCAGCAGCCTNCAAGAATTTTGTTAGAGATGTCCCATCACTTATGGCCTACAC
TGTTACATCTGGACTCTGGATTGCAAGTGTAAGGAAGAAAGTGAAAATGAAAGAGAAAGT
GGAACAAATATTGGCAACAGAGCCCCCAGAGGACAGTTGTCCCTTTTCCAACAAGTTAAG
TGGAAAATGCTGTTGCCATGGGAGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1117
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ANCCTTGGAAAAAATGGNNTTTTAAAAAATNAAAAAAANAANTTTTCAAANCNNNAAAAN
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TTTTTTTAANTTTTTTTAAAAAACCCNCCCCNCNNCCATTTTTAAAAGNGGTTCTNTTTT
NAAAAAAAAATAAANATTGGTTTTTTAAAAAAAAAATTCCCCCCCCCNATTTTTTAAAAN
CCAATTTTTTNTTTAAAAAAAAAAACCCGNNTTTTAAAAAAAAAGNGGGGATTTTTTCCA
NNTTTAAAGGGGGAAAAAAAAAGGGNTTTTTTTTGGGNNAAAAAAAAAAGNCCCCCCCCA
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AAAAAAAAAAAANGGGGGGGGGCCCCCCCGGGTTTTTTTTTTAAAAAAAAAANATTTTTT
GGGGGGGGGGGTTTTTTTTTTTTTNNCCCC
Sequence 1118
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CCCGGGCGGCCGTTTNAAAGGG
Sequence 1119
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TTTNTNTTTNGGGGGTTGCCAAAAAAAAAAA
Sequence 1120
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Table 1

CTTTTGGGGGGCTGGG
Sequence 1121
CCCTTAGCGTGGTCGCGTTCGAGGTACTTTNTTTTTTTTTTTTTTTTTTAATATTTAGTAG
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ACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCGGGCTGAAAAAT
AACCCTTTAGATATCTACAGCTTTAAACTGTGTGCAGTCATGAAAAGCAGACATTAGAAG
TCATTGGCATTTAATAAATTGCAGTAAAATTATACAGTAAATACATTACAATCATTAATA
ATAGGCTTTAATGAGAAGAATTTAATAAATAATCATTAAAAAGACAGCAGAATTTTATTC
TGGTCTCAATATGGTNGCTGCTCTTCTTATCAAATCTATAATAAAACTATNTGACTATNA
TATAGATTTCAGGAGCTAAAAAAAGCCTTATATTTTCAAAATTAAAGAACNATTTTAATT
TTGCNAAATCAATNAGCATTACTGAAGTTTAAGGAAATTTTGGAATAAAATATATGGCAN
TTANATNCCGCCTAAAAAGAATGNAATCTTAANGATTNCTTTTTGGCTCAGGGGCNTAAA
ATTCCA
Sequence 1122
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CCAGTTGCCTGACGAGAGCTCTTCAGCAAAAGCCCTTGTCAGTTTAAAAGAAGGAAGCTT
ATCTAACACGTGGAATGAAAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1123
CGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTTCGAGCGGCCGCCCGGGCAGGTAC
CTTTTATCCCTCAAAGGACCCTTCTTGGGTTTTGAATGGAAGCCTTTATTCCGGTTAAGA
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TGTATCTGCTACCATTTATTCCTATAATTTTAAGAAAGNTGGGGCTTGACATTATACTCA
TTTAGTGAGAGTANATGCCAAAAAAAGTGGAGGGG
Sequence 1124
CCCTTTCGANCGGCCGCCCGGGCAGGACGCGGGTAGGGCAACTTGGATGTATGCTTAGGG
TTCGCAAAAAGTAAACAAAAATACAAGGGAAAAAAATTATTGACAATGAACTGCTTTGGT
AGTGATTTGTGATTTTGTTTTTTCTTGATTAGTAACCAACAGCACAGCCACCAAGAAATT
ATGCACATGTGGGACCACGTCAAGCTGAAGCGTTTGTGCCCAACAAAGGAAACAATAAAG
AAAATAAAAAGGCACACTAAAAATTACAAGTTTGGGATAAGGGATTATTTTTGAAAAGGT
ACCTCGGCCGCGACCACGCTAAGGG
Sequence 1125
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CAAAAATAATTCCATGAAAAAAAAAAAAAAAAAAAAGTACCTGCCCCGGGCGGCCGCTCGA
AA
Sequence 1126
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CTGTTATTTTGAGACTATCCCGCGTACCTCGGGCGGCGACACGCTAAGGGCGAATTCCAG
CACACTGGCGGNCG
Sequence 1127
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Table 1

TTGGCTCAGTGCATGTCACCAAAAATTCTCCAGGGATTTCATAGTCTCGGTGGTGTGGCT
GGCCCAGGACTATCCATGCAGGGAGGCCTGCACCTNTGACAGTCGGCTGCANCTGGGGGT
GCCCATCTTNTGTGCTCTGTGGTACTNCTACACACATAAATTCAGGAAATGACTAGATGA
GCCTGAGTTGGCTTTANTATTAATGTGCAAATACAGTTTTCTATACCAACAAACCC
Sequence 1128
CCCTTTCNNTNNTGCCGCCCGGGCAGGTACTATCGATTGGGTCGGGGGTGATCTATTATC
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TATGTGAAGGAAAAGGCATANTTATATGGTCATCCATGCTGGGGAATATTTNGNAGNTNT
NTTTTGTTGAGAGAAATNGNNCATNTTGGATCAATAGNATTAGACAAATATCTTGNGCAT
CAAGAGACCTGGAAACATG
Sequence 1129
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CAGAAAAAAAGGCCTTAATATCATAAGGTTTTTTTATAGCCCTCAAAACTGATTTTTAAA
TGGAGGTAGGCAACTGAGAAAATAAGCATTTAAATTAGTTTTCACCCCAAAGCCCCCCAA
AATTTTGCTTACAAAATTAGGGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1130
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AAAAATAAGGNAAANAAAAANTTTTT
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Sequence 1132
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CACTCACTATTGCAAAGATAACTCCAAGCCGTGAGTGATTGGCTCCCATGACCTGAACAC
CTCCCACCAGGTCCTACCTTCAGCATTGGGGGTGACAAAGCAACATGAGATTTGGGCAGG
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CATTGCAAAATATAATTATGCCTTCCTAACAGTCCCCAAAAGTCTTAACTCATTCCGACT
TTAACTCAAAAATTCAAAGTTGGCCAGATGCAGTGGCTCACACCTATAATCCCAGCATTT
TGG
Sequence 1133
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GAACTTCATTGATTCATCAATGCTGNCTGGTTTTTTAAACCCA
Sequence 1134
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ATCCTTTCTCTTTTCTTACCTTCCTCTTTGACTCCTTATCTTTCTATGCCAACCCTCTCT

Table 1

AAAAAGTCAGTATGTAATATAGTTGCTCTTTTATTTAAAAAATTTTAAGATTGATATTTG
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AAATGTCATTTTAAGTATAGGAGACAGGTGAAATTGTTCAAGGTTACTACTAAACCAGGG
AATAAGGGAAGCTTAGATTCTTGGNCTTTTTTCAAAAAAGAAAAATTTTA
Sequence 1135
CATGCTCGAGCGGCCCGCCAGTGTGATGGGATATCTGCAGAATTCGCCCTTAGCGTGGTC
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TTGGTCTCACTACCCACATCACCTGGAATGGTTACCAGGCCTCAAAGGACTGCCCCACGG
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Sequence 1136
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Sequence 1137
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Sequence 1138
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Sequence 1139
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Sequence 1140
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Table 1

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CTTAAGANTGTGGGCCCTGAACCATCTGGGGAACTTGTAGCCCAGCCNGTTTCTGGGGCC
CTTATCTTAGACCTACAAAAAGAAACTTTGGGGGTTGGGG
Sequence 1141
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TTCAAGCAATTCTCCTGCCTNAGNCTNCTGAGNAGTGGGGATTACAGGTGCCCGCCACCA
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NNATTTNTANANANCATACTANNNNNGNGGCTTGTTTTGGNNANAGGAGGGGGGGGGGCC
AAACCCCCCNCCCCNCCCCCCNTTTNNCCCCCCCC
Sequence 1142
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AAAAATAAACCATGTTTGCATCTTGGTCTTCTTTCCATTTGGATTCAAAAGTTNTATAGT
GATTCCTCCTAGTAAAATTGCATTTTCTCCCTAGGAGTACCTCGGCCGCGACCACGCTAA
GGG
Sequence 1143
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GGGAAATAGCATTTAAATGGTAAATATGGTAAAGATTGTTTTATGGTTTTTGGGTTTTTT
TTTTTTAATGATCATATTTTTAATGTTACTTTAAAATAGATTAGTGGAATGTGATTCAAT
T
Sequence 1144
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TTTTGCTG
Sequence 1145
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AATTAAAACGAAAATAAAGTAAAAAAAAAAAAAAAAAAAGTACCTGCCCGGGCGGCCGNT
CGAAAGGG
Sequence 1146
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GTTTCGTTAATCAGAAGCTGCAAGTGGGTTTGTTTTATAGCCAGTTTGCTTTTAAATTTG
GCCATGTGGGCTTTAAGTTCAACGTATTTGTGTTCTCTTTATNGTTACTCTCTCCAGAAG
TATTACCCAAACTGTGAAGTTGTGGTTATGGGGATGGCAAACATTCATTCTATTCGGAGG
AGTTTTCAAGTCTNTGCGGTTGCTGTGCACTCAGAATGCCANATCCCGGGAAAGTAAGTC
CTT
Sequence 1147
AGCGGCCGCCCGGGCAGGTACATCTGTCAAAAATCATATTTATGTGAGATGTGTCAATAC
TANACTTGTGTNATTNATGCTACTTAGAANGANGATAAAAAATATCCTGTTTGGCTCCAA
AAAAAAGAAAAGTCAGCCCCTCCTGCACGAGTNGGAGCTGCAACCCTTTANAATTGATAA
TCACAAACCCCTNAGACCCANAGTAAAATAAAAAAAAAGATATGTNACATTAGGCATTGA
TGGAAAAGGACTAGATCCTAGTATAAGCATCCTAATAAAAGGAGAGGTTNAAAGACGCTC

Table 1

TCCAGAACCAGNNTTNCAGACTTTNTATGATAANCTAAATGTGCCANTCCTCGGCCNNTG
ACCACNCTAAGGGG
Sequence 1148
CCCTTAGCGGCCGCCCGGGCAGGTACTATTGAACCAACAGGATATCTTTTTTATTATTTG
CATGAGTTAATCCTACAAACAAAATTAAATACCTCTTTTATAAAACATCTTTTCCAGTGT
TCTAATTGATGGAGATGCGGATCACTCATCTATAAAAAATGACTTACAGCTTCAGCTTAA
TCAGTTGCTATAATGTGAAAACAGGAATGTGTATTTTTTTCAACTAGGTAAAAGGTGCAT
ATAATTTGAATTGTTAAATGTTTTATTAATGAACAAAGTAAACCTTTTAGTAATTTTTAA
ATTACTGGTCTTAGGTGTTTGAAACAAGGTAAAAGTATACATTCCAGTTTTGCCCAAAAG
TCACTTAAAATATCTACAAATTATTTAATCTGTGTGTGGTAACACCATTATTGCTCCAAT
TTCTGGAAAGAGTCTATTTTCAAAGTTTAAAAAAGAGGAAAAACAGCAAAGTGGCTAACC
TTTGCAGTGGAAAGAAAAAGTGTCCTTCATGGGTTACACTTTCATATTTTTATGCAGCAT
TAAGTTATCTACCGTTATGGGGGAACTTGGGGTTT
Sequence 1149
CCCTTAGCGTGGTCGCGGCCGAGGTACCATATTGTTCTTNTTACANNTNTTACTGTCTCA
GNTATAATTTTGCAATGGCGGTTTCNCAACTNGCCTGNCCNNACCCNNNTGTNTCATAAN
TAATCTACGTAAACAAGTTAAAATAGGTAAATGNAATGTGATNAATACTTGNGGACAACC
TGGTCATAATTTANAATCTCAAGGCTATATTAAATAATACATATTTCATTATTNGGGTAT
TTTCCAATANAAATGTATTGGAGGAAAACCTTTCCCANAAAAAAGNGTAACCTTTTTAAN
AAGGNGAATNANNNTTTGTCTAATTCAAAAGCTTATTTAAAGGTTATGTGTAAAACACGG
TNAAAGAACCNTNAAATAAAGAAAGATNTAANATAAAACGTTACCAAAAATAAAGTG
Sequence 1150
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGTTTTAA
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GAGGCCAACTCAGGAGGATTGCTTTAGGCGAGGAGTTGAANACCAGCCTGGGCAACAAAA
AACAAAAAAATTACCCGGGCATGGTGATGTGTGCCTGTAGTCCCAGCTACTTGACAGGCT
GANATGGGAGGATCCCTTGAGCCCTGGAGTTCAAGGTTGCAGTGAGCCATGATCTCCCCA
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ANAGAGGTGGAAGGGCTCANCAAGTGCTTTCCACATTCGCATTCCCTTAAAATCGGGAAT
GCTCTAAAGCTAGAGGACTTTTA
Sequence 1151
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTGGGGTTTTTTTTT
TTTTTTTTTTGAGACGGAATCTTGCTCTGTCACCCAGGCTGGAGTGCAATGGTGCGGTCT
CAGCTGACTGCAACCTCCGCCTCCTGGGTTCGAGATTCTCCTGCCTCANCCTCCCAAGTA
GCTGGGACTACAGGCACCCACCACCACACCTGGCTAATTTTTTTGTATTTTTAGTAAAGA
CGGGGTTTCACTATGTTGGCCAGGCTGGTNTCGAACTCCTGACCTCGTGATCCACCCACC
TTGGCCTCCCAATCTTATTTGCTTTACAAGTCCTGCTTCAGGGTTACCTTCCCTGACCAC
TGCTGCCTCCCTCCCAACATTTCCAAGGGACTGTCATTGCCTTAAGTTATTTTTTCTGTT
NAGNTTTTTTTTTGGCGTTTTTNTTTTTTTTTNAAACAGCGTATTAATCTNTCGCCAAAG
GCTTGGAAATCANTNGCCCAAATTAAAAGCNTTGTTGNAGCCTTGAACTTTCTGGGCTTA
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GGCCTTTAAAATTAATTTNTGGGTAACAAAAAAAAAACTTAAGCCCTANGNAAANCTTTG
GTTTAAAAATNACAAGAGGGACTTNNATNTTNCATTNATACAAATGGAAAANATTAANTT
TCNTCNTTANNANGANAAAGGAAAAAAAAAAAAN
Sequence 1152
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ATTGAGTATCATGTATGCATTCCCTTTTATGATATACAATTAATTGAAGTTATTTCCCCT
TGTATGCAACCATCCACATTTTTCTTCTGACCTTTTCCTCAAGTCTTACAACTACTTTTA
ATGACTGCATTTTGGAGGTGGTCCCAGGAGAACAGATGTTTGCCTTATAATGGNGTTTTT
CCATTTTTATCTTTGATTGNGCAAGGGGGTTGGAAGTATTATTTAGTCATTATATGGATT
CCTCTAAAAATTGTTCAATANAATATATATTCATTTATTCACTTTACTTATTGTTTATTT
ATTGCCTTAGAGTATACCCAAACACNGGAGGATTCAATAATGATCAAGACAGGTCTAATT
TCTGTCCCAAANGAGCTTAAATATGNGAATTAGAAAAGGAATTTT
Sequence 1153
CCCTTAGCGTGGTCGCGGCCGAGGTACTACATAGAAAGGGCTTGGAAGTCTGATTCAGGA
AAGGAAATCAGGAAAGAACAAAGGAAATGAAGGAAGAATAAAAAAGAAGAGAAGTCATTG

Table 1

AAAAAGTATGAAAAAATATGAAACAGATAACAAGAAAGTAGAGGAGATTCCAAAAAATAC
AACCCAGGTTTTCTGCCCTCATTCTATAGAGTCTTGAGAATTGTAGGGTGTAAGAAATAA
AGAATCAAGTCTGAGAGATCCCTTTTGCTTCTTTCTTGTCTCACTGATCTGGAACCCAGG
TTGCCAGCTGGCTATTCACAGGCCCCGCGTACCTGCCCGGGCGGCCGCTCGAAAGGG
Sequence 1154
CCCTTAGCGTGGTCGCGGCCGAGGTACTGCAACTATCACTTGTCATTTGTCTAGGAAGGT
AAAATACAGGAAGTTCCCAACTTAAAAATGGGCTTGACGTAGCAGTCATTTGTAAGTCAC
TTGCTTGGAATTTAGAATGCTTCTTCCCTCTGCAGAGACAGCTTCCATATGGTGATTAGT
ATCCAGTCAGCCCACAGAAGTTATTCAGTCTGTTGCTATAGATGAAATTATCCTTATTTT
TACTTCCCCTTCGAATAGACCACCTACTGTTTCTTCTGAGTGTGGTCTTTTTCTTTTCTC
CTATTCCCTCCTCAATCCTCTTTTTTTTTTTTTTTTTTTNCTGGGTTTCTTCATTATTCTC
TAATTTCTTCTTGGCTCAAAATACTTCAAGTTCTATTGNGGTAGCCTAGATTTAGGGACT
AGTTTGG
Sequence 1155
CCCTTAGCGTGGTCGCGGCCGAGGTACCTGCAGGAACAATATTCCTGTAGCCATGGAAGA
GGGCCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAATCTCCCCGTGGCAACAGGTCCA
GGAGAGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGGAAGGGAGCATGTACTTGCG
CTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAGCAAGAG
GTGGTGAGGTTGATCGGGGTTTATCGATTACAGAACAGGCTCCTCTAGAGGGATATGAAG
CCCCGCGTCCTGCCCGGGCGGCCGCTCGAAGGGCGA
Sequence 1156
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CCTGAGACTGAGTAATTTACAAAGAGTAGAGATTTAAATGGTCAAGGTTCTGCGGGCTTT
ACAGGAAGCATGGTGCCAGCATCTGCTCAGTTTCTGGAGAGGCCTCAGGAAGCTCTTAAT
CATGGCAGAAGATGAAGGGGGAGCAAATTAATCACATGGTGAGAGCAGGAACAAGAGAGA
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TAATGGTATATAAACAAATACAATATATACAATAAAACACCTAAACGCANAGGCTGCTTG
TTATCCACAATANTAATACCAATAG
Sequence 1157
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TTGGGGCAGAAAGCATGGACTTTTAAAGGGGGACTTGGCATGAATGCATTCAGAGGAGGG
AGTGAGCAGTTGGGGGTCTGCGTGACTCGCTTTCGTGCTTAATCTACTGGTGGTCGAGCT
GGCTGCATCACAAGCAGAGCTAGGTTGTATAGTGGCCTTTGTCTCAAGACACTCTCCAGG
TGGGAGAGCCTTCCATCAGGGACATACTTTAGGTTGCAAATTGACTGTTGTCTCTTGAGG
CAATCTCCTTGTGGGAGAGAGTTTCTGCCCTGGAGCTTCAAAAGTAAGCACGTAGTTAGA
TAAGCTTCCAGTGTANNTGAGTGTCTGGTGAAAGGGAAGGTAAAGGTTATGATTGCATTT
TCTGAAAGAGCTAAGGTANGGAAATGGGGAACATAAAAAAAAAAAAAAAAAANAAAGTC
Sequence 1158
GAGAAGGCTTCATTAANGGAATCTCACTGNGAATATCTCCTGAGAGATGGACAATGAAAT
ATCAGNNGGNGGATATGNGTGATAAGCTGATTTCAATATTGAAGTATNGAAATAAAATAT
TCTTTACACCTGAAAAAAAAAAAAAAAAAAAAAGNACCTGCCCGGGCGGCCGCNCGAAAG
GGCGAATNCCAGCACACNGGCGGCCGGNACNAGNGGANCCGAGCTCGGNACCAAGCNNG
G
CGGAANCANGGCATAGCNGNNCCTGGGGGAAAANGGNAN
Sequence 1159
CCCTTTCGAGCGGCCGCCCGGGCAGGTACACCAGCCTGGCGACAAGAGCGAAACTCCATC
ACACACACAAAAAATTAATTAAAAATAAATAAACATTGGTCAAAAATATAAAGCTGTATC
AACTGTATATAAATAATTCAATTAAAATATCATGCATAAAATCTGGGTGTAATAAAAACA
AAGAATAATTTTTTTAAAACCCAAAGCAAGGCAAGGGGTGATGTTACCAAACTGCCATGT
ATCAGAGATGTGATTAGAAGGAAATCCTTCAAGGGGAGCTTATTTATGGTACCTCGGCCG
CGACCACGCTAAGGG
Sequence 1160
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ATACCCTAAATATTTATCAAAATTTTTCACTGCTATTTTCCTCATAGGATTAAAAGGGCT
ATTTATTATTTTTTATAACTACAGCTGACCCTTGAACAACATAGGGGTTAAAGGTGCAGA
TCCCCCGTGCAGTAAAAAAAAAAAAATCATAAAAAACTTTAGATTCCCAGAAAACTTGAC

Table 1

TATTAATAGCCTACTGTTGACCGGAAGCCTTACAAACAGTTAATACACATTTTGTATGTT
GNATGTATTATATAATGTACCTGCCGGGCGGCCGCTCAAAGGGCGA
Sequence 1161
CCCTTAGCGTGGTCGCGGCCGAGGTACTATAAAGCTTTTGTTCACACACACTCTGAAGAA
TCCTGTAAGCCCCTGAATTAAGCAGAAAGTCTTCATGGCTTTTCTGGCTTCGGCTGCTCA
GGGTTCATCTGAAGATTCGAATGAAAGAAATGCATGTTTCCTGCTCTTCCCTCATTAAA
TTGCTTTTAATTCCAAAAAAAAAAAAAAAAAAAAAAGTACCAGTCTCACATTTGGCCCAA
ACCTCAGGATTCTCCCTCTGCCTGTCTTACTTCATGGTACCTGCCCGGGCGGCCGCTCAA
AGGG
Sequence 1162
CCCTTAGCGTGGTCGCGGCCGAGGTACCAACCCTATTTTACAGATGGGAAAACTGAGGCT
CAGAGAGGTTAAATCACTTACACAAAGCCACACAATTTTGAGTGGAGAGCTGGAATGTGA
ATCCAGGCAGTCTGACCCTGCAGCTTATGTGCTTAACGATACTGCCTCTCATGTGGGCAA
AGGATGGCCCAGGAGAAAGGCAGGCCCAGATTCCAAATCTGGCTTGACCGTCTAAGAGGC
TGAGTCTTAACCTCTCTGAGCCTTTGCTGTTTCATCTGTAAAGTGGTCCTCCTGACAGCT
GCCTCCTAGGGTTGTTTTGAGGATAAAGTGAAGTAATGGAGGGCCCTTGGGATATGGTAC
CTGCCCGGGCGGCCGCTCAAAGGGCNAATTC
Sequence 1163
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTTTTCACCCTCTGAAATTACTAAGCAGGCTG
TGGGGTGGTGCTCTGAAACTAGGTAGAAGTCCTCACCCCCCAACAAACCTTTACCAGTGG
TTTTAGCATGCAGAAGATTCTGGCCTGAACCAGTTACTACTACAGAGGCTGCAAAATGAT
GATTTTTTCATTCATTCTTTNGTAAATACCCGGTATTTTTCACAGGATGAATGTACCTGC
CCGGGCGGCCGCTCGAAAGGGCGAATTCCA
Sequence 1164
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TGGAGTGCAGGCAACAGGCCAAGACCCTGTCTCCAAAAAGAAAAAAAGGAATAATTCTAA
AAGACTTATATTGATTTTTTCCCCAATTAACATTAAACGCCTCCACCTGCCCCGTGGGAA
ATTGGGTTGGCATGTCACTGAAAGGCAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1165
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ACTCTTTAAGTAGAAATGAAAGTCATCTGACTGAAAATTATAGCAGTATCTAATTGTTTT
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ATCCTTGGATTTAGGTTATACTGACTTTTATCTTTACCAAACCATATTAACATTTGCATT
TTATAATTGGAATGAGAAATTTAGAGTAAGAGATCTGGATCATGCAGGCAGGCAAGCATC
AACCAACAATACTTTTATGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1166
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CGNTTTNAAANGGGCGNNTTCCANCAAANTTGGCGGGCGTTACTAAGTGGGNTCNCNNCC
NTCGGGACCCGAGCTTGGNCGTATTNTTGGGGAGNACCCCCTCCCNCCCCCNCNTTNTTT
TGGAATAGAAATTCCCCCCC
Sequence 1167
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTCTGTCTTCTAATTTTTAAAATTATTAATG
TCTTCTATTTTTCTAAGGCTGATTTTTTCTAATGTCTGTATTTTTCCTTTTTTTCACATC
TTGACATAAGTAGAGTTCATTTATTTTCATTTATTCTTGTATAATAAAATTACTTAAGGT
TAGGAATAATTAAGTTTTGCTCCCATGTTTTTATGTGTAACAATCTCAATGTTGTATGTC
ATCTACTTCAAAATTTCAAGCTTCCCCTTTAAAATACTGTTTAAAAAACTTTATGAAACC

Table 1

AGTATTTCTCTCAACCCTTNGTGTAATACCTGGTTTTACTTTAAATGTGGTCAAGATAAT
TTAACCTGT
Sequence 1168
CCCTTTCGAGCGGCCCGCCCGGGCAGGTACGCAGGGATATACAAAGGTGAAAAGAAACCT
GAAATATTTGTTGATGGCTGGAATATTTATTTTTTTGATCAAATAGATGAACTGCCTACC
TATTGGTCAGAATGTGGAAAAAATACAGAATCTGTTGGGCAGTTATGGTTGGGCCTTCTT
CGTTTCTACACAGAGGAATTTGATTTTAAAGAACATGTTATTAGCATCAGGAGAAAAAGT
CTGCTTACAACTTTTAAGAAACAGTGGACCTCAAAATACATTGTTATTGAAGATCCCTTT
GATTTGAATCATAATCTCGGAGCTGGATTATCAAGGAAAAATGACAAATTTTATAATGAA
GCTTTTATCAATGGTAGAAGAAGTATTTGGGATTTCCTGGTCAAGGGGATTTCAAANGAC
TACCCCTCAA
Sequence 1169
CCCTTAGCGTGGTCGCGGCCGAGGTACACCTGGTTTCACAGAAAACAAAGCAACTCTTAA
ACACCAGCTGGCAAAATGATAGGGCTTTTCCTTTGAATTANTCACCACAGGTGTGAAAGA
CAGAATGACTAATCCATCTGATTAAACATANACCTTTTAGAAATCAATAACCTTATTTAC
ACAGATGACAACTGCTACTGTTCCAAGGCTCCTAATCATGGTTCAGTTCTCAGGGCCTCA
AGTCTTTTTCCATTCCATCNCANAGTANTACCTGCCCGGGCGGCCGCTCGAAA
Sequence 1170
CCCTTAGCGTGGTCGCGGCCGAGGTACCGCAGCTAGGAATAATGGAATAGGACCGCGGTT
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TCCCAACACTTTGGGAGGCCAGGACAGATCGCTTGAGGTCAGGAGTTCGAGACCAGCCCA
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TANTCCCAGCTACTCGGGANGCTGAAGCAGGAGGATCGCTTGAACCCATGAAGTGGAGAC
TGCAGTGAAGCCGATATCGCACCANAAGNGCTCCAGCCTGGTCGACAGAGTGAAGACTCC
NTTCTTAAGAAAAAATAAAAATAAANGTTGTTNTCTTGAAGAAAAAAAA
Sequence 1171
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAGGAGGAATGTTTGGTTGGGAGAATCACAGC
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GGAATCCATTACCATGTCCTATAAATGACCTCTAGCCATTTTATGATTATTGTTCTCTGT
AAAACTCTTCAAGACTTCAATGAGAAGTTTGTTTATAAGAATTATCTTCTCATACCTTTC
CTTGTGAAGAGCGTATTCTGTTTTTCTATCAGTTCGACATGAAGTCCACATCACATGCTG
TTCTTTTCTAGTTACATGATGTGCCT
Sequence 1172
CCCTTAGCGTGGTCGCGGCCGAGGTACCAACCCTATTTTACAGATGGGAAAACTGAGGCT
CAGAGAGGTTAAATCACTTACACAAAGCCACACAATTTTGAGTGGCAGAGCTGGAATGTG
AATCCAGGCAGTCTGACCCTGCAGCTTATGTGCTTAACGATACTGCCTCTCATGTGGGCA
AAGGATGGCCCAGGAGAAAGGCAGGCCCAGATTCCAAATCTGGCTTGACCGTCTAAGAGG
CTGAGNCTTAACCTCT
Sequence 1173
CCCTTCGAGCGGCCCGCCCGGGCAGGTACGAAGACAGCATCCTTCAATCCCGCCAGCTCA
TGTGCATCTGAGGGTGGGGCTCTGTCTTCATGCTAGAAACCAAACTGCTCTCACAGCTTC
CTGCTAAATCACCACGGCTAACGGATAAGCAGAGACGGACTACCCGCGTACCTCGGCCGC
GACCACGCTAAGGG
Sequence 1174
CCCTTAGCGTGGTCGCGGCCGAGGTACAGATTGCATAATAATTTTTAGATAAATGTCAGG
AACAGAATCACATTCTTAAAAGGCNGAATTTCTATAAACGTGTGTATATGTTGAACAGAT
GAGCAGCTCTGCAAAGATGTGTATAACTGCATTTGAAAANGACAGTGAAAATTTTGGGTT
ACTGTAGATGTCCCACAGTCTGNCTTGGAATTTAGTTCTGTGACTAAAGGAGGCTTACAG
NTGCTCCAATTTTGGTTCTGNGGGGTACCTGCCCGGGCAGCCGCTCAAGGGCGAATTCCA
G
Sequence 1175
CCCTTAGCGTGGTCGCGGCCGAGGTACATGGTCACAACAGATGAGCAACTGATATCACTC

Table 1

ACACATGCTATTAAGAACTGTCCTGTGATAAATAACAGACAAGAAATTCAGGCATCAGAA
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GTTAAACTGTCTCAGGTGCCAGACCCTCCAGATAACATGAATCTGGCCAAGAATTTTCCA
GCACATATTTTTGAGCCAGCTGTGTTGTTAACACCAC
Sequence 1176
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCGCGGCCGTTAAACATGTGTCACTGGGCAG
GCGGTGCCTCTAATACTGGTGATGCTAGAGGTGATGTTTTTGGTAAACAGGCGGGGTAAG
ATTTGCCGAGTTCCCCGCGTACCAATGACTGGTTCCATGATCCCCTAAGAGAACACAACT
TAGGAATGTGGATTCTAATGATAGCTTTATACTGCTTAGGCAAATTTACTTCTGAGCCTT
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ACCTCGGCCGCGACCACGCTAAGGGCGAATTCCAGCA
Sequence 1177
CCCTTAGCGTGGTCGCGGCCGAGGTACACTGAAGAATTAAGCTGTAATGAGGCAACACGC
CTGCAACTTATTCTTTAATAGTTCAGAAATATTAACAATTGGGTAATTTGGGTGAAAGGT
ATAAGGAGCTATAAATGTTATTTCTGCAACTTTTATGTAAATTTCAAGTTATTTAAAATG
AAAAGTTAAAAAGTTTAAAACATAACAGAATAGAACATAACCTATTAAATAAATCTGAGT
CCAGGCATGACACAGTGGTTCATGCCTGTAATTCCAGGGAGGGACTGGGAGGCCGAAGTG
GGCAAATCACTTGAGGTCAGGA
Sequence 1178
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TATTGAATAATATAGAACCAAGATAAGAACCCTAAGAGACTTTAGATGTTTATTTGTTCA
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Sequence 1179
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CNTTTTTGGAAAANAAAATTANGGAATTTAAAAANGGGGGGNGAAAATATTCNNTGCGGG
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Sequence 1180
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GGCNTTAANTTTAAAAAAAAANTTTNNNNCCGGNTTTTGGNNNNGNNNGGNGGGAAAAAA
AAATTTAAAAAA
Sequence 1181
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTAGGCTTTCATAAAAATACAGCAGGGCAAG
AGGACCAAGATGGAGGCAGTGATCAGGGAATCTCAATGAGGGTGAGACTGCGACAAAGAC
TTGAAAAAGGTGGAGAAGCAAGCCTTGTGGGTATTTAGGGTAGCAGTAGTCCAGGCAAGG
GGAACAACTAGTGCAAAGGCTCTAGGAGGCAATGTGTTTGAAGTGTTTTAAGAACAGTAA
GGAGGCTAGTATGGTTAGAACAGAATGAGCAAAGGGGGCCAAAGTGGTAGAAGGTGGGGA
TCAAAGAGGTAATGAGGCCTTTG
Sequence 1182
CCCTTAGCGTGGTCGCGGCCGAGGTTCTAATGAAAGCCAGATAAAGGGATGGACGATCAC
AAGGTGAAGTCCCACANTAGGCTATCTGCAAGCTGAGGAGCAAGGACCANTCATCCAACC
TCAAATAGNANAAAANGGNNNGNAAGCCCGACAGGGCAGCCTTCAGTCTGTGGCTGAAGG
CCCTAGAGCCCCTGGCGAACCACTGGTGTAAATCCAAGAGTCCAAAAGCTGAAGAACTTG
GAGTCCAATGTTTGAGGGCAGGAAGCACCCAGCACGGGAGAAAAGATGGGCCGGAAGACT
CAGCCAGTCTAGCATTTNCACATTTCCCCCGCGTACCTTGCCCNGGCCGGG
Sequence 1183
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTCTTTTTGTGTATTACTTTTCACTTAGC

Table 1

ATAATGTCCTCCAGCTTCATCCATAGCAGCTTCATCCATAACTTCTGGGTGTAGCCATGG
CAAGGGTAAACTGATATGGCACACTGGTGGCATGTCTTCTGGAGAGGTGCTTCCAACTC
TTCCCTGTTTTAGCTAGTCCTCAATTTGTCTGATGTCTGAACCCCACTGCCAGAGTTGAG
TCTTGCCTGCTGAGTCATGTCCAGACTCCTACCTCAGAAGTATGAAGCATAACTGGTGTT
ACAAACACCATCTTCAGAACA
Sequence 1184
CCCTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGAAGCTCATTCTATACCCGAAGAGCA
GTCTCAGAAAGCAAGATTACTTTTGTGTTTTTTAAAAAATGATTCTTTAATGTAANTTTT
CTAAACATTCTGATTGGAAGTAGTGGATTCCTAAATGATTCCAAAGTCATCTGTAATTCT
TCTGTTTTTGTTTTGTTCTGTCTTTTCTTCATTTTGGCTTTGGGTGGGGGAGGGGCAGG
TGACACAAAGGATTTTTTTTTTTTTTTTTTTAATTTTTGGAATCTTTTNCCAATAACCCA
GCTAAAGATTTGCACTGAATACAACTTGTATGCCTTTTGCAT
Sequence 1185
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CCTTCTCGTATCTAGTAAGATTGGCTGGCTCAACTTTCTTCTGTCAAATTATATGGTTAT
TTTTTATATTACCACATCAGCATTATATTAAAAGTGTTTTTAATAGTTGAATGTATTTTG
CCAACTACTAGTATAGACTCAAATTTGCTATTTAATTTTTAAAATACAATTTATTTTGTA
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TGAAGATGAAATTG
Sequence 1186
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CTGCCTGTTTATCATATGCTAGAGTAAACTTACATTCCTTTCTTGTTAGAGAAAAATGAT
GGTAAAATCCATGCATTAATCAAAACTAAAAACATGAAAAGGCAAGCCAACTACAAGAGA
AATACAGTTGGCCCTTGAACAACACAGATTTTGAACTACATGGAGTCCCGTGTACCTCGG
CCGCGACCACGCTAAGGGCGAATTCCAGCACACTGNCGGCCGT
Sequence 1187
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TTCCCAAGGAACTTTTATTGGCTCCATAAGTCAAGTTTGAGTCCTTAAAGGAAAGCACAC
CATTCCCATCAAAGTCCTGGTAAAACAACTAGTTTCTCTAATTGTGTCCTGTTGCAAAAG
AAAACAGATTCTTATTGCACTTGTGCAAA
Sequence 1188
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TGTTCAATGAACATCCCAAGCACCTAGAACAGTTTCTGACACATAAGAAGTATTCAATTA
TGTGCTGGCTGAATGTATGAATTAATAAGTTGAGATTCGATCACTAGTTGAAGTATAAAT
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TCGGCCGCGACCACGCTAAGGGCG
Sequence 1189
CCCTTAGCGTGGTCGCGGCCGAGGTACAATGGCATAGTTGAGTAGTCACCACAGGACCTA
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GACAACGAACTATCAGAATCTATCATACACAGCAATGGTGAACACCTATTCCAGTTGGGG
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Sequence 1190
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AGACAGAATGACTAATNCCATCTNGANTAAANATAGACCTTNNNAGAAATCAATNACNCT
TATNTTACA
Sequence 1191
AATTCGCCCTTAGCGTGGTCGCGGCCGAGGTACTTCTACCATCTTTTGTCTACTTTCGTG
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GCTTGATTACCAATGTTTTGGAGTTTATAAAGCTCAATTCTAACAGAACATGATGATGTA
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TACCTGCCCGGGCGGCCGCTCGAAAGGG

Table 1

Sequence 1192
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AAAGAGTCTCACACTGGACACAAAAATAATTTGAGCTTCAAAATAAACTGCAAGGGATTA
AAACACATAAATTGTGTTAAAATCCACAAGTTCATAATGATACTAAAAAAAAAAAATCTT
GTTGGTTTCCTCTAGAGGCTACTAGAAAATCAGCTCATTATTTCTGATATTGGTTTAAAT
AGAAGAAAGAAAACCAAGCAT
Sequence 1193
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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TNTTCTAATTNAATTCCAAAATACATTCTNTNANCCNTATGCCCTNATACTAGNAACTNG
ATGGTNAGCGGGTAAGTAGGTAGTAGTANAANAACANAANGGGAAATTNGGGGAGCANAA
AAGGGANAAA
Sequence 1194
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AAACGCAGAGGCTGCTGTTATC
Sequence 1195
CCCTTAGCGTGGTCGCGGCCGAGGTACATAGTGTCGCGAACTCAAATCGGCATTTAGATA
GATCCAGTNGGTTTAAACGGCACGTTTTTGCTTATAAAAAAAGTG
Sequence 1196
CCCTTAGCGTGGTCGCGGCCGAGGTACTAAAGGGAAGTTGCTAGGAAATANAGCAGGTAA
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TTCAGTGNTTTTTTGGCATGANTGTNATGGAANAGTAAACAAAA
Sequence 1197
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Sequence 1198
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AAAACAAGACACTCACATACAATGTTTTTTAATGCTTGAAAAGTACCTGCCCGGGCGGCC
GCTCGA
Sequence 1199
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ANAAGAAAGTACCTGCCCGGGCGGCCCGCTCGAAAG
Sequence 1200
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GATTTTAGGCAAATAACCTAACCTCGCTGTGCCTCAGTTTCATCATCTATAAAATGGAAT
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GGTGCGGTGGCTCAACCCTGTAATCCCAGCACTCTAGAAGGCCAAGACAGACAGATCACC
TGAGGTCAGGAGTTCAAGACCAG
Sequence 1201
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AAATTAAGAAAAAAAAAAAAAGAAAAAAAGAAAAAAAAAGTACCTCGGCCGCGACCACGC
TAAGGG
Sequence 1202
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Table 1

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNATTNAANAAANNTTT
NTTAAAANNTTTNTNTNCCAAAAANTTTNNTTTGGAAATNCAAAAAANAAAAAGGTTNNTT
TTNNTNCCNTTAANGANCNAAANTTTNAANAAAAANTTTT
Sequence 1203
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GGGGAGCCCTCAGGAAACTTATAATCATGGCAGAAGGTGAAGCAAGCATGTCCTTCGCAT
GGCAATGGCAGGGAGAAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1204
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CATTCTATATTAAGTAACATTTTATTCAGATCCATATCTAAATAGCAATTTTGTGAGATT
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GCCGCTCAAGGGCN
Sequence 1205
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Sequence 1206
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Sequence 1207
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CCTCGGCCGCGACCACGCTAAGGGCGA
Sequence 1208
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CCCGGGCGGCCGCTCGAAG
Sequence 1209
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GCCTCACCAAGTATTCAACGAGAACATGTAAGTGAAATGCTTCACAAAATGCCTGGTAAA
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TCGGCCGCGACCACGCTAAGGGCGAATTCCAG
Sequence 1210
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TTTTTTGAGGCAGAGTCTTGTTCTGTCNCCAGGCAGGAGTGCANTGGCACGATCTNTGNT
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Sequence 1211
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Table 1

AAGGGGGAAATGAAGGAACTTNCGCACAAGGGGCTGCCCAGCTTTGTGGGGCATTCCAGA
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AGAAACCAGAGCCCAGAAGGGAAAAGTGATTGTCCCAAGATCACACAGCACTGGAGAAAG
TGGATGAGGAGGGGCTGAAGAAGCTGATGGGCANCCTGGATGAGA
Sequence 1212
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ATGCTATGAAGGCCCTTTGAATTCGCTTGACAAGAATGACAGAGATCTACTAGACCCAAT
TTTTAAATAATATTGCTGGTTTTTGCTCAACATGAATTAAAATATGGTGGCTAATGTGCA
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ATGCATTTAATGACACTTAAAATTGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1213
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GGGCTGGGGCAGGGAAAGTGAAAGAGAATCACAGAACATCCTGTAATGACAGAAAAAAGT
CACAATAAATGGTGGGATTATGTCAAAAGGACATGGGATTCAACTTGAAAGATCTTCCAA
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AAAAATATGAATGTATA
Sequence 1214
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TCACAGGANAGTTGCATTTGGGAATANAGTGAACCANTAGGGGCTGTGGAAGGCAGGCTT
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Sequence 1215
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Sequence 1216
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AAC
Sequence 1217
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TCCAGCACATTTTTAAT
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NAGATAATAAAA
Sequence 1219
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CACTANAAAATAAGTTACTATAAAAAGTGGTGGTCTGGGGGCTAAAAACAAAACAAAAAA
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Sequence 1220
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Table 1

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NTNATAACATTNCCATACATACTTAAAAC
Sequence 1221
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TGTGAGCTGTACCTGCCCGGGCGGCCGCTAAGGG
Sequence 1222
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AAAAATAAGGNTACCTTAACTTCCTTTTTTCCT
Sequence 1223
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CAATGTTATTTATAAGCTATTATTTCAAATGATAAAAAATAAATGCATAATACATTTGAT
GATAGAACATTTTTCTTTTT
Sequence 1224
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GNGCCTTGAAGTNATATTTGTGGATAGCTAAAAGCAATTTTTGGTTTATTTGGTTTATTC
TTTGGTTTA
Sequence 1225
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CTTAAAGTAATAA
Sequence 1226
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GCAAAGCAAAAAGCCCGCCAGTAATGTT
Sequence 1227
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Sequence 1228
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Sequence 1229
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Table 1

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ACACTGATGCATACACTATAGTGAAACACTGGCTTTAAGAAAACTGATTAACAGAAAACC
GGCAATTGTTATTTATTTTAAA
Sequence 1230
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Sequence 1231
CCCTTTGAGCCGGCCCGCCCGGGCAGGTACTCCATAATATAATCTTTTAAATGGGCAACT
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Sequence 1232
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AAAATTTTTTAAAAAAAA
Sequence 1233
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Sequence 1234
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Sequence 1235
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Sequence 1236
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Sequence 1237
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AATGGCTAGAAAGTATGGTTTAACTGGACCCTATTATGCCTTTT
Sequence 1238

Table 1

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CACAATCTGAACAGTAGCAGTGAAAGGGAGTTTAAGGTGGGGGTGAGGGAGAAGGGAGTA
ATATGGTTTTTTAGTAATATAGTAATTTACA
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GACCACNCTAAGGGCNAATTTCCAGCACACTGGCGGCN
Sequence 1240
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Sequence 1241
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GAGGCNCCGGNCNGNAACCCCCANCCNNNCCTTTAANAGGGGGGGGCCG
Sequence 1242
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Sequence 1243
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CCTTNGGAAGNTTTNCANCCCTTCCCCCAATTCCTTATCNNCCTTGNGAATTNCCAAAAA
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GAAACCTGGTTTTGGCNTTCCAACCCTTNGNCATTTGNCCATTGGAATACCCCCTCAAGN
AAAGNAAAAGGNCCTTNGNTTTTGTNNGGCCNTTNGTTGGCCCCAANG
Sequence 1244
CCCTTAGCGTGGTCGCGGCCCGANGTACAAATAANGTCTTCCAAGGGTTCAGAATAGAAA
ATGATNTCTTCCAGCTTGGGGACATTTGGGAAATTGGGATTCTTTGGGGAAATGTACGTA
ATCAGTATATTCTGGGAAAACATANTANAGAATGAATNNATAAATTNCATTGAATTNGGA
ATATGTTGTCCATTCTCCCTGTAACTAATGCTATCAAGATANAGTAGAAATACCACATTT
CAAAANCAGCTGGAGTANACAGGTCTTCATAGGCTAGCTTGGAAACCTAATAGCTATTAA
TAATGAAATTTTAATTATACTCTGGATTCTAAACAATGAACACACANTGATCTTTTTGAC
TT
Sequence 1245
CCCTTAGCGTGGTCGCGGCCGAGGTACAGATGTGTCCTTTCTTATAGTCNGTCAATGCTG
GGAAGTAACAGGCAGATGTGACTTCACTTGANCATTTGGANGAANCAAAAAAGGTTGCGC
TTGNTCGNNCCTTAGGGTTTAGATGGGCAAGGACCTTGCTTTTTGCNTCCCCAATTTCTT

Table 1

AGGGTAGNTGTTNTTCTTTGNGTTGCANGGGATNNGTANACCGGTACATCCTTCTTGNNG
GAACCAAGGGGNNNACNTTATGAANTGNAAAAGGGGANGTTCCTTTGTAGTAAANGGCCT
TGGATTGGTTTTCAAANNGGNAAGNTGGGGTTCCACCA
Sequence 1246
CCCTTAGCGTGGTCGCGGCCGAGGATACTTTTTTTTTTTTTTTTTTTTTGNCTAATTACTA
CCTTNTATTCTAATTGTGAACCATGGCCCTGAAAGCTTGATAANCAAGACTTGGCTGAAN
CCAGAAGGGGNAACTAAGTGNGGTTCGGCCAAGNAAAAGGGATTANTTGGGGATGNGAAA
ANTCAANTGGNCTTNTTCCCTT
Sequence 1247
CCCTTGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTANATGA
AAAANCTGTAATTCTTTATTTGAAACAANTGCNTTCAAAAGAANTNAAAACACTTCAAGG
ACTTCTAGTAAACATAAAAGGTCNAACAAACTGTGGCAAAAANTTTTGCAATTNGTANAT
AAGCTAANATAGGGGTTAACNAGTACCCCAGGCCANAATTAAGGNGGNATNNCNTCAANT
ACTTCCANTCANNNAAAAAGGG
Sequence 1248
CCCTTTCGAGCGGCCGCCCGGGCAGGTNCTATCCCTATGAGGCATAATTATAACAAGCTC
CATCTGCCTACGACAAACAGACCTAAAAATCGCTCATTGCATACTCTTTCAATCAAGCCA
CAATAGGCCCTTNGGNTAGTTAACCAGCCCATTTCTTCATTCCAAAACCCCNCCCTGNAA
AGCATTNNAACTCGGGNNGCCANNTTCAATNTCTTACAATNAAATCCGCCNCCCAACCGG
GGCCTTTTAACAATTNCCCTNCCAATATTACCTTAATTTNCTTGGGCCCTTAGGCCAAAT
AANCNTGCAAAAACCTTAACGGNAAACCGGGCAACCTTCCANCCCAAGGNTGCGGCCAAT
TTCNATTAAAATTNCCCTNCNTTCCTACCAANAGGGGGA
Sequence 1249
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TTTTGCAATTCTAGAACTTGGATTTTTTTTTTAACAAAAGTCCCAAAACACCAAAAATGT
AAACAAGATANNGAGATTAATATTGNAGTGGNNGTAATTTAATTAAAGTTATATTTTGGG
TTAATTTTTAACAACTGAAGTCTTATTGTTGAAACTTATTTTTCA
Sequence 1250
CTNTACATGCATGCTCCAGCGGCCGCCATGTGATGGATATCTGCANAATTCCCCTTAGCG
TGGTCNGCGGCCGANGTACTTAGGTGCCTACAACATAAACAGCA
Sequence 1251
CCTGTAGATGCATGCTCGAGCGGCCNGCCAGTGTGATGGATATCTGCAAGAATTCGCCCT
TCGAGCGGCCGCCCGGGCAGGTACGCGGGCAACAGTTAAATCAACAAAACTGCTCGCCAG
AACACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGGTGCTTCATATCCCTCTAG
AGGAGCCTGTTCTGTAATCAATAAACCCCGATCAACCTCACCACCTCTTGCTCAGCCTAT
ATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCTNGGCC
GCGACCACGCTAAGGG
Sequence 1252
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTATTATTATTTCAAATTTAAAAACTTCTTC
TTTTTTAAGAGATAGGGTATCACTATGTTGCCCAGGCTGATCTTGAACTCTTGGCCTCAG
ATGATCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCTCTTATTTGCTTTACAA
GTCCTGCTTCAGGGTTACCTTCCCTGACCACTGCTGCCTCCCTCCCAGCATTTGCCAGGG
ACTGTCATTGCCTTAGTTTATTTTTTCTGTTTTGTTTTTTTTTTGTCGTTTTTGTTTTTT
TTTGAGACAGCGTTCTTAGTCTGTCGCCAAGGCTGNGAGTTGCAGTTGGCCGCAATC
Sequence 1253
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ATCCACACGCTTCANCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCAGC
CTAAATATTTNTTTATAGCAATGCAAGGATGGCCTAACACACTGCCTAAATCAAAATTGC
TATTCACTTCAAGGGTATTTCATTTACCTGACTAGCTTTTTTGGGTGCATNTGGAACATA
ATGTA
Sequence 1254
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GAGTATGGACAGGGAGGCAGGGCAGATACAGTCCTTGCTTCTGGTTTTAAGAGTTCTTCT
GAACCACAATCAACTTCTCCAAACACCCACCTTTGTCTTCTACCACAATAGGGGTCAGAT
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Table 1

TTGAGACTATACCTAAAGGAAGAACATTCTCCTCTGTTGCACACTATTATCCAATTGGAT
AGACCCACATCTAAATGTCTGCAATTACAGTAATGTCAGCTGGGCATTGGTGGCTCATGC
CTGTAATCCCANC
Sequence 1255
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TTTTTTTTTTTTTTTTTTTTTTANAATAACAAAAAATTTTTTACTNAAACATAAANATTTN
CAGANGTTTCCNNACAANCCNTNCAAAATGGTCACAANCTTTTTTNA
Sequence 1256
CCCTTAGCGTGGTCGCGGCCGAGGTACTGTTTTTTTTTTTTTTTTTTTTTTTTTTTAGNT
TTCCTTTTTAATGAGCTCACCCTTTAACACAAAAAAAGCAGGGGTGATGTATTTTAAAAA
AGGAAGTGGAAATAAAAAAATCTCAAAGCTATTTGAGTTCTCGTCTGTCCCTANCANTCT
TTCTTCANCTCACTTGGCTCTCTANATCCACTGTGGTTGGCAGTNTGACCAGAATCATGG
AATTTGCTANAACTGNGGAAGCTTNTACTCCTGCAAGTAAGCANANATCGCACTGCCTCA
ATAACTTGGTTATTTGAGCCNCGTNTTTTTGCAAAAACTACTTTTTCCTANTTTTTCAAN
AATTTACTTTCAATNGTTTTTAAAAAAA
Sequence 1257
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TTAACTGATACAGACTTTTATTCTAAATGCTCACAAGCACAGAAACCAACAAGAAATCAG
ATCTTGAACGAATTTATAATGATTCTTCCAGGAAGCACCGNGGCAGCCACATAAGCCGCT
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AAGACCNAAAAAAAAAAAACAAAA
Sequence 1258
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ATTGGGTTAGGTATCTTTTTTTTTATTTTAGCACCTGATAGCTGTCTTTCTACTGAGTAAA
GAATTATAACTTTTAGATGTCACAGAAAATTAGAGTATTTATTGTCAAA
Sequence 1259
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AAGCAAACTCACTAATGATTATGAACTGAACATAACCAACAGGCTGTTTGGAGAAAAAAC
ATACCTCTTCCTTCAAGTAAGTTTGCCATGCCTACCATATCTGTGAGTGGTATTCTGGAA
TGGCCAAATGGCCCTGGTAGGACTATGGGTCCTGAAGTCGTGCTGCCTGGCTCTGGCCAC
ATCCCTGTGGTGCTTTTCCATCCTGATCTACAGATATTCAGAACTGCAGGGAGTTCCTTT
TAGTCCTGGCAATCTGAACCTGATTTTTTGC
Sequence 1260
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AGTGCACCTTGGAGTCTGTGGAGCTCTCAAGAATATCTCTTTTGGACGTGACCAGGATAA
CAAGATTGCCGTAAAAAACTGTGATGGTGTGCCTGCCCTTGTGCGATTGCTTCGAAAGGC
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TTGATGAAAGGTTGTGAACTGGTGGCTGTGGGTCAAAATCCATCTCACAGNATTTGTTTT
TGGATC
Sequence 1261
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TGATCAACTCTGCTNTTAAAGGACTCTGATGCATTCTTCAGTATGTGAACTGCTTTTTTC
AGCTCCANAATTTCTGCTTCATTCTTTTAAATTCAATCTCTGTTAAATGTATNTGGTAAA
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AATTCTGTCTTGAAAGGTCACAATCNCTGTTTTCTTAAGGGATTGGGGCCCTGGTAACT
TTATTTTAAAA
Sequence 1262
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TTCTAGCTTAGTGAGAATGCAGTATACTTTTTGAAAACTTCGTGCAGGAATCCCTCAAAT
GCTGTAACTAGGAATGGGTCAGTGAAGTTCAAACGACTTTTCCTTGAGGGAGTATTTTAA
TCGGACAAGGGAACTCTTTTTCTTTTGGGCAATGGCCAACAGGACTGAGAAGCCAGAGAG
CTTGCACCTGAGCCATCTCAGCCGTGAGAGTAACAGTCCTAGGAAAATAGATGGGGGCTG
GGGGTAAGGAAAT

Table 1

Sequence 1263
CCCTTAGCGTGGTCGCGGCCGAGGTACTCTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGGTT
TTCTTTGTAGAGACAGGGTCTCACTGTATTGCGCCAGGCTGGTCTTGAACTCATGGGCTC
AAGTGATCCTCCTGCCTTGGGCTCATGAAGTGCTGGGATTACAGGTGTGAGTCACCATGA
CTGACCTATATTTAATTTTTTAAAGATTAGACTGGTGTTAGCTGTAAATAGTTTGAAATA
CCTCTCTGATAGGTGCTAGCTTATCGTTACTCTTAGTGCTTCTTGCATTTGCAT
Sequence 1264
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTGTGTTTAAGAGAAATTCCTAAACTGGAT
ATATGTGGCAGGCTGAAAGCACTGTGAGTTGAAGTCAAGGGGAGAGGTCCAGGCGCAGTG
GCTCATGCCTGTAATCCCAGCGCTTTGGGAGGCCCAGGCGGGAGGGTTGCTTGAGGCCAG
AAGTTTGAGACCAACTTGGGCAACATAGCAAGACCTCGTCTCTACAAAAGATCNNNAANT
NAATANTAATNTAAATTAAAGTTCCTTTGGGCCGNNACCACNCTAAAGGGCGNAANTTTC
CAGCCACCACTGGCCGGC
Sequence 1265
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCTTATTGTTAAAGTGAGTCAGATAAATCTTC
AATTCCTGGCTATTTGGGCAATTGAATCATCATGGACTGTATAATGCAATCAGATTATTT
TGTTTCTAGACATCCTTGAATTACACCAAAGAACATGAAATTTAGTTGTGGTTAAATTAT
TTATTTATTTCATGCATTCATTTTATTTCCCTTAAGGTCTGGATGAGACTTCTTTGGGGA
GCCTCTAAAAAAATTTTTCACTGGGGGCCCACGTGGGGTCATTAGAAGCCAGAAGCTCTN
CTCCAGGGCTCCTTCCCAAGTGCCTANAAGGGTGCTTNTAGGGAAACATTAGGATTCCCA
GCCCAGGGGGCT
Sequence 1266
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TTACCTGTGATTTTGAGACCTATATAGTGAAGGTTTGTTGCCACTTTTTAGTTTCCTCAA
ACATGCAGAAGTAATGAGGTTTGACAGAGACATGAGACTATAAGATGTCTGTCATTGCTG
CCAACCATGGAAAAGATGTTAAGATGTCCAGCTGCCCATAAAATCATATTTTCAAAGTGT
GAGACACGAAGAATATCTTTCTCTTATTTGGAAATATGCTGAAGGATAGGAATAAAGAAA
AGGATTNCAGTAAAATGGGAGNC
Sequence 1267
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NNGGAATNTATTTTNCTTGGCTTNGGTNAAAAACCTCAACAAGTTTTACCTTTNNCCCAG
TTCCCAATTAAATATTAAANAANTTNGGNCAACCGTTTTGTTACCNTCNCCTTTTCNAGG
AAAAAAATTCCTTATTTGGNACCTTNTTTCTTGGNAAATTTTTTNANTAAAANAAAANTG
GGGCCATTTTTTNTTTTT
Sequence 1268
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GTCAGAATCCAAAGAGATGTGAGAATGAAAAGCACAAGTGAGAGCAGTGGGATAGCCAAA
TTTTAAGAGGGTTGTGAGCCAGAGAATATAGGCCGCCTNTAGAAGCTGCAGAAGGCCGGG
GTGGACAGAGTCTCCCTGCGAACCTCCAGAAGCAGCACAACCCTGCCCACTCACGGTAGA
CTCTCGATCTCCGGGCTGTAGAAATAATACATCTGTGCTATTTTAAG
Sequence 1269
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTAAAAGGTGATGCTAATACTTTAAAATGTT
TAAGANATAAGATTTAAAAAGCATTTGTAAATTGTATACTTGCANANGTCCGTNCTACAT
TGGCATTTTGGAACAAGGNACATTAATTGGTT
Sequence 1270
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CATACCAAAGCCGTCGCCTTGGNCACCG
Sequence 1271
CCCTTAGCGTGGTCGCGGCCGAGGTACAATTTTTAGTCAAGGGATTGTTTGATACTCTTT
AAGTTCACTGCCAGGCCTACCACTTATCTCTGTCCCAGGAGGAGAGTTCCTTGTAATGAG
AGGTTTTTAAGACGTCCTTTGTTCTGGGATGAATCATAGGGAATGACTGCCTTTGGAGCT
CAGGATATTAAACTGAGTGGTGTCAAATATTNCCAGGATCAATTCGACAATGCCATGTGT

Table 1

ACCTGCCCGGGCGGTCGNTCNAAAAGGGCNGAATTTCCANCACACTGNCGAGNCGTTACC
TANTTGGATTCCCGAGTCTTCTGNTTCCAAAANTCTTTTGGCGGTTA
Sequence 1272
CCCTTAGCGTGGTCGCGGCCGAGGTACTCAATGTCACATTNNCATAGGAAAGGTTATATA
TACACTATACACTTCAACCTTGAAATGTGGACCCAAAAAACATTCTATTTTTCAGTAATC
NATTGAATTTNGGTGAGGGGTCCNACACCCTCAAATCCTAANTTTATCACANAAAAAGCC
CNTNCTTGGCTGCCAAGCGCTGGCNGATGAACTTTGTNTTGCTGNANCTCTTNATGANTT
GGATNCCANAGTNTCNTGATGATCCTNTTCAATGTTTANGAGCATNTGACCNGNCATGNT
GTAGNGGANTGACTTTC
Sequence 1273
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAAAAAACNTTTNAAATTAAAAA
ACTCAAAAAAAAAANAAAAATGAGCATTTTAAAAAANGGAAANANTTNNAANNNNNNNG
GNAAAAAAAAAAAAAAANNGNAAAANNAAAANTNNNGNATTGNTTTTTTGGCAANTNANC
AANATCNTCCCCCTGAAAAAAAAAAAGTTTTTTTTTT
Sequence 1274
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AGCAGAATCTGTTCCATCCCTCTCTTCTTGTCTTCATCTGTTCTATGTCTGTCTTTGTTC
AAATTTCCCCTTTATATAAGGATAGCAATCATATTGGATTAGGCCCAGTCCTAATGACCA
GATCTTAACATTTGCAAAGGCCCTATTTCTCACTAAGGTCGTATTTACAGGTATAAAGGG
TGTAGACTTTAACATCTTTTTGGGGGAAGACACAGTTCAATCCGTAACAAGATGTTAAGT
CCTTTCCTCTCCTAAA
Sequence 1275
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Sequence 1276
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTATAAAAGGTTGAGTAAAAACAGGAAAGCGT
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GTATATTTTTATGCATTTTT
Sequence 1277
GTACCAACACAATTGTTAATTTCCTCACAGGCTNAAGGCATTCTGGGAAGCTATACAGGG
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GGCTAGGACAGGTGGNGGNGGTGGCCGGGTTTNAGGNTCTNCAAGGGACCCTNTGCAGAT
GCCGGGGCCCTGTTTATTCTGAGCAC
Sequence 1278
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CTTAGTTTTCCAAAACAAAAATGTTTAGGGCAAGAGTAACATTATTTTACATTATTGCAT
CTCAGTGAAAAATAAATGGCAACAAAATTCTTATATCTGCTTCTGCAGTTAATCTGTTCA
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AGGGGGACTATTGTAACAGGGCTGTGCACATAATTGTGGATGATTTTCTTTGATACAACA
ACAAAACTTGGTGGAT
Sequence 1279
CCCTTCGAGCGGCCGCCCGGGCAGGTACAATGTGATTTATCAATTAATTAAATTTGAATT
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TCATTAATAATTTGATAATTAAATGGTCCTGAATGGTTAGCCATGTTCTCCGCATTTAAA
TAAATAGTATAAACATAAATGAAAATATTAAAGTAATTTCAACGTGATAGAGACCGCTTA
TTTTTAGTTCAGGTAGAGTTCCAACCTAATGGTAATTAAGATTCCAGATCCGAAAGATGT
CATGTGAATATTGCTCTGAAAAACCAAAATTAAAGCTTTCTTAAAG
Sequence 1280
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTNGAAGGCA

Table 1

ATTTAATAAGATTTGAGCATAGATATTAAACTTAGCATGGACAGAGAAACTTATTTNTTG
GGGGACTGGCATAAGTGAAAGAACAGAATCAGTNTGACCAGAGAGAGCATAAAAACTTT
Sequence 1281
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GGCTAATAGAAAAAAAAGAGCAGTTTTAAAATATGTTTTATGTAACCTATTTTCATTGTT
TTTCATTTTGTTGTTGCCGAATAGTAGTTGTTCTAAGTAAATACAGGTCTCAATTTCACT
ATGAATAAAAAAAAAAAAAANGAAAAAAAAAAAAAGTACCTTGGCCGCCGACCACGCTAA
GGG
Sequence 1282
CCCTTAGCGTGGTCGCGGCCGAGGTACTCTTTCTTATTTTCTTAATCAATACAGCTAAAG
GTTTGTCAATATTGTTGATCTTTTTAAAGAACTAAAATTTTGTTTTGTTGATTTCCTTTA
TTTTTTTTTTCTGTTTTATTTATCACCACTCTTATTTTTAGTATTTCCTTCCTTCTGGTA
GCTTTGGGTTTAGTTTGTTCTTAAGTTCCTTAGGTGTAAAGTTACGCTGTTGAAATGAGA
TCTTCTTATTTAATGTATGCATTTATAGCTCTAAATTTTCTCTTAGCACTGGTTTCACTG
CATGCTCTAAGTTTTGATA
Sequence 1283
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NNANNCTNGTTTGGCCNNCCAAANNNCTNGGATTANNNGNNTGAACCANCNNACCCANNT
TTTAAAANCNNAATNTTTTTNNGGNAANNTNANANANCNNNCCCAAGGANTTAAANGGGN
GGGAAAAACNTGGANNTTTGGNTTTTTTTTT
Sequence 1284
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GTACTTGGTCTCTACCTCAGATAATTCTTCTTTGAGCTTTTGAGTAGCTTCTCCTTTTTC
ACTTAGTTCTACATGTATTCTATGCAGTGAGGTTTCAGATGCAGACAATCTTGACTGAAG
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TTCTTCATTATGTTTCTCCT
Sequence 1285
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AAATTGTGTAGTATAAAAAGAATGCTGTCCTGGTTGTTTTTTGTAGAATATGGAAGTCCC
TGCAGTAAGTAGGCAACATGCTACCCTTCTATTCAACACAGCACTAGAACAAGGCAAGTG
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ACCTNCATCCACACCCACAGCTCANGTTAAGCTGCAAAAGTTACACATCTTCTCTAGGCC
ATACACCCACGTAGCATCTTTCTCTAATGGTACCTGCCCGGGCGGCCCGCTCGAAAGG
Sequence 1286
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GCCTGGTGCCTCATCAGGTGTAAGTTCTTATAACCACTCTTGGCAAATTTATTAAAGACA
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GGATGAAAGCCAGGATTCCTGGGATGAACAGACAGTGGCAATTAGGATGTGAAGACAGGT
CACAACCTATTACTATGTCTAAAAACGACCAGAGCAGAGAGCCAGAAGAGAATAAGCCTG
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GATCTAACCTGGAANGGGCTAAAAANTGGCTTGGTTCTGAGTTTTTTTT
Sequence 1287
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CTTTTATTTCCAGTTTCTTGGACCAGAACAATAAAATACATAAGACATCGTTTCTATATG
GTCATATACTATATAGAATAAAGAATTGTTATGTAAATTATTAAATGAGTATACAGACCT
TTACATAAAAACTAAGGTACTTTTTTTTTTTTTTTTTTGTTTTTTTTTTTTTT
Sequence 1288
CCCTTAGCGTGGTCGCGGCCGAGGTACCTTGTGCAGACCGCCTACCTCATCCTGTGACTT
AGAATGCCTAACCTCCTGGGAATACAGACCAGTAGGTCTCAGCCTTATTTTACCCAGCCC

Table 1

TTGCTACATTCAAGAAGGAATCACTCTGGTTCTAATGCCTCCGACAGAATGGTCAGATTC
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GTGTTACAATGAAGTATATCATCACTGC
Sequence 1289
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AGAGGTTTAATGGACTCATAGTTCCATGTGGCTGGGGAGGCCTCACAATCATGGTGGAAG
GTGAAAGGCACATCTTACATGTTGGCAGGCAAGAGAGAAATGAGAGCCAAGCAAAAGGGG
AAACCCCTTATGAAATCATCAGATCTCGTTAGACTTATCCACTACCACAAGAACAGTGTG
GGGGAAAGCACCTCCATGATTCA
Sequence 1290
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TACATCCACAACTACACATTATTTATTTATTTATTTTTTGCAAATCCCAATTCCCCAGAA
ATGGTCCTCACCTCATTGACATATGCAGGAAGAGCCAAGGGGGAAACAGCAACTTGGAAA
TGACTATGACAGACTAACACAAAGGACAAGAAATGGCTCTCATGGGATGTAGGTGGAAGG
AGAGGCCTCTGGCATTGGCAGCTCCCTACCAGAGGTGTCCTGCCCTCTGTTCTCTTGGGG
TAAGGGAGCCACTGGGCAGGAGTAGGCA
Sequence 1291
CCCTTTGAGCGGCCGCCCGGGCAGGTACATAAGCTCTGCCTATCTNTGNGGNATGGATCC
TACATCCACAACTACACATTNTTTATTTATTTATTTTNTGCAAATCCCAATTCCCCAAAN
ATGGGCCTCACCTCATTGACATATNC
Sequence 1292
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTTTTTTCCTCTTTTTTTTTTTTTTTTTTTA
ATTCTGAGATTTCCCCAAGCTGTGGATTCTTCCTACTCCTTAANAAAAAAACTTTGGTTT
TATTTAACATCTACACCTTTTNGTCAGTTGTGTTAGCGTGTTTTCCACCCCATTTTATTA
TACTCTTAAAAGATGTAATTGTTGTCATTTTTGAACAGTTAAACATNTTTGNGTATAAAA
AGAACCCCAATGGTTTTAGTTATNGCTTTGTAAATTTTTATTTTTTANTTTTACCTAAAN
AAACTTTCAACTAATCAAATAAGGGAAAGAAACTGTCTTTT
Sequence 1293
CCCTTAGCGTGGTCGCGGCCGAGGTACTACCTGTTTAAGGACATACCAGAAAAAAAGTAT
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CTGAAATTATGCAACACTACTAGATAACCCCTGGATCAAAGAGGAAATCAAAAGGGAAAT
TTCACACTGTATTGTAAAGAGAGGAGACTTTTATGCCAAAATACAGTAAGTCTTTTAGTC
AGATAAAATTAATAATCTTAAATTCCATTCATGTTAAAGAAGAAAGACAATTAAGAAATC
TGACACTAATCAGAAGAAATTAGGAAAACGAATAAGTAAAAGAATCTGAAAAGGAGAAAT
AAAA
Sequence 1294
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CNCTCAGAGCCNTCCTACAAAGGCAGTGGCAAAGCTTCNTTACCGTGACATTTGTTNAGT
ANTAAACTTTGCCTNGGCACGCGNCNTCCTGNAAANTGTNTTTGTTTTGGGCCTATTTCT
TGCTGAGNTNCCCTTTANNGGNTTGTNCCTTCGNNTTTTTCATTTCNANCTAATTTNGCC
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Sequence 1296
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Table 1

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Sequence 1297
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Sequence 1298
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CT
Sequence 1299
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Sequence 1300
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ATTGGACAGGACATAA
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Sequence 1303
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Table 1

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Sequence 1310
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ANNGGGGAGCNNACCTTCTGCTTCCTTTTAATCCCAGATCNGAGGCCAAGGG
Sequence 1311
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Sequence 1312
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Table 1

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TGAGGAGTGAAATCTAAATGAAGATTTAGCTTAGAAAGCATGAAGATAGTATGTTCCAAT
TTTAAATAAAAATTATATTGTCTGAAAGACAATACAATTTTAGTACCTCGGCCGCGACCA
CGCTAAGGG
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CTAAGGG
Sequence 1316
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Sequence 1317
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Sequence 1318
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CGTTT
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Table 1

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GGTGGCCTATAATGGGCCTTCACCTTGTGAACATGTGANCCAATTCTNCTTAACAAACGC
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Sequence 1320
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Sequence 1321
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AAA
Sequence 1322
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TACAATTAGCACCTCTAGCCATGGGGCAGGAAAAGGGGGAGGAAGGGACAGGAATGCTTT
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CGA
Sequence 1323
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Sequence 1324
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Sequence 1325
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Sequence 1326
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Table 1

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Sequence 1327
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Sequence 1328
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Sequence 1329
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Sequence 1330
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Sequence 1331
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Sequence 1332
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Table 1

CA
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Sequence 1334
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Sequence 1335
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Sequence 1336
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Sequence 1337
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Sequence 1338
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ATAAAAGGNTTATAANAATCTTACC
Sequence 1339
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTAAAAATTTCCACTATCAGAAGATCCTGATT
AAAATAAAGAAATACATAAAACTCAAACAGTAAGTCAATGTGATTATTTGTTTCATTTCA
GAAGATCTATGGGTCCCACTGCCCGCCACACGTAGTCTCCTGGGTTCTCAACGAAGTGTG
ACCAGCTCTTCTGAAGAGGTAGGGTGAATGGCGACTGTGTTGTCA
Sequence 1340
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTAACTATTTGTTTCTTCTACGATAATTGGT
TTGTTGTGACTTTATCTACCTAGAGTAAATTTTGGCAATTTGCATTTTTCTCAAAATAGT
TTTTGAATTTATTGTGTAAAATTGCTCAAAATAGTCAATTTAAACAAATTTCCTGTTTTA
CTATTTCCCCCTTGTCATTTAAATTTTTGTATTTGTGCTTCCTCCCGCGTACCTGCCCGG
GCGGCCGCTCGAAAGGG
Sequence 1341

Table 1

CCCTTTCGAGCGGCCGCCCGGGCAGGTACTTTGACTATTTTTTAGCAACAAATTACTTTT
GACACACAGCACAATTGATTTAACACTTCCAATTTTGGAACTATTGGATAAATAATGATG
GGATTTAAATAAAGCAATCCGATTCTACTATTACAGCATAGGGTCTCTTGTAGTCCTCTT
AGTAAAAACTATTGTGACACTTCCTTCTTTCTCCAAATATTCGGCCTGGAAAGACCTAAA
TACAATGCAGGGATTGAATCAAATTCACACATTTTTTTCCTACGGAAACAACAACCTTT
CTTGCTTATATTTAACAAAAACTAGTATAGATT
Sequence 1342
GGTCCGTGGTGCGGGATCGAGATTGCGGGCTATGGCCGCCGAAGGTTTTTCGTCAGTACT
GGGATATCCCCGATGGCACCGATTGCCACCGCAAAGCCTACAGCACCACCAGTATTGCCA
GCGTCGCTGGCCTGACCGNCGCTGCCTACAGAGTCACACTCAATCCTCCGGGCACCTTCC
TTGAAGGAGTGGCTAAGGTTGGACAATACACGTTCACTGCAGCTGCTGTCNGNGCCCGTG
TTTGGCCTCACCACCTGCATCAGCGCCCATGTCCCGCGAGAAGGCCGACGCCCCCTGAAC
TACTTCCTNGGTGGCTGCTCCNGANGCCTGACTCTTGGAACACGCACGCACAAACTACCN
GGATTGGCGCCCGACGNCTGCGTTGTACTTTGGCATATCGGGNCTTCCTGGTCAAGAATG
GNCNCGGNTTGGAGGGGCTGGNNAGGGTGTTTGNAAAAACCCAATGTTTNAGCCCTTGTG
CCTTGCCGGGGACCTTTCAGCCCTGCAATAATGCGTCCCAGAAATAAAATNNTGTGGTCT
TGGTGTNNGAAAAAAAAAAAAAAAAA
Sequence 1343
CGCCCCGCGTCCGAATGCAGTGAAAGTGACACTGCCTGACCTTCAAGACTAGATCATCAA
AGGTGCTACAGCTTCTGCTTTGGCTTACCCTCTCTGTCGTGGGACACTCACCCTTGGACC
CAATCTCCACACTGTGAGAACTTCTATGCTACCTGGAGAGGCCTTCTATAGATATTTCAG
TCAACAGGCCTAGTTAAAGTTTCAGCCAGCGTCAACCACCCAACATGTGGGTGAGTGAAC
CCTCAAATGATTGCAGCTCCCAGCCTTTGAGTCTTCAGTTGCGGTCCCAGTCATTGAAAC
AGAGTCAAGCTGCCCCCGCTGTGATTTATCTGAATTTCTGACCCACTGGGAGCATAATAA
ATGATTGTTTTATGTTNAA
Sequence 1344
GGGAGTCGACCCACGCGTCCGTCCAGAATTTCTAGAGTGGGTGGGCATGATTCCAGTCAA
TGGGGGACCGCCCGTGTCTAAGCATGTGCAAAGGAGAGGAGGGAGATGAGGTCATTGTTT
GTCATTGAGTCTTCTCTCANAATCAGCGAGCCCAGCTGTAGGGTGGGGGGCAGGCTCCCC
CATGGCAGGGTCCTTGGGGTACCCCTTTTCCTCTCAGCCCCTCCCTGTGTGCGGCCTCTC
CACCTCTNACCCACTCTCTCCTAATCCCCTACTTAAGTAGGGCTTGCCCCACTTCAGAGG
TTTTGGGGTTCAGGGTGCCTGNTGTTTCCCTTTNCTGTNCCCAGGTCATTCCAAACCCTT
CTGTTATTTATTANGGCTGGNGGGAAGGGTTTTTTCTTCTTTTTTCTTTGGAACCCTGCC
CCTGTTCTTTACACTTGCCCCCATTCCTTAAANCTCATACAAGAATTTNCATCNATNGGG
GGGCAATGGGNTTGGAAGCAAAAAGGGGCTTCCNTTAACCCCGGGCAAGGCAAAANGCAA
TTNGGTAAAANGGANGCACCTNCCCCCCTTTTCTTNGNCCCCTTNCTTAANTTTTNAATA
AAANAACCNGGGTTTTNTANTTTTTTAAAAAAAAACCTGTTTTNTTANCANAAAAAAAAA
AAAA
Sequence 1345
TAGCANTTCAGCCCTGACCTGGGTCCGCAGCCTCCAGGGCAGGGGCTGGAGTGGGTNTCT
CAAATTAGTGCTAATGGTGGTCANAACTGACTACNCAGACTCCGGCCCATC
Sequence 1346
CCCTTAGCGTGGTCGCGGCCGAGGTACTAGATTGGGTGTGTGTATTAAGAGAAAGACAGG
AGTCAAAGATAGTTCCAAAACTTTTGAACAGAACACTGGATGAATACTGTTTACTGAGAT
GGGGAACACTTAGAGAAAAATGCATTTGGAAAGCAGAAATACGATCAAGACTTCCATTTT
TGATACATTAAGCTTGGTATGTTTAATTCATAGCTATATAGAGGTATTAAATTGGCAGGA
CAAAATCATAGCTAGAGATAAAAATTTAGAGTTCACCAGTGTAAAGATGATATTTGATGG
CACAGGATGGACTTTCTTCTGGGATTTGAGTATACATAGAGGAAAGATGTGAGGATTGAG
CACCAGGGGACTTCAACATTGACAGGCTCAACAGAGGAGAATTCCCAAGAGGATGAGGTT
CCACCTTTAGGACCCGCCAAAGAAGACTTCCCAGACAAAGTACCTGCCCGGGCGGCCGCT
AAAGGGCG
Sequence 1347
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTAACTATTTGTTTCTTCTACGATAATTGGT
TTGTTGTGACTTTATCTACCTAGAGTAAATTTTGGCAATTTGCATTTTTCTCAAAATAGT
TTTTGAATTTATTGTGTAAAATTGCTCAAAATAGTCAATTTAAACAAATTTCCTGTTTTA
CTATTTCCCCCTTGTCATTTAAATTTTTGTATTTGTGCTTCCTCCCGCGTACCTGCCCGG

Table 1

GCGGCCGCTCGAAAGGG
Sequenc 1348
CCCTTAGCGTGGTCGCGGCCGAGGTACAAATTACTCTGTAATATTGCTTTCTATTAAAAG
GGTGTGGTTTTTTTTTTTGTTGTTTTTTTTTTTTTTAGCTAGTCCAGTGGTCTTTTTGAT
GTTGGTTCAGCTTAGTGGTTCTCAACCCTGGAACAACCCGTANACCCACCTGGGGAGCTC
TTAAAATTATCAAGTGCCTACCCCACCTTCCAAGATTCTGATTTAAATCCTGTAGTGTTT
TTAAGGCACCCCAGGTGATTGTAATGTACCTGCCCGGGCGGCCGCTAAAGGG
Sequence 1349
CCCTTAGCGGCCGCCCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
NAAAAAAANGGNTAAAANNAANTTTTTNTTTNCCCCCNAANGGGAANGGGGNTNAANTNN
NAAANNTTTANNTTTTGGNAAAAAAAAAAAAATNNNANTTTNAAAAANCCCNGGGGGNGN
TTTTTTTTTAAAAAAAANNNNTAAANANNTTTTTTTNGGGGGGGTTAAAANTTTTTTTTT
NNGGGNCAAAAAAAANNNNCCCCNTTTTNNCCNTTTTNAAAAAANGGAAGGGGGGNNNNN
NTTTTANNTNNCNNTTTNAAAAAAAAANTNNTNANGGNNTNNNNATTTTTTTAAANNNAAN
NNNNNNNGGAAANNTTTTAAAAAAGGGAAAAAAAAAAANGGTTTTTTTTTTTNNNGNGGC
CAACCCNNGGTGGNGGAAAAGNNACNCCNCCNAGTTTTNCCCCTGGGNGGAAAAAGNTTT
TTTAAAAAAA
Sequence 1350
CCCTTAGCGTGGTCGCGGCCGAGGTACTTCGTCTTCTAATTTCAAAAATATAACTTAAAA
ATGTAAATATTCTATATGAATTTAAATATAATTCTGTAAATGTGTGTAGGTCTCACTGTA
ACAACTATTTGTTACTATAATAAAACTATAATATTGATGTCAGGAATCAGGAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAANGTACCTGCCCGGGCGGCCAAGGG
Sequence 1351
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAGTATTATGTATCCATAAAAATTAAAAAAT
CTTTAAAAATGCATATGGGGGTCAGTAGGTAAAAGAAAAGAGAACCAAGAGAGCTGCAGC
GGGGAGCACAGCTTGCTTTAAACATGAGATCCAGCTCAGTGATCATGCGGGGGAAAAGGC
CCGGCATTGCTGGAACTCCTAATATTTAAAAAGATGATGGAAACTTGAAATTTTATATTT
AATCTTCTCATTTTTTAAGTGTTGGCAATGTATTGAAGACTTTGAAGCCTCTCTGCTGGTC
AAACAAGATGTATCTGTAGGCTGGATTTAGTCCACAGCTGGCCAGTTTGAAAACTGAATC
CTGCTAGCCTTAATTTAAATTTTTTTAAATTTAATTTGCTTTGATTCCTGCCTCCTGCTC
AAAAAAATCTTCAATGGCTCCCCCTGTCTGCAAGGNAAAAGTCC
Sequence 1352
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACA
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AACAGAAGATCTTCATTTATGCAACAAGTCAATCATTTGCAGTATGTATGGAAAATAAAA
ATCTAAGGTAAGTCAAACATACAAACTCTACCTNTTGCTTTCTCCATTANAATATACACA
TTGGAAATCTAAGTTCCAAACAGTTCCTNTNTACTGAANATAGTGAAATTTAGTGCAAGC
CCCCTAATTACCAATTTTTTGG
Sequence 1353
CCCTTTCGAGCGGCCGCCCGGGCAGGTACATTGGTTTGATCTGGAAAGGCAGGACAACCC
AAAGCGGGCTGGGGACAGTTCCAAGTTATAGGAGGTTTTCCAATTGGCAGTTCGTTGAAA
GAGTTTATCTTAAGACCTGGAATCAATACAAGGGAGTGTGTCTGGGTTAAAATAAAGGGG
TTGTGGAGATCAAGGTTCTTATTAGGCAGATGAAGCCTCCAGGTAGCAGGCTTCAGAGAG
AATAGATTGTAAATGTTTCTTATCAGACTTAAAAAGGTCCCAGACTCCTAGTTAATTTTC
TAGTGGATCAGGAAAAAGACCTGGACAGGGAAGAGG
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TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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NANANAAANANNNNATNAAANNANTTTTTTNANAAAAAATTCTTTANNAAAGGGGGGAAA
AAAAAAAANNTNNAAAAAAAAANTTTTTT
Sequence 1355
CCCTTAGCGTGGTCGCGGCCGAGGTACAGAACCTGCCTGAGTATGACCTCTCCACCTTAT
AGTTTATGAATGTCTTGTTTGTGAAAGTGACTATAACCCAAACTTTTTTTTTTTAAAGAG
GATTTGGAAGTTGTATGGATTTTTTGTTATCTTCACTTTACTGCATAGGAAACAATCTAC

Table 1

CTCATCATTTAAAATGACATGGGTGTCGGTTTTGTAGATCTTTGGTTTTTTTGTCAGGTT
TAATTTCAGTTAACAAAATGTAAAACATGACATTCCCTGCAGATATTGTTGTATACCAGT
ATGGTTTCTTCTCTTTCTTTAAATGTTTTTGGCCATCAAGTA
Sequence 1356
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AAAAAAAAAAAAATTTTTTNNAAAAAAAATTTTTNTTNNNTNAAANTTTAANTTTTTNAA
AAAANCCANGGGNTTTTTTTTNAAAANNTTTTTNCCNGTTANGTTNTTNAAAANNANTTG
GGGGGGGGGNCTTTTTTNTAAAAAANGGGNNNNNCCGNCCCGNAAAAAAAAAAN
Sequence 1357
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAACACTTTAAAAAGTGAATTTTAAGCTATGT
GAATATCTCAATAAAAACATTTTTTAAATAAAAACAATTCCCAAAGGCCTGGAAATTCAG
GAACATAATTCAAAATAATTTATGGATCAAAAAATAAATCATATAAAGATCTGAGAACTA
CAATGTAAAAATATAGAAAAAAGTCATAACAATATTAGAAAAAAATTTGAGCTGGATAAC
AAAAATAGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1358
CCCTTAGCGTGGTCGCGGCCGAGGTACTTACATGGAAATAAGTGTTAAGAAAAGGATTGC
TTATTGGTAGCATATAGATTTAGAGTCAGGAATGATGGTGATTTCAAACAACCACAGAAC
GTCCACATGGGTGGCTGGCCAGGATAGTGACACCTTTGCTTTCTAATGGCTTAGTGTACC
TGCCCGGGCGGCCGCTCGAAGGG
Sequence 1359
CCCTTAGCGTGGTCGCGGCCGAGGTACAAAGAAAAAGCTAAGGAACGGTATGTATATTAA
TCCCTTTATTAAAAATGTAAAAAGCCAAAAGCAAGATAGACGCAGATATGTGCCAAAATA
TGTATTTTTTTTTCCTGGAACAAATCACAAGAAATGTAATAACAGTTACAGTGAGAGGAG
CCTTTGACATCTCTTTCTAAACTATTTGATATCATTTGTATACTAACGATGTACCTGCCC
GGGCGGCCGCTCGAAGGG
Sequence 1360
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GTGCTGGCTAGAGAAAGTTAAAAATTTCTGTTAGCTTTGCATTGAGCTTTTTAATATCAT
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TAGGCCAAATGTTACAAAATAGATAAAATTACCTGACCAGTGAAGTGTGTTCCTCAGTCG
CCATGGANCCTCAGATTTGAACTCCCAAAAAAAAAAAAAAAAAAAAAGNN
Sequence 1361
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AGGAGGCCAAGATGTCTCCCTAAAACTTAGTCTCTGTCCTATTTACTTTGTTTATAAGAC
TGTGACCTAACTTCCCATGGCCAATTCAATCGACTAGGTTATCTTTACTCCAATGGACCC
AGGCCTTTTCCCAGTCAATCCATGTCCAACCCTTCATCTCCAGCGTGATCACTCAACTCT
TCAACATGCCTGCTTGCTGCAGGNTTAAAACCACACCCACCATCCTGTGCTTNCCCCTTA
ATCGCCCATTGATGCCCCGCANGGTAAAATAAAAACTA
Sequence 1362
CGANGTACATGAAAATGGCTGTTTTTCCCCACATTANTCAGCTCTGGATTTTGCATGTGT
GGGGCTTTTTTTTTTTTTTTGATAGTTATTTGTTTTTTATTTTAAAAATTTATTTNGCCAA
CCCAGTANAGAACAGCTGAGCATNTTCTCATGTATTTATTGGCCATTTGCATTTCTGCTG
CTTATTGGCCATGTATTTATNGGCCATTTGCCGTCTGCTGTGAAATGTCTTAAATTNTTT
GCCCATTTTTCTAGTGATAAAACACTGAAGCACATTTTTAAAAGA
Sequence 1363
CCCTTAGCGTGGTCGCGGCCGAGGTACATTTAAAAGGTGATGCTAATACTTTAAAATGTC
ATAAGATATAGATTNAAAAAGCATTGTAAATTGTATACTAGCAAAAGTCGTCTANATGGC
ATTGNACAGGACATAATGTAAAACAT
Sequence 1364
CCCTTAGCGTGGTCNCGGCCGANGTACTTAAACTTTTTCAGCCTACTACTGCACACCTAG
GCTATGTGGTATAGCTACCTTGTATATGTGGNCTGTCACTGACTAAAACTTNGTTACACA
GNGTATGACCCTACTATTCANCCTTGAGAAGATGGAAATGCTGNCATTTGCAACAATATG
GATGAACCTGGAGGACATTAAATTAANTGAAATANGCCAGGCACAGAACGACAAGTAACA
CATAATC

Table 1

Sequence 1365
CCCTTAGCGTGGTCGCGGCCGAGGNACTTTTTTTTTTTTTTTTTTTTNTTTNACTTNATTN
TACTTTAAGTTCCAGGATACATGTGCAGAGTATGCAGGTTTGTTACAGGTATACATGTGC
CATGGTGGTTTGCTGCACCCATCAACCCATCACCTAGGTTTTAAGCCCCACATGCATTAG
GTATTTGTTCTAATGCTCTCCCTCCCCTTAACAGCAGTTTTTCTATAGGNCAAAACAAAT
TTGGGAACCAGAATNGNCTACTGTCTTTATATAAATGATCATTACGATTTGGGANGAGGG
TTTTTTT
Sequence 1366
CCCTTTCGAGCGGCCGCCCGGGCAGGTACCACAACGTTTCTACTCTATTGTGTAAGCTTT
AAATACAAAAATACCACAACCACTCCCGGACTCCTCCATTATTTCAGTAATACTGGCTGC
CCTAGTTTTTCAGGATACATCATGCAAATAAGTTCTTTTATTTTTCAAATTATTTTATTC
CTAAAGTATCTTTAATTTTTCTTTTTGGTTATACAGCTTATAGAATAAACAAGTCACAAG
AATCTTCATTTGTTTCTAAAGTATATAATTTTACAAAAGTTGTTTTACTCAATGTGAATT
AAAATTTGCAAGGTCTAAAAAAATAAAAAAATTTTAAAAAGTAAAAAAAA
Sequence 1367
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAATATATTATGAAGCATGACCACTTTATTTT
GAAACTTAGCAATTGTATTGCTGGGGTTTATTGTATCTGTAGCATGTCACTGATTATTTC
AGTTAGTTTTATAATGATTTTTAAAAAACATATCTATTTGGAATAAGATACAGCAACAAT
CATTGCTATTGACTTGTTCAACCCCTTAGTTACACTGTATGATCAACATATAACAAGATA
CAGTGGGAATGGCCCATACAGTATATTACTGTTGTGTGATGATTGGCTTTGGAAGCAGTT
TGATTTTGAAATGCTTTGATATTCTAATTGACATGGAACAA
Sequence 1368
CCCTTAGCGGCCGCCCGGGCAGGTACATATGATGGGGCCAATGCACAATACTTTTATCAC
AATCAACTTTTTCTTTGTATCCCTATTTCAATGAGCAGTCAGTCTCAAGAGGTTACTGCA
TTTCAGTTCTAACTAGACATTTGTACTTGTGATCACACTACGGGAATCTCTGTGGTATAT
ACCTGGGGCCATTCTAGGCTCTTTCAAGTGACTTTTGGAAATCAACCTTTTTTATTTGGG
GGGGAGGATGGGAAAAAGAGCTGAGAGTTTATGCTGAAATGGATTTATAGAATATTTGGA
AATCTATTTTAGNGTTNGTTCGNNTTTTAACGGTCATTCCT
Sequence 1369
CCCTTAGCGTGGTCGCGGCCGAGGTACAGCTTTCTCTGCCTCACGTTTCAAGCTTAATGC
ATCATCTTAATTCATCTTTCGACATCTATTTCTACTACATGCTGCTCTCTTTCTCTATCT
TACATCTCCCAGAATGTTTTATTTCAACAAATTGCTAATCTGTGCCAGGCATTGTTATTA
GCAAAATGATAAGCCCTGCATGTAGCAAAGTTCCTGCCTTCACTTGCATATGCATTAACA
AGCTCTGATTAGTCCCACTTAAAAACCATTTGTTCCCCCGTCATGCAGAACTCCATTGCC
AAGCCACACAACACCCCAGCCAGTAGGGTAGCAGCTNCCTGGAGCAAGGGA
Sequence 1370
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TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTTTTTTTTTTTTTTTTTTTTT
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AANNNAAAAGGGGNTTTNAANGGANTTGGNNTTTTTTTTTTTTNGNCCNNGGNAACTTTNA
AATTTTTTTAAAANCCNGNAAAAAAANTTT
Sequence 1371
CCCTTTCGAGCGGCCGCCCGGGCAGGTACTGTCGTTTCCTTCCTACCTCGTCCTCACCCC
ACCCCGAGTGAAACTTTTCGAGTGTGAACCTTACTTTTTTCCCGTTCTCCTCAAGGCAGT
TTGAACGACACAGGTTTGGAAGGAATAGTTAACTCTCCAGTATTATTGGAACATCTGGAC
ACCACCAACAAAAAAATCTTAGAAAAGGGTCATTTAAGGCCTATAAAAAGTGCCACCTTTC
CCAGAATTAATTCAGAGAGAAAAATCTTATCTGCCTCCTGGCAGCTACAGCGCANAAAGT
ACCTCGGCCGCGACCACGCTAANGGGCGAATTNCCAGCACACTGGCGGCC
Sequence 1372
CCCTTAGCGTGGTCGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTT
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GCGGGNANANAAGGTNCANNATTNTTTNAAANNTNANTTTTTANCAAAAAAAACAAAANT
TTANCCCAACANNTTATTTTTAACAGCAANANGTAAAAAANCCCAANCNACNTTCCANNT
AANAAAATTTTTTT
Sequence 1373
CCCTTAGCGTGGTCGCGGCCGAGGTACAGCTATTCTCAATGGATAATTCTATAAAATATT

Table 1

TAAAGAAGAATCAACACCAGTTCTCCACACTCTCCTCTAGAAGAAGAGGAGGATGGAATA
CCTTCCCCCTTAATTTATGAGGCCAATATTACCCTGATGCCAAATCCAGACAAAGATATT
GTCCCCCAAAATAAAACTAACGATCATAGATAAATACCCTCTTATAAATTTAGATGCAAA
ATCTTAAGCAAAATATATTAGCAAAATGGAATTCAACAATGGAATAAACCTATTATACCA
CCAAGTGGGAATTTATTTCTAGCTATTGCAAGACTAGCTTGGACCTTTTGAAAATTGATT

Sequence 1374
ATATCTGCAGAATTCGCCCTTTGCGGCCCGCCCGGGCAGGTACTGGGAATACAGGCATGA
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AATATCATTTCTCTCTTATAGGTTTTTGGTTTTAACCAATCTATTTTAAAAGGGGCAATT
CAAGGATTATGGTTTATATGGNGGGATTTCTGTTTGAATATGATCAAATGTTCACTGGAG
AACAAGCAATAATTTGCAAAAGGCATATNTATGCCTTACATTAAATGTGGATCCTCTTCT
AAAACTAGAATAAGCATCAGTTCAGTCACCCAACGGTGGGAAG
Sequence 1375
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGGATATGATTGGCCGGCGAATCGTGG
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TCCGCACTAGAAAGTTCATGACCAACCGACTACTTTCA
Sequence 1376
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CAATTAAAACAACAAATAAATAAACAAAAATGCCCAACAAGGAAGAGAACGGGAAGTCAT
AGGCAATCTCATTCATGAACATAGATTAAAAACACCTGAAGTATATACATACCCACACCC
CCGACATGAATACATATGAGATGTGTAAATGTGAATACTTACATGTATGTATATGAAAGC
AAACCAAATCAAACAATGTAAAATAAAAATAACACATNATGACTGACTGGCATTTGTCCC
AAGAATGCAAAGCTACTTGAGAAAATCTATTAATTCATCAATTTAATACTTTAAAAGAG
Sequence 1377
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AAATTTTCACAGTAATATATGAAAGAACAGACTTTACACTTCTTTTGCACAGAATTATCT
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AATTTATTACATAAGCTATACACACAAAATGAAATCCTAGTTATAAAAGATGCATCTAGA
AGAATAATTTATAATAAACCAACAAAAATGAGAATGTGTATCTCCAGGAATATAAATATA
TTTAAATGTTCTCAGTGACTGGCATTGCTTTATGCATTACATAAGATAGTATGTACCTGC
CCGGGCGGCCGCTCGAAAGGG
Sequence 1378
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AGGTCAGCCACTGTTTGTTTACAAAATCAGGTAACTAACTGCATACACTTTTTCTCTTTC
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CCCGGGAGTTAGCCCCCTGGTAATAGCTGTAAACTTCCAATTTCTAGCCATACGCTCAGC
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AGCAGTTGGACTTTTTAAAAATTCAGCAAAGTGGTTCCCTCTCTTAGGGACAGTCAAAAC
CAAGTCACTTAGGTAGTACCTGCCCGGGCGGCCGCTAAGGGCGAAT
Sequence 1379
CCCTTTCGAGCGGCCGCCCGGGCAGGTACGCGGGGTGAATGGAATGCCTTGCAATATGAA
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AAAAAAAAAANGTACCTCGGCCGCGACCACGCTAAGGG
Sequence 1380
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CTTATAGAAGACACCTGGGTTCTTATATCTGCTTCTGAATCGATCTATTGTAATGNNGTT
ATTTTGGCTGAAGTATGTTGAAGAAAATACTACCTTACAAAGATATGTATTTTCA
Sequence 1381
CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAGCCATTGAATAAGCCTCTTCCTTTTTTTT
GCTCAAACATTCCACATCCTTGTGGATTCCCCTGCATTGTTTGTTTTATATAACATTTGA
TATTTGTTGTANCTTGTATATGAACATAATTTTCTTTAGAGGTAGTCACTGTTCTCTCCA
GTATGACCCAGGTTTCTTGACTCTGAGTAATGCACCTTCTATAACTATCTAAATTTCTAT
TGAAGCTTTTTGGATTATGAGTATGCTGACTTTTCACGATTGGCTGGTGCATGTTTAGAC

Table 1

TTAAATGTCATATCCTTCATGTCTCAAAGCCAAAATAGTAACATCTCATCTCAGAACANG
AGCTGTGACCACATGCCAATATATGTGTCACAAAGTCTACATATGTTACATTCCTTGGAA
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GATTGGGCACATTTAAGACAGTAAACGGGGAAAGGTGGNGAAAATCTATAAGAAAGATGC
TGTATCTTGAGAATTGGAAAAATGANGAATCNTGACATGGTTTGAAAAATCAT
Sequence 1382
CCCTTTCGAGCGGCCCGNCCGGGCAGGTACCAAAATTCATTCAAGAAGAAATAGATACCA
GCCTGAGCAACATGGCAAAATCCCATCTCTACAAAACATCAAAAAAAAAAAAATTAGTCC
GGGCATGGTGGTGCACACCTGTAATCCCAGCTTGTCAGGAGGCTGAAGTGGGAGGATCAC
CTTGAGCCCAGGGANGGTCANGGATGCAGTGAGCCATGGGTCTCACCACTGCACTCTAGC
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AGCCCTATATCTATAGAAACTTAANAGTGCTGGGGAGATATAGGTATTATTATCCCTCAA
TTTTACNAGATGGTGAAAATTGAGGGTTCANAAGAAGTAAAAGTCTATTGCTCAAGGTCA
TGGTGGCTAAGAATATTGGCANANNCATGAATTCAAAATCCAGGGTTTTTTTGATTCTTT
ATTCCAAGGGGTCCTTTNNTAGCAATACCCTTGGTTGNCCTNTTAAAGAATTGCANTTCC
NTTTTTTACTAANAAAATTGGTTCCCTTGGCCCAAATCNTAAATGTTCNAACNTTCAACC
CCANTTTTTTTTTTAAAGCACCTATGNNTTGGGNGTTTTATCANGCATTAATNTTGNATT
GGCTTTTGGAAAANACCGNGTNTCNTNTNGGGGAAAGGGAAAAAAAAANTTTTTTTTCCA
ACTTGGCCCTTCGGNCCAANTTGGGAAAAA
Sequence 1383
CCCTTAGCGTGGTCGCGGCCCGAGGTACTTTGTGTTGTTGGTATCCAAAATTAGGACTCT
GAGATTCTTGTGTATTCAGAGAATTTTTAGTAGGAAACAAGGACAAATTTGCATATGAAA
TGAAAATAGTTATTACATGACAAAATATGTAGATCTGATTTCTAGAAACTGAATTAGTCC
AAAACAAGTAAGAGTGGGAAAAGCAGTAAAAAGTTCTTCTTGAATATTGCTGTTGTCATC
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AAGAAAGTTTAGGATTTTACAGGNGTTCTGAAATACTGAATCTTAATTCANGTATTTCAA
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TAAAAGATCTCTTTTTTGGGAGCCTGCTNTNTTTAACAGTTTTTCCCAANNTTGGGTTTT
GTTTTTGGAAAACANGAAAATATNTGGTNCNTAAAAGCCAANCTTTTANTTCTATTANNA
GGGTTTTCTCGCCTCANAANAAACCNNTNAAAAATTTANGTTTAAATTGGGNANGGGAAC
CCCGNGNAAAAAAAAAAAAAAAAAA
Sequence 1384
CCCTTGAGCGGCCGCCCGGGCAGGTACCTCACTCATCTCATCCTTGGCTCAGCCCTGCTG
GTTAGTATTTAGTATTTATTTTAGTAAGATATTTGTGTCTGTATGATGGTCAGAGTTGAA
CTGATCTGGCTTGTCATTTTTCAGTAATAAAAAAAGTTACTGAATTTAATTGTTGAATAT
GATGCATATCTCATTCATTACGATTTATCAGAAACCAAAGATTTAAATTGCCTAGATTTG
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Sequence 1385
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NCAGTTTTTATTTAAAAAAAAAAA
Sequence 1386
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Table 1

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Sequence 1388
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Sequence 1389
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Sequence 1390
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Sequence 1391
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Sequence 1392
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GACCACGCTAAGGG
Sequence 1393
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Table 1

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Sequence 1394
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Sequence 1395
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CATTCTTTTATAAAAATGACCCATAGGCTAAAAAT
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GAGTGNTTAACCTACAA
Sequence 1399
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ATGGCTATTTCCTAAGTTGTAAAGTNCTGCATTTATAANTGCCANTGTTGNAAGGTGGTG
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Sequence 1400
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Table 1

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Sequence 1402
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Sequence 1404
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Table 1

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CTGTG
Sequence 1410
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Table 1

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Sequence 1418
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Sequence 1419
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Table 1

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Sequence 1421
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Sequence 1422
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Table 1

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Tabl 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

>Sequence 815
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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 2

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Table 3

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Table 3

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Table 3

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Table 3

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CA
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Table 3

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TGGAACTCTCTGTAAGTCCAACTTGGTTTCGCGGACATAATTGTCCGGAT
TCCGGCTCAGCATCTTCACCTTCATCTCGGTTGCTCTTC
>36.1
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Table 3

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>37.1
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GACT
>38.1
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TGTCCAGGTGAGTTGA
>39.1
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CTTAATTATTTAATATTTTGATAGTCAATTACCTAAGACACGGCATCGTC
ACTGACCAATCAGAAGAGATGCCAGTAGTTGGGC
>40.1
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>41.1
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>42.1
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>43.1
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Table 3

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>46.1
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>47.1
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GGGGAAACCTTGTTCGTGCCAGC
>47.2
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>48.1
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>51.1
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TGCTTGTTGTGATGATCTCATACTTTGTAGTTGTTCTATCTGCAGCACTG
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>52.1
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Table 3

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>53.1
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>54.1
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>56.1
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CTTTAAATGCTACCAAACTGGAACGAGTATTTGCAAAACCATTCCTTGCT
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>58.1
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>59.1
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>59.2
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>59.3
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Table 3

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>61.1
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>62.1
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>63.1
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>63.2
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GGCCTTCAACTTGACTTCGGCTTGC
>65.1
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>67.1
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>68.1
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Table 3

>69.1
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>70.1
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>72.1
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>73.1
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>74.1
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Table 3

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>79.1
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>79.2
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>82.1
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>83.1
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CA
>85.1
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Table 3

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>86.1
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>87.1
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>88.1
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>91.1
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>94.1
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GAGCACTGTGCAATTGAGTCAACAAGGTCTCAACTACTGACTGGCTAAGA

Table 3

TGGGGCCTGCCCTTGGCCAACTTCACCATACAGTTTAGAGCAATCTTTAA
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>95.1
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CTGTGTGAGCTGTGCGCTCCCGACTGGGAAATGTCTAACTCCATCGAAAA
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>99.1
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GGT
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Table 3

GCTGAAGATTTTAGATTTCTACCTATTAGAAATGAATATTCACTGAGGTT
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CAAAA
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Table 3

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>112.1
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>114.1
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Table 3

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>122.1
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Table 3

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>123.3
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>124.1
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>131.1
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Table 3

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>138.1

Table 3

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CAATCTCCACACCCATCTTTACTCTGAGCCAAGGAAGTGTCTGTTCTTGT
GCTGAGTTTCAGGGGCCTTCAGCTTGCGGGAAATCCCGAAGATGGCCAAA

Table 3

GACAACTGAACTGTTCGTTGCTTCCAGGGCCTGCTGATTCTTGGAAATGT
GATTATTGGTTGATGCGGCATTGCCCTGACTGCCGAGTGCA
>149.1
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TCAGAGGGGTGAAGAGCAGTATCTTCAGAGGCCATCCAAGTTTTAGCATA
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GAAAGAAATCAAGAATTGGG
>150.1
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AGCCTGGTAGCTCGGT
>151.1
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AAAAGAGGGC
>152.1
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ATTCTCCTGAGAATGATATTCCTATGGAGATCACCACGGCAGAACCACAG
GTTTCCGAGGCAGTATATGACTGTGTTATTTGTGGACAGAGTGGCCCCTC
CTCTGAAGATCGACCTACTGGATTAGTTGT
>153.1
GGTGGCGGCCGAGGTACACCTGCAACTGTGCGAATGGTCCTGTTGCCTCC
TGCATTTTGGCCTCTGTTCTATAAAGGAAGAGTAAAGATGGAGCTCCTCC
TGCCTCCATCACGAAAGCACATATCATCTGTCCCTTTGGATTTTACTTCC
AGGACGCGTGTCGTCCCCAGCGTGTGTTGCCTTATGGTGCCGGCAGAGCC
TCAGCTATCTGCCTGGGAAGTCGGATGTCCTTGGAGAGAATTTGGAATGC
AGATAATTTTTCTTATTTCTTGAGAGCTTACTTTAATCAGCATGACACTA
CCTAAACACTGAAGATGGCCTTATATTAGTAAGATTTGCACAAAATTAAG
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GAAGTAATGGGATCACATATATATGTAAG
>154.1
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CCCTGCTCGCGGTTGCCCTTGAGGTCAAAGCT
>155.1
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CTTGAAAAGACTTCAGTCTCCGCTCCCCTGTTGATCTCATGGAGTGGGGA
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CTCTTTGTTGATCTCATGGAGTGGGGAATGGGAATTGAACCAGAACTGGA
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ACC
>156.1

Table 3

ACCGGGCTGGCGGTCGCCCGCTCTGGTGCTTGCATCTTGGCTTCCTATAG
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ACAATGTTCTTGTTGTTCCTTGGGTTTCTTAATGATTTCTGAATCATCAT
TATTAATTATGGAATTCTCTGGTCGAAAAGTCACATTTGGTTTTCTCCTC
AGTTTCTCACATCTTTTTTCTTGCAGCTCTTTCTCAGCTCTTCTTCCTTG
CCTTTTTTTACTGTCCTTTCCTTGTCTTACTTCAGGT
>157.1
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CCGAGTCGCCTCTCCCCGCGT
>158.1
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AGCCCCATGGGTCCACCAGGATGAGGTGTTTAACTCTATCAGGGT
>159.1
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GTATAACATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTT
ACACCGCCGACCATGGTTACCATATTGGGCAGTTTGGACTGGTCAAGGGG
AAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGG
TCCAAGTGTAGAACCAGGATCAATAGTCCCACAGATCGTTCTCAACATTG
ACTTGGCCCCCACGATCCTGGATATTGCTGGGCTCGACACACCTCCTGAT
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>160.1
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AAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGG
TCCAAGTGTAGAACCAGGATCAATAGTCCCACAGATCGTTCTCAACATTG
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GTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAA
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>161.1
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ACAGGATATAACCCATTGGCAGTGCATTGATGTGGGGATGTGCAACTGAA
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>162.1
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ACGTAGAAATTTGCCTCTTTCCACTAGGAATGTATCACGCCAAATTTTGG
CCTTCTTGTTTGTTCGAAACCTGTTACCTGGCTTTTCTGGGTCCAGAAGT
TTGAGGACAGACTTGCCGTCCACATCAGGAGGTGTGTCGAGCCCAGCAAT
ATCCAGGATCGTGGGGGCCAAGTCAATGTTGAGAACGATCTGTGGGACTA
TTGATCCTGGTTCTACACTTGGACCACGAATAAAAAAAGGCACACGAATA
TCAAAGTCATATGGCATGGATTTCCCCTTGACCAGTCCAAACTGCCCAAT
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Table 3

>163.1
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>163.2
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>164.1
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AGTATTTAGCCCAGAGGGTTGTGGTGAAGTGT
>165.1
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AAGGGTGAGAAGAGATGTCTGAATCCAGAATCGAAGGCCGTCAAGAATTT
ACTGAAAGCAGTTAGCAAGGAAAGGTCTAAAAGATCTCCTTAAAACCAGA
GGGGAGCAAAATCGATGCAGTGCTTCCAAGGATGGACCACACAGAGGCTG
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TTAGTTTGCAGTTACCCCTAAAGGTGACCAATGAT
>166.1
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GGATCCATCCCATTGGATGGAGAAGAAAGGTGGACAGCCTGTTCGTCTCT
CATGTCAGCCTAGGGCTGGGAACAGTTTGTGAGGACTTATCTGTTGTACC
T
>167.1
AGCGCAAGTAGGTCTACAAGACGCTACTTCCCCTATCATAGAAGAGCTTA
TCACCTTTCATGATCACGCCCT
>167.2
CCCCTACCGCCAATCCCTTTTTACAATAAAACAGGACCGAAGGGTCCAAA
C
>167.3
ACCTTGAAACCCCTAACCGAAGTTACCCTTCGGGCCCGCTTCTTAAGAAA
CTAAGG
>168.1
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TCCTAGGACAGTTCGCGGAAGAAGTGGCTCACGCCTTCCAGAGCCACATC
ATCGCGGTCGAAATAGAAGCCCAGAGAGAGGTAGGTGTAGGAGGCCTGCA
GGTACCTCGGCCGCTCTAGAAC
>169.1
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GGCACATAGTAAGCAT
>169.2
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>170.1
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TCCAGGGAGAAAACAAGCCATGACCATTGTTGGTTGGGAGACTGAAGGTG
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ACCCTTTGGTGGAGCCTGAAAAAAATCTGGGCAGAATGTAGGACTTCTTT
ATTTTGTTTAAAGGGGTAACACAGAGTGCCCTTATGAAGGAGTTGGAGAT
CCTGCAAGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAAACAATG
AGGAACATTTCATTTGACCCAACATCCTTTAGGAGCATAAATGTTGACAC
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Table 3

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>171.1
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GTAGTCCAGTTGGCTTAGCAGTAGTTTCGTTGGGGGGGAGCCGAGGTTCC
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GAAA
>172.1
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CTCTGTTTTCATTGTGACACACTGAGTTAATAAAGCACTTACTGAGGGAG
CCAGAGCCCAAACTCTAAATGTGCTGTAGAAAAAGGGCCAAGTCATTGAC
TGCACCACTCCTTCAGCCAGAGGTAGAAAGGATTTACTCTTCAGCCATCT
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GAATACAGTCTGAGAAAGGCCTGGGCAAAGGGAGGCAGAGGGACTGAAGG
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>173.1
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CACCAAGATGTGGGTAAATGAAAATTATTAGTTCAC
>174.1
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CAGTAAATAAAGGCTAAGATTCAACAAGCATTTATCCAGCCTTTCCTCAA
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>175.1
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AGCGTGTGTGGGAAAGTCTTCCTCCGTCATTCATTCCTGGACAGGGACAT
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CAA
>176.1
ACGCGGGGTGCTGTGAAGAGCTTTGCATTGTGGGAAGTCTTTCCTTTCTC
GTTCCCCGGCCATCTTAGCGGCTGCTGCTGGTTGGGGGCCGTCCCGCTCC
TAAGGCAGGAAGATGGCGGCCGCACAGAAGACGAAAAAGTCGCTGGAGTC
GATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGGAAGTG
>177.1
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Table 3

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>178.1
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AACCACTTTTCCTCTTTCCTCTGAAATATCAGAAGTTAAAAATCTACTCT
GAGTTATATGTGCATCAATTTTAGACATATTGCTGATTTTATTATGAAAA
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AGACCAGCACTGCTTGACCCATGTGTATACACATGTGTGCTTTGT
>179.1
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CCTTGGGCTTCATGGGGTTGGCATTGAGGATCCCTACGACAGTCCCCTGC
TCCGTCTTCCAGAGCGCTTTGTGAACTTCTCCAAATAAGAACAAGGACAC
ACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTT
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>180.1
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TGTGAATTTGCGTGACTGTGAGT
>181.1
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GGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCACTATTC
ACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCACCCAATC
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TGATCAGTTT
>182.1
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ATGGAATTAAGATCCACCTGGTGTGATGAATAAACCCAGACTCTCAGCAA
CGCAGGAAAAAAAACAAAAACTGGCTGGCGATCTGGAGTAAAGGATCCTC
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ACTGGGAGAGCCGAACTAAAAGTCTTTTAGCACGGGT
>183.1
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GAAAATGGTAGAAACCAATGGAAAGAACAATATACTGGATATTCAGTTGG
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Table 3

TAAATGAAGAAAAGCACAAAGAACTAATAGAGAAAAAGGAGAT
>184.1
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>185.1
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>186.1
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CCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGGATCCCTACG
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TGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTTCTTCAAT
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CTCCTACTACTGGATTGGGATCCGAAAGAACAATAAGACATGGACATGGG
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>188.1
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>188.2
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>188.3
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>189.1
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CTCACACAAAGCCTGTTTGGTGGTCTCTTCACATGGACGCGCGCGACATT
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Table 3

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>190.1
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ATTGGGGAAACTTTGCAATGCCCCGAAGACTTAACTCCCGATGAGGTTGT
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TCACACATGGAAAGCGAGGAGTTGAATGGTGCATACAAGGCCATCCCCGT
TGCCCAGGACCTGAACGCGCCTTCTGATTGGGACAGCCGTGGGAAGGACA
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>191.1
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GTTACAGAGGGGTTCATTGCAGTGAAGGGCGGGTTCTGCAAAGACAAACA
GGTCTCACAGATAGTTGCCCCCGCGT
>193.1
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C
>194.1
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>195.1
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TTAAAGTTTATAAAAGTAAAATCAAATACATTTTTTTTTCAAAAAAAAAA
AAAAAAAAAAAAAGT
>196.1
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TGAAGATTTAGATTTATTTGAAAACACTTAGTCTAATTTATATTAGTGCA
GAAAAATCACATTCAATAAACCACAATTGTAGAAGAGACAGATAAGTGTG
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CCTCACTCGGATCCCCCCGCGT
>197.1
GCAGGGCGGTATGCCGCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGT
GGAGCGCCTCACTAACTCCATGATGATGCA
>198.1

Table 3

CTTGCTCAGCCTTTCCAGGCCCCTCTGATGAGCTCTCTAATCAGCAGGAC
CAAGGTGTGAATGTGGGAATGAACATGGATCCATCCCATTGGATGGAGAA
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GTTTGTGAGGACTTATCTGTTGT
>199.1
GTACTTGCTCAGCCTTTCCAGGCCCCTCTGATGAGCTCTCTAATCAGCAG
GACCAAGGTGTGAAGTGGGAATGAACATGGATCCATCCCATTGGATGGAG
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CAGTTTGTGAGGACTTATCTGTTGT
>200.1
AAGATGGCCAGAGAGAAGCTGGAAGAAATAGATTGGGTGACATTTGGGGT
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GCATATGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTG
TTCTTATTTGGAGAAGTTCACAAAGCGCTCTGGAAGACGGAGCAGGGGAC
TGTCGTAGGGATCCTCAATGCCAACCCCATGAAGCCCAAGGATGGTTCAG
AGGAGCGTGACTGTGAGT
>201.1
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CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCA
>201.2
CTGATGAGCAACTTGGACAGCAACAGGGACAACGAAGGTGGACTTTCCAA
GAAGTACCTGCCCGGGCGGCCCGCTCTAGAACTAGT
>202.1
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AGACTAGGGTTGGAGATGGGATGGGTGGGGCAAGGGATGGAAAGGAAAAG
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GAAGATCAAAGTTCCCTCCAAACCTAATTTGATGTTTTATTACTAAAAGC
AAAGACCAGTATGGT
>203.1
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TCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAGAAGACGAAAAAGTC
GCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGGAAGT
ACCT
>204.1
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TGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
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GTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGC
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>205.1
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TGGAAACTGAATGATCTTCGTGACCTGACACAATGTGTGTCCTTGTTCTT
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GTGTGTTTATCTATCGATCATCCTCAGAAGGTCTTAATTATGGGTGAAGC
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Table 3

>206.1
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GTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCA
CTATTCACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCAC
CCAATCTATTTCTTCCAGCTTCTCTCTGGCCATCTTTTCCTTGATCTGAG
ACAGTCTGATCAGTTT
>207.1
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CCAAAAACGTTTGAGTCCTAGTTTTTTTCTGTCATTCTCATCAACTACCC
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CCAATCATTATTGGGAAGAAAGTCAATTATATTAGAAATGGTTAAGAGCT
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>208.1
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GGATTAAAACAAAGGTCATCTGATCTCCAATCATTATTGGGAAGAAAGTC
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TGATTTAAAAAGAT
>209.1
CGCGGCGGCGGACGAGGTACACGACATAGGCACATGTGCAAACACAAAGA
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TCACGTAAGATGGAGACTGTCCCATTCCTCTGAAGTTGCTGGAAGGACAT
TTCCCAGGAAGAAACAATTCCTCACTGCCTATAAACTGTAGTCACATGTG
GGATAGTCAATAGAACATGAGAATCAGAACAATCTGGGCAAATGGGTATG
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>210.1
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GGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTTTTCCACTATTC
ACACTCTGTGGCGTAACCTTCTTCAATATAACCCCAAATGTCACCCAATC
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TGATCAGTTT
>211.1
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ACATTGTGTCAGGTCACGAAGATCATTCAGTTTCCATATGCTGAAGGTTT
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GTCACCCAATCTATTTCTTCCAGCTTCTCTCTGGCCCCATCTTT

Table 3

>212.1
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TAATTTTTAAATGTTTGACACACAGTCTCTGATAAATGATCATTCACCAA
TCACCGATTACTCTCCTTGCTCTGTTAAGTGTGACACTGTCCCTTTGAGA
ATCTGGCGACAGCTATGTATCCCATAACCACACACCCCAAAAAAAAAA
>213.1
GGCGGCCGTTTGAGAAGCCAGCGCTCACCCACCCGGGGTCTCTGTGCATT
GACCTTTGGGTGCTGACTTGGAGAAAAGCACAAACACGACCAGTCCCCCC
GCGTACCTCGG
>214.1
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AGAAGTAATACCTGATTAATTAGAATTCCCAACCCTCATCAAGTGTGTGC
TTATATAGAAGAAACCCAGTAAATGTTTGTTGATTGAAAGATATTAATAC
TCTTGCTTGGATGAGAGTGAGGAAAAAGGTATTAGTATTGGCTTTTCAC
>215.1
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CTTTGTCTTTGTCATGGAAGCCGCGAGCGTAGAGGTTCCGCGTGCTCTGC
CGGACTTGAGCAGGTCACTGGGTCCTTTACACTTGTGAATTCGAAGCTTG
CCAGATGTATCCTCAATGCATTGCCACTTCTGCCCCGGTTGTTCACAGGC
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GCAAAAGTTGAGAAGCTCAAACCATTAGAGGTAGAGCTGCGACGCCTAGA
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>216.1
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CGTGCTCTGCCGGACTGTGAGCAGGTCACTGGGTCCTTTACACTTGTGAA
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CGGCCTGCGCAGCCACCTCAAGATCACAGATTCTGCTGGCCATATTCTCT
ACTCCAAAGAGGATGCAACCAAGGGGAAATTTGCCTTTACCACTGAAGAT
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GA
>217.1
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TTTTAGCTGAATGAGTGGCCACTCATAGAGAGATTGCATTTCTGGCTTCC
CTTGCAGCCATAGGTAGCCATGGGACAAAGTTCTAACCCAGGGGGGGTCC
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AAAAAAAAAAAAAGT
>218.1
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CTAAATTGAATCCGACTGGGCGTGCCCCTCCTCGGAACACAACAGTAGAC
CTTAATAGTGGAAACATCGATGTGCCTCCCAACATGACAAGCTGGGCCAG
CTTTCATAATGGTGTGGCTGCTGGCCTGAAGATAGCTCCTGCCTCCCAGA

Table 3

TCGACTCAGCTTGGATTGTTTACAATAAGCCCAAGCATGCTGAGTTGGCC
AATGAGTATGCTGGCTTTCTCATGGCTCTGGGTTTGAATGGGCACCTTAC
CAAGCTGGCGACTCTCAATATCCATGACTACTTGACCAAGGGCCATGAAA
TGACAAGCATTGGACTGCTACTTGGTGTTTCTGCTGCAAAACTAGGCACC
ATGGATATGTCTATTACTCGGCTTCTTAGCATTCACATTCCTGCTCTCTT
ACCCCCAACGTCCACAGAGCTGGATGTTCCTCACAATGTCCAAGTGGCTG
CAGTGGTTGGCATTGGCCTTGCATATCAAGGGACAGCTCACAGACATACT
>219.1
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CCGCGTACCTCGGCCGCTCTAGAACTAAGTGGGATCCCCCGGGCT
>220.1
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TGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTGGCCATG
GAAAAAGAAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAG
AACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACTTGTTGAT
GCAGAATACACCAAAAACCAGGCCTGGAAATCTATGAAAGATACCTTAGG
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ATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTC
TTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATT
CTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCAATCAAAACAG
ATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGAT
GT
>221.1
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GATACTACATATTCAAAGATAACTTACTGAAGCTTGTTCACAGAACCAAG
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CCCCAAATGCTCTTCAGGATTTAAATAACAATTTTTAAAAGACACTTAA
CACCACAAAATGGAATTTGCTGGCATGACGCGAACAATACGGTTACTCCA
GATGCTGTATTCAAACTGTATGGGTCCGTTGAAAAAATAGATATAACCAT
TTTTCTCATAGACAGCATCTACTTTATCACCAATTCCTGGGAAGTCTTCT
TCTATTAGTCTCGGATAGTCTTTATCCATAATATGGCTAGTATCATCATA
TCTCCAGACCTGGTTTCCTGAGAACAGGAGAGTCTTGCCTGTATCCTCAA
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GATATTTTTTTGGGATAACCTTCCAAAATGTCATAACCAT
>222.1
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CCATATCTCCAAAAGATTGATCCGACAGCTGATACAAGTTTTTTGGGCTG
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GTTTATGGTCTAATTATAGACCAAGAAAAGAGCCTCTTATTGTCTCCATC
TTGATTTCCGTGGCAGCCAACTGCCTCTATGCATATCTTCACATCCCAGC
TTCTCATAATAAATACTACATGCTGGTTGCTCGTGGATTGTTGGGAATTG
GAGCAGTTTTTC
>223.1
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CCGACATGAGAAACCTGAGATTTTCACTGAGTTGGTGGTCAGCAATATCA
CAAGGCTCATCGATTTACCTGGAACTGAGTTGGCTCAGCTGATGGGGGAA
GTGGACCTTAAGTTGCCTGGCGGGGCTGGCCCAGCATCAGGATTCTTCCG
GTCTCTCATGTCTCTCAAGCGAAAGGAAAAAGGAGTGATATTTGGGTCCC
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Table 3

>224.1
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GTGCAGTTAACTTCCAGGAGTTCCTCATTCTGGTGATAAAGATGGGCGTG
GCAGCCCACAAAAAAAGCCATGAAGAAAGCCACAAAGAGTAGCTGAGTTA
CTGGGCCCAGAGGCTGGGCCCCTGGACATGTACAGACTCTCATTTTATGA
TGTATCCTACTGCATCAGGACATTTGTGTCAATGTCAGGTGACGAGGGGA
AATGAAAGTGATGAGACGATGAGAGGAGTGAAATACCAAGGACGCCATAC
TAGGAAACCCAGGTCTATTTGTTATCAGAGTAAGGATCAAGCCAGATAGC
CTGTTATGTAATTTCTCCGATAAAAGATTTTGAAAGCAGGTGCTGTGGGC
ATCTGTATGGGGAATCGCACTCATAGAATTATTTTCATTTGTAAATATTT
GGTATCAGGCCAAGCAAGGGAAAGAAGCTTTACTGTATTACCATCTTT
>225.1
CGCTCCCCGCGGTGGCGGCCGAGGTACTCACAGTCACGCAAATTCACAGT
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CAAGAGCTTCACCCATAATTAAGACCTTCTGAGGATGATCGATAGATAAA
CACACCTCCTCTGAACCATCCTTGGGCTTCATGGGGTTGGCATTGAGGAT
CCCTACGACAGTCCCCTGCTCCGTCTTCCAGAGCGCTTTGTGAACTTCTC
CAAATAAGAACAAGGACACACATTGTGTCAGGTCACGAAGATCATTCAGT
TTCCATATGCTGAAGGTTTTTCCACTATTCACACTCTGTGGCGTAACCTT
CTTCAATATAACCCCAAATGTCACCCAATCTATTTCTTCCAGCTTCTCTC
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>226.1
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AGAAACTTGCAGGGCTTCCTATGATACCTCTGCTCCAAATGCAAAACGTA
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TTAGATAAGATAAGGCTAATATCACTGACTGATGAAAATG
>227.1
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ACAGAAATCAGAGGAGCCATCGGTGTCAATACCCTTCCTACAAACTGCAT
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TGATGACCAAAGTGACAAGGGT
>228.1
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TAGAGGGAG
>229.1
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CTT

Table 3

>229.2
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TTTAAGAAGTTTTTACAACAGGCTGGGGGGGGGGGGTTACACC
>230.1
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CATGG
>231.1
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CAGCCTCCCCCAGACCACATTCCTTGGATTACAGCTGT
>232.1
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>233.1
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AAAGG
>234.1
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ACGC
>234.2
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>235.1
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CACTTCCCGCGT
>236.1
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TCGGTTATGTAAATTCATATATGTATTTTTGGAATCAGTTCTTATAAACA
GCTCGATTCAGTTTTAGCTAAATTTATAGTCTAGGTAGTATGTTACATTT
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AGAAATATACTTTTCTATTAAAGATCTGT
>237.1

Table 3

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GGGGCTGGCCCAGCATCAGGATTCTTCCGGTCTCTCATGTCTCTCAAGCG
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GGTTTGTTTAGAGT
>238.1
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>239.1
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>240.1
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>241.1
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TATAAAAGTAAAATCAAATTACATTTTTTTTCCAAAAAAAAAAAAAAAAA
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>242.1
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Table 3

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AAAAAAAAAAGT
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Table 3

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Table 3

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>262.1
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Table 3

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>269.1
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Table 3

>277.1
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>283.1

Table 3

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>291.1

Table 3

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Table 3

AGCCAGTCCATTACTCACAGTTTGACCACTCTGACAGTGATGATGATTTT
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>298.1
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TACTCAGTCCCAGGGACTTCTCCAATAGCGACAACTCTGCGGCCGCCGCC
ATCTTC
>299.1
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TGCGTCATGGATTTAAGGTCTTTTAATCACCTTCGGTTTAATCTCTTTTT
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>300.1
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CAAGTATTTCTGACTCCCAAGATTGCCGTTTCCTAAAGAGCAATTCTTCT
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T
>301.1
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>304.1
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>305.1
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>306.1
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Table 3

TCCTGGAGGTTCAAAGAATTGCAGGAGGGTAGAAAAGCACCTGGGTCGGG
TGCAGACTGCGGAGCGGGCCCTACCGTGTGCGCAGAAAGAGGAGGCGCTT
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TCGTTGCTTCCAGGGCCTGCTGATTTTTGGAAATGTGATTATTGGTTGTT
GCGGCATTGCCCTGACTGCGGAGTGCATCTTCTTTGTATCTGACCAACAC
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>307.1
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CCCCGCGT
>309.1
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AACCTATTGGG
>309.2
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>312.1
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>315.1
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Table 3

GAACAATACACATTCTTATTAGCAACAGTTATAAGTAGGTTTTCAAAGAA
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>316.1
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>317.1
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>319.1
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>323.1
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>324.1
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>325.1
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Table 3

CCTGCAGAATCACCAGATTATTTTGTGGATTTTCCTGTTCCATTTTGTGC
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>326.1
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>329.1
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>330.1
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>331.1
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Table 3

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>332.1
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>333.1
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>335.1
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>336.1
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>338.1
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>339.1
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>340.1

Table 3

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>341.1
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>342.1
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>343.1
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>344.1
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Table 3

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>346.1
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>351.1
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>352.1
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GAGTCCAGGGAAGCAGTGGTAACAACGCAGAGTACCCGGGGAAAAAAGGC

Table 3

AAATAGAATGAGAACCATATTATGT
>353.1
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>354.1
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TTCTGTTACTCCATTTTTTTCTCTCCATATTGTATGCCTGAAGTGAGCTG
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>358.1

Table 3

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>365.1
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Table 3

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>368.1
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>371.2
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Table 3

>372.1
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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TTTTTCAGAGAGTGGTGCAGCGCCAGACATTTTGCACATAAGGCACCAAA
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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CCAAAGCAAATCCAGCTACTTCTCTAGCTGAGAGGGTGGAATGACTCCAA
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>735.1

Table 3

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Table 3

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Table 3

>748.1
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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 3

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Table 4

>1
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Table 4

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Table 4

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>8

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Table 4

>10
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>41

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Table 4

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Table 4

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Table 4

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NNN

Table 4

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>53
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Table 4

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CGGTGCCTCATGCCTGTAATCCCAGCACTTTCGGAGGCCAAGAAGGGTGGCTTGAGATGAG
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GCCAGGGCAACAGTGAGACTCAGTCTCAAAAATAAACAATAAAATAAATAAATAAATGAATGT
NNNNNNNNNNNNNNN
>55
>56
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CCTTTTGAGGTCCCACGAGAATATATAAGAGCTTTAAATGCTACCAAACTGGAACGAGTATTT
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GGGACTAGATTAATTGCAAACATTTTAGTTATATGTGTAGAGCTTTATTGTTACTCCTTTTAGC
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Table 4

CATAACATTTAGAATAATGATGTCAATTTTTTACAACTGAATTTATTTCTAGTGCTTTACTTATA
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NNN
>57
>58
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>59
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GGTGACAGAGCGAGACTCCGTCNNN
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Table 4

CTCTTATGTTATCTTTAATATTACTTTGAATAATGATTGCAATGATGTTTCTTCCTGTGATTCCA
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>61
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>62
>63
>64
>65
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>66
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>67
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>68
>69
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Table 4

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>70
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CAAGACAGACTGAACTAAATTAGAGTATTTTTCTTGGTCCACTTCTTCATATGGGTTCACTTTT
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Table 4

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>71
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GATTTCACAGGC
>72
>73
>74
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ATAAGCATACATGTCTACACATGACTACACAAATGCAAACCTTTGCAAACACATTATTATGCTT

Table 4

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>77
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>79
>80
>81
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>82
>83
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>85
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Table 4

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>87
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Table 4

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Table 4

>98
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

>123
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>178
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>224

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>232

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>233

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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NNNNNNNNNNN

Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>719
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>855

>856

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>932

Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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>1037

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>1038

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>1039

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>1040

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>1042

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Table 4

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>1043
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>1044
>1045
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Table 4

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Table 4

>1060
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>1062
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>1063
>1064
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Table 4

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Table 4

>1076
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>1081
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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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Table 4

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